BAT RESEARCH NEWS

VOLUME 63: NO. 1 SPRING 2022

BAT RESEARCH NEWS

VOLUME 63: NUMBER 1 **SPRING 2022**

Table of Contents

Front Cover

Eastern Red Bat (*Lasiurus borealis*) chasing a Sphinx Moth. Drawing courtesy of Chester O. Martin. Originally illustrated as a t-shirt design for the 9th Annual Mississippi Bat Working Group Mist Net Event, 2012. Thank you, Chester, for sharing your artwork.

BAT RESEARCH NEWS

Volume 63: Number 1 Spring 2022

Publisher and Managing Editor: Dr. Margaret A. Griffiths, 8594 Berwicke Circle, Bloomington, IL 61705; E-mail: margaret.griffiths01@gmail.com

Editor for Feature Articles: Dr. Allen Kurta, Dept. of Biology, Eastern Michigan University, Ypsilanti MI 48197; E-mail: akurta@emich.edu

Editor for Recent Literature: Dr. Thomas A. Griffiths, 8594 Berwicke Circle, Bloomington, IL 61705; E-mail: thomas.alan.griffiths@gmail.com

Emeritus Editor: Dr. G. Roy Horst

Bat Research News is published four times each year, consisting of one volume of four issues. *Bat Research News* publishes short feature articles and general interest notes that are reviewed by at least two scholars in that field. *Bat Research News* also includes abstracts of presentations at bat conferences around the world, letters to the editors, news submitted by our readers, notices and requests, and announcements of future bat conferences worldwide. In addition, *Bat Research News* provides a listing of recently published bat-related articles. *Bat Research News* is abstracted in several databases (e.g., BIOSIS).

Communications concerning feature articles and "Letters to the Editor" should be addressed to Dr. Al Kurta (akurta@emich.edu), recent literature items to Dr. Tom Griffiths (thomas.alan.griffiths@gmail.com), and all other correspondence (e.g., news, conservation, or education items; subscription information; cover art; back issues) to Dr. Margaret Griffiths (margaret.griffiths01@gmail.com).

The prices for one volume-year (4 issues within a single volume) are:

Institutional/Group subscriptions	US $55.00
Individual subscriptions:	
printed edition (U.S.A.)	US $30.00
printed edition (outside U.S.A)	US $40.00

Subscriptions may be paid by check or money order, payable to "***Bat Research News***." Please include both mailing (postal) and e-mail addresses with your payment, and send to Dr. Margaret Griffiths at the address listed above. To pay by credit card (Visa or MasterCard only) or for further information, please go to the *Bat Research News* website at http://www.batresearchnews.org/ and click on the "Subscription Information" link.

Many **back issues** of *Bat Research News* are available for free download from the *BRN* website at http://batresearchnews.org/. Other back issues may be available by contacting Dr. Margaret Griffiths (margaret.griffiths01@gmail.com). Thank you!

Bat Research News is ISSN # 0005-6227.
Bat Research News is printed and mailed in Bloomington, Illinois, U.S.A.

This issue printed March 24, 2022.

Book Review

Runkel, V., Gerding, G., and Marckmann, U. 2021. The Handbook of Acoustic Bat Detection. Pelagic Publishing, Exeter, UK, 196 pp. [ISBN 978-1-78427-220-3] Price (soft cover), $54.36 (USD).

Bats are among the most diverse groups of mammals. They are the only ones with the capacity of real flight, and they emit sounds to find food, hunt, and move through the environment. Bat echolocation is unique among mammals in that bats' pulses cover a wide range of the ultrasound spectrum. Additionally, most bats emit these sounds constantly while they are active. The ability to emit sounds that do not overlap with those of most other animals make bats ideal to be studied and monitored through acoustic methods. Moreover, technological advances have created cheap and easy-to-use bat detectors with highly sensitive microphones to detect ultrasound signals. As a consequence, acoustic bat studies have increased exponentially in numbers in the last decades and the field of bat acoustics has been revolutionized. However, as this field grows, it is necessary to have both good documentation on the best practices and general recommendations for those interested in exploring the field.

This book addresses the most important topics and recommendations on the techniques, methods and equipment needed to carry out successful bat surveys and monitoring programs. It covers a variety of subjects, from acoustic research to environmental impact assessments. It consists of 14 chapters that go from explaining the basic principles and best practices of bat acoustic recording, to a simple explanation of the physics of sound. Chapter 1 explains the three principles of signal transformation available in bat detectors: heterodyne, frequency division, and time expansion. It briefly mentions the newest technology available, full spectrum in real time recording, which is the method with the highest recoding fidelity of bat calls that does not use any signal transformation. This chapter also introduces three main strategies for carrying out acoustic samplings. Active recording, the first strategy, is the identification and data recording of bat calls while the survey is being done. It is usually performed using heterodyne detectors. Passive recording, which is the automatic recording of the acoustic data by a detector left unattended in the field, is the second strategy. The data are analyzed after the sampling. The third survey strategy is mobile acoustic recording, which refers to the use of mobile transport (bicycle, car, motorcycle) while carrying out the survey. At the end of the chapter, its authors compare the applicability of acoustic surveys with other bat sampling techniques including mist netting, telemetry, and roost site monitoring.

Chapter 2 gives a very general overview of the different questions that can be addressed with the use of acoustic surveys. It gives some recommendations on how to prepare the sampling design and detector settings for each particular purpose. The most important consideration here is whether a researcher is interested in obtaining quantitative or qualitative data, since this will determine the setting used for the bat detector as well as the time and geographic extent of the study. For example, surveys can be done for single nights if we are interested in assessing general activity or in detecting particular habitat uses like flight paths. Longer term monitoring is necessary if we are interested in a deeper understanding of bat ecology and behavior, or in ensuring the recording of rare and highly mobile species. Important topics are apportioned here including best practices to

carry out wind turbine assessments, with special emphasis on standards set by environmental agencies in Germany and other European countries. Finally, the chapter closes with an important analysis on how to plan biodiversity assessments. Here, several figures are used to exemplify the influence of the temporal coverage of the sampling on the number and type of bat calls recorded. This issue is particularly important because most biodiversity assessments have to maximize the use of financial resources to document as many species as possible at the least expensive cost.

Chapter 3 describes the different spatial strategies that can be used to design an acoustic survey, which can be summarized as a combination of systematic versus random sampling, stationary versus mobile surveys, and points versus transect designs. In order to decide on the best strategy to follow, the user must consider the extent of the area to be sampled, its complexity in terms of habitat types and the terrain, the time frame to be covered, the replicability of the study especially when comparisons with other areas/times might be needed, and the effort and economic resources that can be invested. This chapter is illustrated with figures that help the reader understand the fundamental of each sampling design over a landscape representing different habitat elements.

In Chapter 4, the issues of selecting manual (mostly done with heterodyne or frequency division devices) versus automatic (implemented mostly with time expansion and real time recording) are covered. Here, a few tables give a good and quick summary of the main considerations to select between these two recoding options. The chapter ends with a section discussing the main differences between them, and how to overcome some of the drawbacks that each technique has.

Chapters 5–8 address a very controversial but pivotal issue on bat acoustics, the identification of the recorded calls. These chapters briefly summarize the advantages and disadvantages of manual versus automatic identification of bat calls, and how some of the most popular call parameters are measured for identification purposes. For manual identification, the biggest disadvantages are the subjectivity of the person who identifies the calls because the accuracy highly depends on the expertise of the person doing the analysis. Because of this, the precision or uncertainty for the identifications cannot be measured and compared with identifications from other sources. The popularity of automatic identification has increased in recent years, mainly because it allows the processing of large amounts of data, something that is not possible with manual identification, and it is possible to assign a degree of certainty to the identifications. However, it also has raised a lot of controversy on whether an algorithm is better in identifying patterns than are human eyes (based on the looks of spectrograms). The main obstacle in automatic identification is the need for a good quality and balanced dataset as reference material to train the algorithms; while the main obstacle for both approaches is the high overlap of several call parameters between some species groups. Another problem for call identification is the great variability inherent in the ecology and behavior of each individual bat and each species. Sex, age, habitat, and even the climatic variables have an effect in the final outcome in the propagation of sound, and therefore, in the final shape of the call. These chapters present a good introduction to all the factors that need to be considered when bat calls are identified to avoid mistakes and misidentifications.

Chapter 9 goes over the different characteristics and settings that need to be considered when choosing a bat detector. It starts with a discussion of the pros and cons of having a manual or an automatic system, information that complements the first chapters. Then, it covers important elements that will affect the quality of the detectors and

the recordings: recording distance and amplitude, triggering systems, recording quality, and weatherproofing. The authors cover the different factors that influence the performance of the detectors, some within the detector itself, and others being external factors. When selecting a bat detector, it is important to have a clear objective for its use. There is no right or wrong selection as choice of a detector will depend on the goal of the study, the bat community or targeted species, seasonality, and even the habitat to be surveyed. It is important to have a detector of good quality but the properties of the bat calls and the environment will also influence the quality of the recordings, as well as the recording distance and capacity of the detector. The settings selected at this point will have a strong influence on how we can analyze and interpret the data, as is discussed in the next chapters of this book.

Chapter 10 gives recommendations on the analysis and interpretation of the results from studies using acoustic data. This chapter addresses a common theme found in other chapters of the book, namely on how the different decisions we make over the different steps in setting up a study will ultimately influence the results. This is one of the longest chapters and it covers some of the problems with collecting and analyzing acoustic data. For example, false negative species identifications are particularly common in short surveys. False negatives are when a species is not recorded but is, in fact, present in the study area. This is not a trivial question as survey design can have a great effect on the ability to detect rare and/or highly mobile species. Another common problem addressed in this chapter is on how to report averages of activity when interpreting acoustic data. The chapter explains that this can be done in a number of ways, including counting the total number of recordings, counting the number of pulses, counting the number of calls, counting the total time of activity, and even by creating temporal sub-samples of recording nights. To select the best method to detect species activity, it is necessary to consider the time that each method requires, the amount of detail that can be obtained from each of them, and the characteristics of the recording habitat and the settings used on the detector. Comparisons of activity among species are difficult to make using this technique because the nature of the calls of each species highly influences its likelihood of being recorded, and thus counting numbers of calls will not necessarily always reflect species' level of activity. The chapter ends with a set of recommendations on data standardization, metrics for quantitative or qualitative analysis, and selection of activity indices. Additionally, it offers some strategies for dealing with a large amount of data.

Chapter 11 provides a good overview of the data needed for standard environmental impact assessments. It addresses how much detail should go into the reports. It covers data presentation, and even offers suggestions on how to produce graphs and figures that make these types of reports more easily interpreted by decision makers. Chapter 12 goes over the best practices on acoustic monitoring for wind energy developments. There is a good analysis on how the different technology used in these developments might affect the results from acoustic monitoring programs. It shows how some of these drawbacks can be overcome to deliver better estimates of fatalities. Toward the end of the book, Chapter 13 explains the different types of calls produced based on their function (echolocation, feeding, social) and their structure (CF, QFC, FM-QCF, FM). It briefly covers the concept of "guilds" and how bat calls are adapted to exploit a particular niche in terms of habitat structure and feeding preferences. Finally, Chapter 14 complements all the information given so far by detailing some of the physics of sound such as how sound travels through the air, how sound waves are captured by the different detector systems covered in the book, and how we

eventually portray that sound in the different types of software through the implementation of sonograms and oscillograms.

In general, this book is very complete and it covers the most important topics in the field of bat acoustic sampling. It is important to emphasize that some chapters cover the most important topics and methods used mostly in Europe, giving examples of species from that continent. However, some recommendations and preferences in the selection of detectors, settings and even sampling designs may differ in other countries, especially in the tropics where a wider range of bat guilds, families and species are present. Overall, however, it is a good book for those who want to develop a general understanding of the implications of bat acoustic detection as well as for those advanced users who want to refresh their understanding of the many concepts involved.

—Veronica Zamora-Gutierrez
Ecología Integrativa
CIIDIR Unidad Durango, Instituto Politécnico Nacional, Durango, Dgo., 34220, Mexico
e-mail: zamora.gtz@gmail.com

RECENT LITERATURE

Authors are requested to send reprints (PDF files) of their published papers to the Editor for Recent Literature, **Dr. Thomas A. Griffiths**, (e-mail: **thomas.alan.griffiths@gmail.com**) for inclusion in this section. Receipt of reprints is preferred, as it will facilitate complete and correct citation. However, if reprints and/or PDF files are unavailable, please send a complete citation (including complete name of journal and corresponding author e-mailing address) by e-mail. The Recent Literature section is based on several bibliographic sources and for obvious reasons can never be up-to-date. Any error or omission is inadvertent. Voluntary contributions for this section, especially from researchers outside the United States, are most welcome and appreciated.

ANATOMY/HISTOLOGY

Andronowski, J. M., M. E. Cole, T. L. Hieronymus, R. A. Davis, L. R. Usher, and L. N. Cooper. 2022. Intraskeletal consistency in patterns of vascularity within bat limb bones. The Anatomical Record, 305(2): 462– 476. https://doi.org/10.1002/ar.24694 [jandronowski@mun.ca]

Crane, M., I. Silva, M. J. Grainger, and G. A. Gale. 2022. Limitations and gaps in global bat wing morphology trait data. Mammal Review, 52: 165–176. https://doi.org/10.1111/mam.12270 [mattecology@gmail.com]

Eilam-Altstadter, R., L. Las, M. Witter, and N. Ulanovsky. 2021. Stereotaxic Brain Atlas of the Egyptian Fruit Bat, 1st Ed. Academic Press, 154 pp. [ISBN hardcover 9780128192979] [ISBN eBook 9780128192986]

Sulser, R.B., B. D. Patterson, D. J. Urban, A. I. Neander, and Z.-X. Luo. 2022. Evolution of inner ear neuroanatomy of bats and implications for echolocation. Nature, 602**:** 449–454. https://doi.org/10.1038/s41586-021-04335-z [rsulser@amnh.org]

Toledo, K. S., A. L. Peracchi, and M. R. Nogueira. 2022. Morphological variation of the brachial plexus in four phyllostomid bat species (Chiroptera, Phyllostomidae). The Anatomical Record, 1– 22. https://doi.org/10.1002/ar.24874 [karentoledoo@live.com]

BATS AND FOLKLORE

Arapu, V. 2021. Bats and diseases in the context of the SARS-CoV-2 pandemic and magic medicine practices: perceptions, prejudices and realities (historical, zoological, epidemiological and ethnocultural interferences). Revista de Etnologie şi Culturologie, 1: 5–12. (in Romanian, some English translation) [no author email address provided]

BATS AND FUNGI

Pereira, M. L. S., J. L. V. R. Carvalho, J. M. S. Lima, E. Barbier, E. Bernard, J. D. Bezerra, and C. M. Souza-Motta. 2022. Richness of *Cladosporium* in a tropical bat cave with the description of two new species. Mycological Progress, 21: 345–357. https://doi.org/10.1007/s11557-021-01760-2 [cristina.motta@ufpe.br]

BATS AND RADIATION

Tovstuha, I., O. Timofieieva, V. Kovalov, and A. Vlaschenko. 2022. Effect of ^{90}Sr and ^{137}Cs concentration on hematological parameters of bats in the Chernobyl Exclusion Zone (Ukraine). Acta Chiropterologica, 23(2): 371–376. (published 14 February 2022) [olhatimofieieva@gmail.com]

BEHAVIOR

Bosia, T., F. Villalobos, and S. Schmidt. 2022. Evidence for vocal diversity during physical interference at the perch in sympatric *Carollia* species (Chiroptera: Phyllostomidae): a key to social organization and species coexistence? Zoological Journal of the Linnean Society, 194(2): 457–477. https://doi.org/10.1093/zoolinnean/zlab040 [sabine.schmidt@tiho-hannover.de]

Brown, B. K. G., and G. G. Carter. 2022. Do bats use scent cues from guano and urine to find roosts? Animal Behavior and Cognition, 9(1), 106–118. https://doi.org/10.26451/abc.09.01.09.2022 [brown.6531@osu.edu]

Goldshtein, A., L. Harten, and Y. Yovel. 2022. Mother bats facilitate pup navigation learning. Current Biology, 32(2): 350–360. e4, https://doi.org/10.1016/j.cub.2021.11.010 [yossiyovel@gmail.com]

Hernández-Pinsón, H. A., S. Chaves-Ramírez, and G. Chaverri. 2022. Seasonality in the emission of contact calls in Spix's disc-winged bats (*Thyroptera tricolor*) suggests a potential role in mate attraction. Acta Chiropterologica, 23(2): 413–420. (published 14 February 2022) [andres.hernandezpinson@gmail.com]

Jones, G. 2022. Animal behaviour: Mother bats teach their pups to help build independence. Current Biology, 32(2): R74–R76. https://doi.org/10.1016/j.cub.2021.11.042 [gareth.jones@bristol.ac.uk]

Piskorski, M., and K. Sachanowicz. 2021. Different songflight calls of *Pipistrellus kuhlii* and *Pipistrellus lepidus* (Vespertilionidae, Chiroptera) in Europe. Journal of Vertebrate Biology, 71(21058): 1–9. [no author email address provided]

CONSERVATION

Ballesteros-Correa, J., and J. Pérez-Torres. 2022. Silvopastoral and conventional management of extensive livestock and the diversity of bats in fragments of tropical dry forest in Córdoba, Colombia. Agroforestry Systems, https://doi.org/10.1007/s10457-021-00698-4 [jballesteros@correo.unicordoba.edu.co]

Barros, M. A. S., L. Iannuzzi, S. I. L. de Holanda Silva, A. Otálora-Ardila, and E. Bernard. 2022. Factors affecting searcher efficiency and scavenger removal of bat carcasses in Neotropical wind facilities. Journal of Wildlife Management, 0:e22198. https://doi.org/10.1002/jwmg.22198 [barrosmas@gmail.com]

Biassi, D. L., R. Baldissera, D. Galiano, R. de Souza Rezende. 2022. Effects of pine forest management practices on bat functional traits in a subtropical region. Acta Chiropterologica, 23(2): 421–431. (published 14 February 2022) [davidbatsc@hotmail.com]

Browning, E., R. Freeman, K. L. Boughey, N. J. B. Isaac, and K. E. Jones. 2022. Accounting for spatial autocorrelation and environment are important to derive robust bat population trends from citizen science data. Ecological Indicators, 136: 108719. https://doi.org/10.1016/j.ecolind.2022.108719 [ella.browning.14@ucl.ac.uk]

Cryan, P. M., P. M. Gorresen, B. R. Straw, S. Thao, and E. DeGeorge. 2022. Influencing activity of bats by dimly lighting wind turbine surfaces with ultraviolet light. Animals, 12(1): 9. https://doi.org/10.3390/ani12010009 [cryanp@usgs.gov]

Dekker, J., W. Steen, H. B. Bouman, and R. E. van der Vliet. 2022. Differences in acoustic detectibility of bat species hamper environmental impact assessment studies. European Journal of Wildlife Research, 68(14), https://doi.org/10.1007/s10344-022-01562-1 [r.van.der.vliet@buwa.nl]

Díaz, M. M., M. D. Miotti, A. and S. Gamboa Alurralde. 2021. Los murciélagos del dique Escaba y sus alrededores (Tucumán, Argentina): investigación, educación y conservación. (Bats of Escaba Dam and its surroundings (Tucumán, Argentina): research, education, and conservation.). Fundación Miguel Lillo, 26: 127–148. [no author email provided]

Gorman, K. M., S. M. Deeley, E. L. Barr, S. R. Freeze, N. Kalen, M. S. Muthersbaugh, and W. M. Ford. 2022. Broad-scale geographic and temporal assessment of northern long-eared bat (*Myotis septentrionalis*) maternity colony-landscape association. Endangered Species Research, 47: 119–130. https://doi.org/10.3354/esr01170 [katiegorman@vt.edu]

Kusuminda, T., A. Mannakkara, R. Gamage, B. D. Patterson, and W. B. Yapa. 2022. Roosting ecology of insectivorous bats in a tropical agricultural landscape. Mammalia, 86(2): 134–143. https://doi.org/10.1515/mammalia-2021-0056 [t.kusuminda@gmail.com]

Laforge, A., L. Barbaro, Y. Bas, F. Calatayud, S. Ladet, C. Sirami, and F. Archaux. 2022. Road density and forest fragmentation shape bat communities in temperate mosaic landscapes. Landscape and Urban Planning, 221: 104353. https://doi.org/10.1016/j.landurbplan.2022.104353 [frederic.archaux@inrae.fr]

Lorenzo, C., C. Lorenzo-Monterrubio, J. E. Bolaños, and G. Tapia-Ramírez. 2022. Use of abandoned buildings by mammals in tropical forest sites with no forest control. Therya Notes, 3: 18–23. http://mastozoologiamexicana.com/ojs/index.php/theryanotes/article/view/185 [gloria.tapia@estudianteposgrado.ecosur.mx]

Lukesova, G., E. Voslarova, and V. Vecerek. 2022. Mammals at rescue centres in the Czech Republic: Trends in intake and outcome, causes of admission, length of stay and release rate. Journal for Nature Conservation, 67: 126156. https://doi.org/10.1016/j.jnc.2022.126156 [lukesovag@vfu.cz]

Mellado, B., L. de O. Carneiro, M. R. Nogueira, and L. R. Monteiro. 2022. The impacts of marking on bats: mark-recapture models for assessing injury rates and tag loss. Journal of Mammalogy, 103(1): 100–110. https://doi.org/10.1093/jmammal/gyab153 [lrmont@uenf.br]

Mirts, H. E., J. P. McLaughlin, T. J. Weller, A. M. White, H. S. Young, and R. Sollmann. 2022. Bats in the megafire: assessing species' site use in a postfire landscape in the Sierra Nevada. Journal of Mammalogy, 103(1): 111–123. https://doi.org/10.1093/jmammal/gyab129 [rsollmann@ucdavis.edu]

Mohd-Azlan, J., J. Y. Yong, N. N. M. Hazzrol, P. Pengiran, A. Atong, and S. A. Aziz. 2022. Local hunting practices and perceptions regarding the distribution and ecological role of the large flying fox (Chiroptera: Pteropodidae: *Pteropus vampyrus*) in western Sarawak, Malaysian Borneo. Journal of Threatened Taxa, 14(1): 20387–20399. https://doi.org/10.11609/jott.6977.14.1.20387-20399 [sheema@rimbaresearch.org]

Petriello, M. A., C. M. Edgeley, C. L. Chambers, and M. E. Lee. 2021. Factors influencing support for bat management and conservation in the wildland-urban interface. Human Dimensions of Wildlife, https://doi.org/10.1080/10871209.2021.2018630 [michael.petriello@dal.ca]

Reusch, C., M. Lozar, S. Kramer-Schadt, and C. C. Voigt. 2022. Coastal onshore wind turbines lead to habitat loss for bats in Northern Germany. Journal of Environmental Management, 310: 114715. https://doi.org/10.1016/j.jenvman.2022.114715 [reusch@izw-berlin.de]

Shrestha, L., M. S. Sarkar, K. Shrestha, P. S. Aung, X. Wen, Y. Yongping, H. Zhipang, Y. Xuefei, Y. Shaoliang, and N. Chettri. 2022. Mammalian research, diversity and conservation in the Far Eastern Himalaya Landscape: A review. Global Ecology and Conservation, 34: e02003. https://doi.org/10.1016/j.gecco.2022.e02003 [Nakul.Chettri@icimod.org]

Tena, E. and J. L. Tellería. 2022. Modelling the distribution of bat activity areas for conservation in a Mediterranean mountain range. Animal Conservation, 25: 65–76. https://doi.org/10.1111/acv.12719 [e.tena@ucm.es]

Vogeler, A.-V. B., I. Otte, S. Ferger, M. Helbig-Bonitz, A. Hemp, T. Nauss, K. Böhning-Gaese, M. Schleuning, M. Tschapka, and J. Albrecht. 2022. Associations of bird and bat species richness with temperature and remote sensing-based vegetation structure on a tropical mountain. Biotropica, 54: 135–145. https://doi.org/10.1111/btp.13037 [anna.vogeler@alumni.uni-ulm.de]

DEVELOPMENTAL BIOLOGY/ONTOGENY

Nojiri, T., V. T. Tu, J. H. Sohn, and D. Koyabu. 2022. On the sequence heterochrony of cranial ossification of bats in light of Haeckel's recapitulation theory. Journal of Experimental Zoology B (Molecular and Developmental Evolution), 338: 137–148. https://doi.org/10.1002/jez.b.23042 [dsk8evoluxion@gmail.com]

DISEASE

Aguilar Pierlé, S., G. Zamora, G. Ossa, A. Gaggero, and G. P. Barriga. 2022. The *Myotis chiloensis* guano virome: Viral nucleic acid enrichments for high-resolution virome elucidation and full alphacoronavirus genome assembly. Viruses, 14(2): 202. https://doi.org/10.3390/v14020202 [sebastian.aguilar@inorevia.com]

Becker, D. J., G. F. Albery, A. R. Sjodin, T. Poisot, L. M. Bergner, B. Chen, L. E. Cohen, T. A. Dallas, E. A. Eskew, A. C. Fagre, M. J. Farrell, S. Guth, B. A. Han, N. B. Simmons, M. Stock, E. C. Teeling, and C. J. Carlson. 2022. Optimising predictive models to prioritise viral discovery in zoonotic reservoirs. The Lancet Microbe, https://doi.org/10.1016/S2666-5247(21)00245-7 [colin.carlson@georgetown.edu]

He, W.-T., X. Hou, J. Zhao, J. Sun, H. He, W. Si, J. Wang, Z. Jiang, Z. Yan, G. Xing, M. Lu, M. A. Suchard, X. Ji, W. Gong, B. He, J. Li, P. Lemey, D. Guo, C. Tu, E. C. Holmes, M. Shi, and S. Su. 2022. Virome characterization of game animals in China reveals a spectrum of emerging pathogens. Cell, https://doi.org/10.1016/j.cell.2022.02.014 [shuosu@njau.edu.cn]

Joffrin, L., A. O. G. Hoarau, E. Lagadec, O. Torrontegi, M. Köster, G. Le Minter, M. Dietrich, P. Mavingui, and C. Lebarbenchon. 2022. Seasonality of coronavirus shedding in tropical bats. Royal Society Open Science, 9: 211600. https://doi.org/10.1098/rsos.211600 [lea.joffrin@gmail.com]

Jones, D. N., N. A. F. Ravelomanantsoa, C. J. Yeoman, R. K. Plowright, and C. E. Brook. 2022. Do gastrointestinal microbiomes play a role in bats' unique viral hosting capacity? Trends in Microbiology, https://doi.org/10.1016/j.tim.2021.12.009 [devinjones18@gmail.com]

Leopardi, S., E. Barneschi, G. Manna, B. Zecchin, P. Priori, P. Drzewnioková, F. Festa, A. Lombardo, F. Parca, D. Scaravelli, A. Maroni Ponti, and P. De Benedictis. 2022. First detection of West Caucasian Bat Lyssavirus infection in a domestic cat, Italy, 2020: ecological and sanitary implications. International Journal of Infectious Diseases, 116, Supplement: S72. https://doi.org/10.1016/j.ijid.2021.12.169 [no author email address provided]

Liu, B., X. Chen, L. Zhou, J. Li, D. Wang, W. Yang, H. Wu, J. Yao, G. Yang, C. Wang, J. Feng, and T. Jiang. 2022. The gut microbiota of bats confers tolerance to influenza virus (H1N1) infection in mice. Transboundary and Emerging Diseases, pp. 1– 19. https://doi.org/10.1111/tbed.14478 [fengj@nenu.edu.cn]

Magalhães, L. M. D., K. J. Gollob, B. Zingales, and W. O. Dutra. 2022. Pathogen diversity, immunity, and the fate of infections: lessons learned from *Trypanosoma cruzi* human–host interactions. The Lancet Microbe, https://doi.org/10.1016/S2666-5247(21)00265-2 [waldutra@icb.ufmg.br]

Moreira Marrero, L, G. Botto Nuñez, S. Frabasile, and A. Delfraro. 2022. Alphavirus identification in Neotropical bats. Viruses,14(2): https://www.mdpi.com/1999-4915/14/2/269 [sfrabasile@fcien.edu.uy]

Mohammadi, Z., A. Tabarraei, F. Ghorbani, A. Khajeh, H. G. Kami, S. Shahabi, and U. Olsson. 2022. Recently discovered Iranian population of *Rousettus leschenaultii* (Chiroptera; Petropodidae), highlighting the essential need for taxonomic expertise in applied medical sciences. Journal of Health Sciences & Surveillance System, 10(1): 62–70. https://jhsss.sums.ac.ir/article_48115.html [tabarraei@goums.ac.ir]

Mukai, Y., M. Horie, S. Kojima, J. Kawasaki, K. Maeda, and K. Tomonaga. 2022. An endogenous bornavirus-like nucleoprotein in miniopterid bats retains the RNA-binding properties of the original viral protein. FEBS Letters, 596: 323–337. https://doi.org/10.1002/1873-3468.14290 [mhorie@vet.osakafu-u.ac.jp]

Muzeniek T., T. Perera, S. Siriwardana, D. Bas, F. Kaplan, M. Öruc, B. Becker-Ziaja, I. Perera, J. Weerasena, S. Handunnetti, F. Schwarz, G. Premawansa, S. Premawansa, W. Yapa, A. Nitsche, and C. Kohl. 2022. Full genome of batCoV/MinFul/2018/SriLanka, a novel alpha-coronavirus detected in *Miniopterus fuliginosus*, Sri Lanka. Viruses, 14(2): 337. https://doi.org/10.3390/v14020337 [muzeniekt@rki.de]

Toth, G., T. Görföl, S. Boldogh, Z. Lanszki, Á. Balázs-Nagy, F. Jakab, and G. Kemenesi. 2022. Concept of resampling: protocol for the field-based detection and characterization of the european filovirus (*Lloviu cuevavirus*). International Journal of Infectious Diseases, 116 (Supplement), S68-S69. https://doi.org/10.1016/j.ijid.2021.12.161 [no author email address provided]

Van Brussel, K., and E. C. Holmes. 2022. Zoonotic disease and virome diversity in bats. Current Opinion in Virology, 52: 1–11. [edward.holmes@sydney.edu.au]

DISTRIBUTION/FAUNAL STUDIES

Abdullah, N. I., N. F. Khodri, N. A. Tajul Arifin, M. R. Abdul Rahim, S. H. A. Razali, N. D. Amat Darbis, and S. Md Nor. 2021. Small mammals of Tekai Tembeling Forest Reserve (TTFR), Jerantut, Pahang, Peninsular Malaysia. Journal of Sustainable Natural Resources, *2*(2): 12–21. [shu kor @ukm.edu]

Aguilar-Romero, R. J., C. M. Escobedo-Bonilla, I. G. Martínez-Álvarez, C. P. Ley-Quiñónez, C. E. Hart, K. A. Zavala-Félix, R. Leal-Moreno, G. Suzán, A. A. Aguirre, and A. A. Zavala-Norzagaray. 2022. First ecological report of bat diversity present in Sierra de Navachiste protected area, Sinaloa, Mexico. Revista Bio Ciencias, 9: e1208. https://doi.org/10.15741/revbio.09. e1208 [anorzaga@gmail.com]

Amick, P. K., K. Sam, G. Drumo, P. S. Toko, and V. Novotny. 2022. Bats can reach 3626 m a.s.l. in Papua New Guinea: altitudinal range extensions for six rainforest bat species. Mammalia, 86(2): 150–155. https://doi.org/10.1515/mammalia-2020-0169 [amick.peter@gmail.com]

Argoitia, A., and M. Collett. 2022. Bats in wetlands: composition and structure of assemblage in Reserva Natural Don Luis, Esteros del Iberá, Argentina. Mammalia, 86(2): 144–149. https://doi.org/10.1515/mammalia-2021-0042 [anto.a_25@hotmail.com]

Arias-Aguilar, A., and M. J. R. Pereira. 2022. Acoustic clue: bringing echolocation call data into the distribution dilemma of *Pteronotus* (Chiroptera: Mormoopidae) complexes in Central America. Biological Journal of the Linnean Society, 135(3): 586–598. https://doi.org/10.1093/biolinnean/blab148 [ariasaguilar.a@gmail.com]

Brinkley, E. R., S. M. Weier, D. M. Parker, and P. J. Taylor. 2021. Three decades later in northern Kruger National Park: multiple acoustic and capture surveys may underestimate the true local richness of bats based on historical collections. Hystrix, the Italian Journal of Mammalogy, 32(2): https://doi.org/10.4404/hystrix-00319-2020 [sinaweier.univen@gmail.com]

Da Silva, L. C. N., T. B. Vieira, A. S. Q. A. Oliveira, P. Mendes, F. P. Peixoto, M. Oprea, and L. M. de Souza Aguiar. 2022. Bat species of a karstic region in the Brazilian savanna and extension of the *Hsunycteris thomasi* (Phyllostomidae: Lonchophyllinae) distribution. Mammalia, 86(1): 27–36. https://doi.org/10.1515/mammalia-2021-0019 [liriannens@gmail.com]

Ding, C., D. Liang, W. Xin, C. Li, E. I. Ameca, and Z. Jiang. 2022. A dataset on the morphological, life-history and ecological traits of the mammals in China. Biodiversity Science, 30(2): 21520. [jiangzg@ioz.ac.cn]

Furey, N. M., V. T. Tu, A. T. Hitch, A. Pimsai, C. Kimashalen, B. Vuthy, Y. Raksmey, C. Sarak, S. A. Borthwick, L. Ch'ng, S. Sinly, G. Csorba, I. Saveng, G. J. D. Smith, C. Dany, and I. H. Mendenhall. 2022. First records of seemingly rare bats (Mammalia: Chiroptera) in Cambodia, with a revised checklist of species for the country. Acta Chiropterologica, 23(2): 345–369. (published 14 February 2022) [neil.m.furey@gmail.com]

Mathis, V. L., and D. L. Reed. 2021. Two new recent country records of mormoopid bats (Chiroptera: Mormoopidae) from Long Island, the Bahamas. Florida Field Naturalist, 49(1): 13–17. [vmathis@flmnh.ufl.edu]

Meheretu, Y., H. Meinig, O. Mikula, N. Hermes, M. Wale, A. Tadele, I. Kaipf, and J. Bryja. 2021. Small- and medium-sized mammals of the Kafa Biosphere Reserve, Ethiopia. African Journal of Ecology, pp. 1–14. https://doi.org/10.1111/aje.12961 [meheretu.yonas@mu.edu.et]

Núñez-Novas, M. S., R. Torres, A. Rodríguez-Durán, and J. M. Zorrilla. 2022. Spatial distribution of bat species on Hispaniola Island, the Greater Antilles. Acta Chiropterologica, 23(2): 443–454. (published 14 February 2022). [m.nunez@mnhn.gov.do]

Palacios-Mayoral, V. D., L. Palacios-Mosquera, J. D. Echavarría-Rentería, A. M. Jimenez-Ortega, and H. Mantilla-Meluk. 2022. Presencia confirmada del murciélago marrón de Chiriquí, *Eptesicus chiriquinus* (Chiroptera: Vespertilionidae), en el departamento de Chocó, Colombia. Revista de la Academia Colombiana de Ciencias Exactas, Fisicas y Naturales, https://doi.org/10.18257/raccefyn.1594 [e-victor.palacios@utch.edu.co]

Pilatti, P., R. Moratelli, L. M. S. Aguiar, and D. Astúa. 2022. Distribution and morphological variation of *Xeronycteris vieirai* Gregorin and Ditchfield, 2005 (Chiroptera, Phyllostomidae). Acta Chiropterologica, 23(2): 475–497. (published 14 February 2022) [diego.astua@ufpe.br]

Risch, T. S., and S. S. Scherman. 2022. A record of the northern yellow bat, *Lasiurus intermedius* (Chiroptera, Vespertilionidae), from Ometepe Island, Nicaragua, and bat diversity implications for this region. Ecotropica, 24: 202201. https://www.ecotropica.eu/index.php/ecotropica/article/download/40/27 [trisch@astate.edu]

Simal, F., L. Smith, O. Doest, C. de Lannoy, F. Franken, I. Zaandam, D. Simal, and J. M. Nassar. 2022. Bat inventories at caves and mines on the islands of Aruba, Bonaire and Curaçao, and proposed conservation actions. Acta Chiropterologica, 23(2): 455–474. (published 14 February 2022) [jafet.nassar@gmail.com]

Tanshi, I., B. C. Obitte, A. Monadjem, and T. Kingston. 2022. Hidden Afrotropical bat diversity in Nigeria: Ten new country records from a biodiversity hotspot. Acta Chiropterologica, 23(2): 313–343. (published 14 February 2022) [iroro.tanshi@uniben.edu]

Wang, J., K.-C. Wong, S.-N. Chek, K.-M. Vu, H.-H. Chan, J. Liang, H. E. Xiangyang, and L. Zhang. 2022. New records of bat species and their conservation status in Macao, China. Acta Theriologica Sinica, 42(1): 125–130. http://www.mammal.cn/EN/10.16829/j.slxb.150521. [15537369278@163.com]

ECHOLOCATION

Görföl, T., J. C. Huang, G. Csorba, D. Győrössy, P. Estók, T. Kingston, K. L. Szabadi, E. McArthur, J. Senawi, N. M. Furey, V. T. Tu, V. D. Thong, F. A. A. Khan, E. R. Jinggong, M. Donnelly, J. V. Kumaran, J. Liu, S. Chen, M. Tuanmu, Y. Ho, H. Chang, N. Elias, N. Abdullah, L. Lim, C. D. Squire, and S. Zsebők. 2022. ChiroVox: a public library of bat calls. PeerJ, 10: e12445. https://doi.org/10.7717/peerj.12445 [tamas@gorfol.eu]

Hase, K., Y. Kadoya, Y. Takeuchi, K. I. Kobayasi, and S. Hiryu. 2022. Echo reception in group flight by Japanese horseshoe bats, *Rhinolophus ferrumequinum nippon*. Royal. Society Open Science, 9: 211597. https://doi.org/10.1098/rsos.211597 [kazuma.hase01@gmail.com]

Malmierca, M. S. 2022. How the bat brain detects novel sounds (commentary on Wetekam et al., 2021). European Journal of Neuroscience, 55(3): 895–897. https://doi.org/10.1111/ejn.15606 [msm@usal.es]. (Editor's note: Wetekam et al. citation included in the previous issue's Recent Literature of *Bat Research News*.)

Salles, A., S. M. Lee, and C. F. Moss. 2022. Sound evoked fos-like immunoreactivity in the big brown bat. IBRO Neuroscience Reports, 12: 197–202. https://doi.org/10.1016/j.ibneur.2022.02.005 [angiesalles@gmail.com]

Sulser, R. B., B. D. Patterson, D. J. Urban, A. I. Neander, and Z.-X. Luo. 2022. Evolution of inner ear neuroanatomy of bats and implications for echolocation. Nature, 602: 449–454. https://doi.org/10.1038/s41586-021-04335-z [rsulser@amnh.org]

ECOLOGY

Andersen, B. R., and K. Geluso. 2022. Roost characteristics of bats in the pine ridge region of Nebraska. Northwestern Naturalist, 103(1): 30-41. [gelusok1@unk.edu]

Ayala-Berdon, J., R. Vázquez-Fuerte, A. Guillén-Servent, I. L. López-Cuamatzi, and M. Martínez-Gómez. 2022. Changes in activity along the year in a community of insectivorous bats inhabiting a montane ecosystem of central Mexico. Mammal Research, https://doi.org/10.1007/s13364-022-00620-y [jorgeayalaberdon@gmail.com]

Baqi, A., V.-C. Lim, H. Yazid, F. A. A. Khan, C. J. Lian, B. R. Nelson, J. S. S. Seelan, S. Appalasamy, S. I. Mokhtar, and J. V. Kumaran. 2022. A review of durian plant-bat pollinator interactions. Journal of Plant Interactions, 17(1): 105–126. https://www.tandfonline.com/doi/full/10.1080/17429145.2021.2015466 [jayaraj@umk.edu.my]

Bogoni, J. A., V. Carvalho-Rocha, and P. G. da Silva. 2022. Spatial and land-use determinants of bat species richness, functional diversity, and site uniqueness throughout the largest Tropical country, Brazil. Mammal Review, 52: 267–283. https://doi.org/10.1111/mam.12279 [bogoni@usp.br]

Colorado-Durán, W. B., E. K. Espinosa-Francisco, F. Sierra-Vázquez, and A. A. Castro-Luna. 2022. Dispersal of *Hoffmannia excelsa* (Rubiaceae) by the Toltec fruit-eating bat (*Artibeus toltecus)* in central Veracruz, México. Therya Notes, 3: 6–9. [castrolun@gmail.com]

Da Silva, F. P., M. A. Montes, A. C. L. Garcia, E. A. Fischer, and L. G. da Silva. 2022. Distribution modelling and habitat requirements of *Micronycteris sanborni* (Phyllostomidae) across the South America dry diagonal. Acta Chiropterologica, 23(2): 433–441. (published 14 February 2022) [lucas_gonc@yahoo.com.br]

Froidevaux, J. S. P., G. Duarte, A. Fonseca, V. Zina, S. Conde, M. T. Ferreira, and M. R. Fernandes. 2022. The location and vegetation physiognomy of ecological infrastructures determine bat activity in Mediterranean floodplain landscapes. Agriculture, Ecosystems & Environment, 332: 107929. https://doi.org/10.1016/j.agee.2022.107929 [jeremy.froidevaux@stir.ac.uk]

Froidevaux, J. S. P., A. Laforge, L. Larrieu, L. Barbaro, K. Park, P. C. Fialas, and G. Jones. 2022. Tree size, microhabitat diversity and landscape structure determine the value of isolated trees for bats in farmland. Biological Conservation, 267: 109476. https://doi.org/10.1016/j.biocon.2022.109476 [jeremy.froidevaux@stir.ac.uk]

Klüg-Baerwald, B. J., C. L. Lausen, B. Wissel, and R. M. Brigham. 2022. Meet you at the local watering hole? No use of an artificial water resource, and evidence of dehydration in hibernating bats in the prairies. Acta Chiropterologica, 23(2): 405–411. (published 14 February 2022) [Mark.Brigham@uregina.ca]

Kruszynski, C., R. de Andrade Moral, C. Míllan, T. R. Diniz-Reis, M. A. R. Mello, and P. B. de Camargo. 2022. Diet composition of bats in a human-modified tropical landscape. Acta

Chiropterologica, 23(2): 395–404. (published 14 February 2022) [rafael.deandrademoral@mu.ie]

López-González, C., and C. Ocampo-Ramírez. 2022. External ears in Chiroptera: Form-function relationships in an ecological context. Acta Chiropterologica, 23(2): 525–545. (published 14 February 2022) [celialg.dgo@gmail.com]

Mas, M., C. Flaquer, X. Puig-Montserrat, X. Porres, H. Rebelo, and A. López-Baucells. 2022. Winter bat activity: The role of wetlands as food and drinking reservoirs under climate change. Science of The Total Environment,154403. https://doi.org/10.1016/j.scitotenv.2022.154403 [mmas@mcng.cat]

Mushabati, L. M., S. J. Eiseb, P. Benda, and T. M. Laverty. 2022. Effects of lunar phase and temperature on bat activity and species richness at varying altitudes in the Kunene Region, Namibia. African Journal of Ecology, pp. 1– 14. https://doi.org/10.1111/aje.12968 [seth_eiseb@yahoo.co.uk]

Neubaum, D. J., and K. Aagaard. 2022. Use of predictive distribution models to describe habitat selection by bats in Colorado, USA. Journal of Wildlife Management, 86: e22178. https://doi.org/10.1002/jwmg.22178 [daniel.neubaum@state.co.us]

Novella-Fernandez, R., J. Juste, C. Ibañez, J. Nogueras, P. E. Osborne, and O. Razgour. 2022. The role of forest structure and composition in driving the distribution of bats in Mediterranean regions. Scientific Reports, 12: 3224. https://doi.org/10.1038/s41598-022-07229-w [r.novella@tum.de]

Rolland, V., S. A. Schratz, D. R. Istvanko, and S. E. Harrod. 2022. Evening bats (*Nycticeius humeralis*) use bird nest boxes as day roosts in northeastern Arkansas. The American Midland Naturalist, 187(1): 84–89. [harrodsara@yahoo.com]

Saldaña-Vázquez, R. A., F. Villalobos, J. R. Hernández-Montero, D. Ferreyra-García, and J. P. Molina-Rodríguez. 2022. Ecoregions occupied are more related to diet diversity than body mass in Artibeina bats. Acta Chiropterologica, 23(2): 387–393. (published 14 February 2022) [romeoalberto.saldana@iberopuebla.mx]

Stevens, R. D. 2022. Dietary affinities, resource overlap and core structure in Atlantic Forest phyllostomid bat communities. Mammal Review, 52: 177–191. https://doi.org/10.1111/mam.12271 [richard.stevens@ttu.edu]

Uhrin, M., G. Nusová, and P. Kaňuch. 2022. Linking activity of common pipistrelles, *Pipistrellus pipistrellus*, in an urbanised area with a nearby mass swarming site. Urban Ecosystems, https://doi.org/10.1007/s11252-022-01222-x [marcel.uhrin@gmail.com]

EVOLUTION

Gardner, N. M., and T. A. Dececchi. 2022. Flight and echolocation evolved once in Chiroptera: comments on 'The evolution of flight in bats: a novel hypothesis'. Mammal Review, 52: 284–290. https://doi.org/10.1111/mam.12286 [ngardner@mail.wvu.edu]

Muñoz-Romo, M., E. M. Vilar, M. Dewynter, B. K. Lim, and R. A. Page. 2022. Revealing hidden sexually dimorphic male traits in the little white-shouldered bat, *Ametrida centurio* Gray 1847 (Chiroptera: Phyllostomidae). Mammalian Biology, https://doi.org/10.1007/s42991-022-00227-5 [munozml@si.edu]

GENOMICS

Baeza, J. A., M. E. Rodríguez, and J. Ortega. 2022. A genomic portrait of *Sturnira parvidens*: mitochondrial chromosome, repetitive elements, and microsatellite discovery. Journal of Mammalogy,103(1): 82–90. https://doi.org/10.1093/jmammal/gyab117 [baeza.antonio@gmail.com]

Farias, J. C., S. Vasconcelos, G. Oliveira, N. Santos, and C. G. Sotero-Caio. 2022. Complete mitochondrial genome of the greater round-eared bat, *Tonatia bidens* (Chiroptera: Phyllostomidae) from Brazil and phylogenetic relationships within the family. Mitochondrial DNA, Part B, 7(2): 323–325. https://www.tandfonline.com/doi/full/10.1080/23802359.2022.2030820 [cfarias.joao@gmail.com]

Fernandes, A. P., A. Águeda-Pinto, A. Pinheiro, H. Rebelo, and P. J. Esteves. 2022. Evolution of CCR5 and CCR2 genes in bats showed multiple independent gene conversion events. Viruses, 14(2): 169. https://doi.org/10.3390/v14020169 [up201900698@edu.fc.up.pt]

HIBERNATION

Boyles, J. G., E. M. Johnson, N. W. Fuller, K. A. Silas, L. Hou, W. F. Frick, and L. P. McGuire. 2022. Behavioural microclimate selection and physiological responses to environmental conditions in a hibernating bat. Canadian Journal of Zoology, 100(3): 233–238. https://doi.org/10.1139/cjz-2021-0193 [jgboyles.lab@gmail.com]

IMMUNOLOGY

Fernandes, A. P., A. Águeda-Pinto, A. Pinheiro, H. Rebelo, and P. J. Esteves. 2022. Evolution of TRIM5 and TRIM22 in bats reveals a complex duplication process. Viruses, 14(2): 345. https://doi.org/10.3390/v14020345 [up201900698@edu.fc.up.pt]

MIGRATION

Rogers, E. J., L. McGuire, F. J. Longstaffe,. J. Clerc, E. Kunkel, and E. Fraser. 2022. Relating wing morphology and immune function to patterns of partial and differential bat migration using stable isotopes. Journal of Animal Ecology, pp. 1– 12. https://doi.org/10.1111/1365-2656.13681 [bethrogs@gmail.com]

NECTARIVORY

Diniz, U. M., N. L. S. Fischer, and L. M. S. Agular. 2022. Changing the main course: strong bat visitation to the ornithophilous mistletoe *Psittacanthous robustus* (Loranthaceae) in a Neotropical savanna. Biotropica, 54: 478– 489. https://doi.org/10.1111/btp.13070 [ugomdiniz@gmail.com]

González-Gutiérrez, K., J. H. Castaño, J. Pérez-Torres, and H. R. Mosquera-Mosquera. 2022. Structure and roles in pollination networks between phyllostomid bats and flowers: a systematic review for the Americas. Mammalian Biology, 102: 21–49. https://doi.org/10.1007/s42991-021-00202-6 [kevingg2010@gmail.com]

Karimi, N., S. Saghafi, K. Keefover-Ring, S. M. Venter, C. Ané, and D. A. Baum. 2022. Evidence for hawkmoth pollination in the chiropterophilous African baobob (*Adansonia digitata*). Biotropica, 54: 113–124. [nkarimi@wisc.edu]

Rebolledo Contreras, M. 2021. Polinización de *Mucuna mutisiana* (Kunth) D.C. por murciélagos *Glossophaga soricina* y *Glossophaga longirostris* (Phyllostomidae: Glossophaginae) en el Bosque Seco Tropical (BsT) al norte de Colombia. Revista Novedades Colombianas, 16(1): 77–99. https://doi.org/10.47374/novcol.2021.v16.1945 [merieler@uninorte.edu.co]

NEUROPHYSIOLOGY

Yu, C., and C. F. Moss. 2022. Natural acoustic stimuli evoke selective responses in the hippocampus of passive listening bats. Hippocampus, pp. 1–12. https://doi.org/10.1002/hipo.23407 [cynthia.moss@jhu.edu]

PALEONTOLOGY

Izvarin, E., A. Ulitko, S. Panina, E. Zazovskaya, and A. Nekrasov. 2022. Voronin Grotto (Middle Urals, Russia): Analysis of vertebrate assemblage with taphonomic remarks and reconstruction of the Late Bronze Age and Early Iron Age human environment in the east end of Europe based on small mammals. Quaternary International, https://doi.org/10.1016/j.quaint.2022.02.031 [izvarin1982@mail.ru]

Kimura Y., D. Fukui, M. Yoshiyuki, and K. Higashi. 2022. Conservation paleobiology on Minami-Daito Island, Okinawa, Japan: anthropogenic extinction of cave-dwelling bats on a tropical oceanic island. PeerJ, 10: e12702. https://doi.org/10.7717/peerj.12702 [ykimura@kahaku.go.jp]

Piskoulis, P., and K. Chatzopoulou. 2022. The fossil record of bats (Mammalia: Chiroptera) in Greece. Pp. 93–111 *in* E. Viachos, Ed. Fossil Vertebrates of Greece, Vol. 2. Springer, Cham., xxiii + 724 pp. https://doi.org/10.1007/978-3-030-68442-6_4 [Hardcover book ISBN 978-3-030-68441-9; E-book ISBN 978-3-030-68442-6]

Rosina, V. V., S. V. Kruskop, and M. Pickford. 2022. Odontological characters of African molossid bats (Molossidae, Chiroptera, Mammalia) in the context of studies of the Miocene bat

assemblages from Berg Aukas I, Namibia. Communications of the Geological Survey of Namibia, 24: 17–32. [rossina@mail.ru]

PARASITOLOGY

Fernandes, T. F., J. N. dos Santos, F. T. de Vasconcelos Melo, T. J. Achatz, C. T. McAllister, C. C. Bonilla, and V. V. Tkach. 2022. Phylogenetic relationships of *Ochoterenatrema* Caballero, 1943 (Digenea: Lecithodendriidae) with descriptions of two new species. Parasitology International, 102575. https://doi.org/10.1016/j.parint.2022.102575 [jeannie@ufpa.br]

Gómez-Corea W., F. G. España, D. Mejía-Quintanilla, and M. R. V. Alvarez. 2022. Bat fly-common vampire bat association in Honduras: prevalence, mean intensity, infracommunities and influence of the biological characteristics of the host (Diptera: Hippoboscidae; Chiroptera: Phyllostomidae). Zoologia (Curitiba), 39: e21018. https://doi.org/10.1590/S1984-4689.v39.e21018 [wilsongomezcorea@gmail.com]

Hrycyna, G., C. L. C. Dos Santos, J. M. M. Rebêlo, and G.Graciolli. 2022. A new species of *Hershkovitzia* (Diptera: Nycteribiidae) from Maranhão, Brazil. Annals of the Brazilian Academy of Sciences, 94(1): e20191161. https://pubmed.ncbi.nlm.nih.gov/35018991/ [gabrielahrycyna@gmail.com]

Hugot, J.-P., C. Feliu, and A. Ribas. 2022. Human parasites as tracers of the evolution of their hosts. Infection, Genetics and Evolution, 105262. https://doi.org/10.1016/j.meegid.2022.105262 [hugot@mnhn.fr]. (Editor's note: contains a few parasites shared by bats and humans)

Di Benedetto, I. M. D., V. N. Debarbora, A. P. Benitez Ibalo, E. B. Oscherov, A. G. Autino, S. Nava, and J. M. Venzal. 2022. Morphological and molecular analysis of *Ornithodoros hasei* and *Ornithodoros* sp. cf. *O. mimon* (Acari: Argasidae) from northeastern Argentina. Systematic and Applied Acarology, 27(1): 71–80. [no author email provided]

Ramírez-Chaves, H. E., A. J. Folleco-Fernández, and A. Cardona-Giraldo. 2021. Registro de la pulga *Hectopsylla pulex* (Haller, 1880) (Siphonaptera: Tungidae) en el murciélago mastín común *Molossus molossus* (Pallas, 1766) (Chiroptera: Molossidae) en el departamento del Cauca, Colombia. Revista Novedades Colombianas, 16(1): 67–75. https://doi.org/10.47374/novcol.2021.v16.1894 [hector.ramirez@ucaldas.edu.co]

Sato, H., and E. Mafie. 2022. "Visiting old, learn new": taxonomical overview of chiropteran trypanosomes from the morphology to the genes. Parasitology Research, 121: 805–822. https://doi.org/10.1007/s00436-022-07423-9 [sato7dp4@yamaguchi-u.ac.jp]

Sullivan, C. F., J. L. Occi, J. R. Brennan, R. G. Robbins, M. Skinner, A. B. Bennett, B. L. Parker, and D. M. Fonseca. 2022. First report of the bat tick *Carios kelleyi* (Acari: Ixodida: Argasidae) from Vermont, United States. Journal of Medical Entomology, tjab232, https://doi.org/10.1093/jme/tjab232 [cfrank@uvm.edu]

Tai, Y. L., Y.-F. Lee, and Y.-M. Kuo, and Y.-J. Kuo. 2022. Effects of host state and body condition on parasite infestation of bent-wing bats. Frontiers in Zoology, 19, Article # 12. https://doi.org/10.1186/s12983-022-00457-w [yafulee@mail.ncku.edu.tw]

Vieira, T. M., S. de Oliveira Silva, L. Lima, G. Sabino-Santos, E. R. Duarte, S. M. Lima, A. A. S. Pereira, F. C. Ferreira, W. S. de Araújo, M. M. G. Teixeira, R. L. Ursine, C. M. F. Gontijo, and M. N. Melo. 2022. Leishmania diversity in bats from an endemic area for visceral and cutaneous leishmaniasis in Southeastern Brazil. Acta Tropica, 228: 106327. https://doi.org/10.1016/j.actatropica.2022.106327 [no author email address provided]

PHYSIOLOGY

Edwards, P. D., R. Boonstra, C. O. Bosson, N. J. Harms, P. M. Kukka, C. K. R. Willis, and T. S. Jung. 2022. Effects of capture on stress-axis measures in endangered little brown bats (*Myotis lucifugus*). Journal of Mammalogy, 103(1): 91–99. https://doi.org/10.1093/jmammal/gyab135 [thomas.jung@yukon.ca]

Hornok, S., R. Berkecz, E. Sós, A. D. Sándor, T. Körmöczi, N. Solymosi, J. Kontschán, and A. Hunyadi. 2022. Arthropod moulting hormones (ecdysteroids) are present in the blood of insectivorous bats. Mammal Review, https://doi.org/10.1111/mam.12283 [hornok.sandor@univet.hu]

Muñoz-Garcia, A., M. Ben-Hamo, S. Pilosof, J. B. Williams, and C. Korine. 2022. Habitat aridity as a determinant of the trade-off between water conservation and evaporative heat loss in bats. Journal of Comparative Physiology B, 192: 325–333. https://doi.org/10.1007/s00360-021-01425-2 [munozgarcia.1@osu.edu]

Paksuz, E. P. 2022. Hematology and plasma biochemistry of greater mouse-eared bat *Myotis myotis* (Borkhausen) (Chiroptera: Vespertilionidae) in Turkey. Trakya University Journal of Natural Sciences, 23(1): https://dergipark.org.tr/en/pub/trkjnat/issue/27380/962609 [epinarpaksuz@trakya.edu.tr]

Ramos-H., D., M. Williams, and R. A. Medellín. 2022. Inter-taxon and seasonal variations of mineral concentrations in soft tissues of frugivorous phyllostomid bats in a mineral-limited ecosystem. Acta Chiropterologica, 23(2): 377–386. (published 14 February 2022) [danielramosh7@iecologia.unam.mx]

POPULATION BIOLOGY AND GENETICS

Grimshaw, J. R., J. D. Manthey, N. S. Paulat, R. D. Stevens, and D. A. Ray. 2022. Landscape level patterns of genetic diversity of bat species of greatest conservation need in Louisiana. Occasional Papers, Museum of Texas Tech University, No. 380, pp. 1–12. [jenna.grimshaw@ttu.edu]

Jakab, E., S. Bücs, C. Jére, I. Csősz, R. I. Jakab, F. Szodoray-Parádi, and O. Popescu. 2022. Low population structure and genetic diversity in *Rhinolophus blasii* at the northern limit of its

European range: Are there undiscovered colonies? Acta Chiropterologica, 23(2): 301–311. (published 14 February 2022) [endre.jakab@ubbcluj.ro]

REPRODUCTION

Alonge, M. M., L. J. S. Greville, P.A. Faure, and G. E. Bentley. 2022. Immunoreactive distribution of gonadotropin-inhibitory hormone precursor, RFRP, in a temperate bat species (*Eptesicus fuscus*). Journal of Comparative Neurology, pp. 1–11. https://doi.org/10.1002/cne.25291 [mattina.alonge@berkeley.edu]

Kazeem, E. O., O. G. Samuel, and O. O. Bankole. 2022. Reproductive cycle in the male African fruit bat (*Epomops franqueti*). Journal of Entomology and Zoology Studies, 10(1): 395–402. https://doi.org/10.22271/j.ento.2022.v10.i1e.8959 [no author email address provided]

Novaes, R. L. M. 2022. The ecological cost of reproduction in the proboscis bat. Frontiers in Ecology and the Environment, 20(2): 75–75. https://doi.org/10.1002/fee.2479 [no author email address provided]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Csorba, G., and N. M. Furey. 2022. From greener times: a new species of thick-thumbed *Myotis* from Phnom Penh, Cambodia. Acta Zoologica Academiae Scientiarum Hungaricae, 68(1): 85–97. https://doi.org/10.17109/AZH.68.1.85.2022 [csorba.gabor@nhmus.hu]

Salomon, G. R., A. L. Gaglioti, L. P. B. Machado, A. O. T. Carrasco, and R. P. Mateus. 2022. Note on the phylogenetic position of *Eptesicus* species in the Vespertilionidae family (Chiroptera) using Brazilian bats and RAG2 sequences. Brazilian Journal of Biology [online], 84: e258210. https://doi.org/10.1590/1519-6984.258210 [rogeriopmateus@gmail.com]

Uvizl, M., and P. Benda. 2022. Intraspecific variation of *Myotis emarginatus* (Chiroptera: Vespertilionidae) inferred from mitochondrial and nuclear genetic markers. Acta Chiropterologica, 23(2): 285–300. (published 14 February 2022) [marek.uvizl@gmail.com]

Volleth, M., S. Müller, K.-G. Heller, V. Trifonov, T. Liehr, H.-S. Yong, R. J. Baker, F. A. A. Khan, and C. G. Sotero-Caio. 2022. Cytogenetic analyses detect cryptic diversity in *Megaderma spasma* from Malaysia. Acta Chiropterologica, 23(2): 271–284. (published 14 February 2022) [heller.volleth@t-online.de]

TECHNIQUES FOR STUDYING BATS

Appel, G., U. D. Capaverde, Jr., L. Q. de Oliveira, L. G. do Amaral Pereira, V. da Cunha Tavares, A. López-Baucells, W. E. Magnusson, F. B. Baccaro, and P. E. D. Bobrowiec. 2022. Use of complementary methods to sample bats in the Amazon. Acta Chiropterologica, 23(2): 499–511. (published 14 February 2022) [giu.appel@gmail.com]

Brewer, C. T., W. A. Rauch-Davis, and E. E. Fraser. 2021. The use of intrinsic markers for studying the migratory movements of bats. Animals, 11: 3477. https://doi.org/10.3390/ani11123477 [efraser@grenfell.mun.ca]

Doty, A. C., A. D. Wilson, L. B. Forse, and T. S. Risch. 2022. Biomarker metabolites discriminate between physiological states of field, cave and white-nose syndrome diseased bats. Sensors, 22(3): 1031. https://doi.org/10.3390/s22031031 [adoty@csub.edu]

Hooper, S. E., S. K. Amelon, and C.-H. Lin. 2022. Development of an LC-MS/MS method for non-invasive biomonitoring of neonicotinoid and systemic herbicide pesticide residues in bat hair. Toxics, 10(2): 73. https://doi.org/10.3390/toxics10020073 [shooper@rossvet.edu.kn]

Mancini, M. C. S., F. Hintze, R. de Souza Laurindo, R. de Macêdo Mello, and R. Gregorin. 2022. Tradition vs. innovation: comparing bioacoustics and mist-net results to bat sampling. Bioacoustics, https://www.tandfonline.com/doi/abs/10.1080/09524622.2021.2008494 [mthmancini@gmail.com]

Rolfes, J. W., J. A. Encarnação, and N. I. Becker. 2022. Going bald — The hairy affair of timing in telemetry studies: moulting activity in European bat species. Acta Chiropterologica, 23(2): 513–523. (published 14 February 2022) [nib@inatu.re]

Whiting, J. C., B. Doering, and K. Aho. 2022. Can acoustic recordings of cave-exiting bats in winter estimate bat abundance in hibernacula? Ecological Indicators, 137: 108755. https://doi.org/10.1016/j.ecolind.2022.108755 [whitingj@byui.edu]

Yoh, N., T. Kingston, E. McArthur, O. E. Aylen, J. C.-C. Huang, E. R. Jinggong, F. A. A. Khan, B. P. Y. H. Lee, S. L. Mitchell, J. E. Bicknell, and M. J. Struebig. 2022. A machine learning framework to classify Southeast Asian echolocating bats. Ecological Indicators, 136: 108696. https://doi.org/10.1016/j.ecolind.2022.108696 [tallyyoh@gmail.com]

WHITE-NOSE SYNDROME

Arant, P. L., M. J. Lacki, J. M. Lhotka, and J. W. Stringer. 2022. Summer populations of northern long-eared bat in an eastern Kentucky Forest following arrival of white-nose syndrome. The American Midland Naturalist, 187(1): 71–83. [mlacki@uky.edu]

Căpătînă, D., B. Feier, O. Hosu, M. Tertiș, and C. Cristea. 2022. Analytical methods for the characterization and diagnosis of infection with *Pseudomonas aeruginosa*: A critical review. Analytica Chimica Acta, 339696. https://doi.org/10.1016/j.aca.2022.339696 [ccristea@umfcluj.ro]

Grimaudo, A. T., J. R. Hoyt, S. A. Yamada, C. J. Herzog, A. B. Bennett, and K. E. Langwig. 2022. Host traits and environment interact to determine persistence of bat populations impacted by white-nose syndrome. Ecology Letters, 25: 483–497. https://doi.org/10.1111/ele.13942 [at.grimaudo@gmail.com]

White, J. A., P. W. Freeman, M. I. Shehan, and C. A. Lemen. 2022. Decline of the northern long-eared myotis (*Myotis septentrionalis*) in the eastern Great Plains after the arrival of white-nose syndrome. Western North American Naturalist, 82(1): Article 8. [Available at: https://scholarsarchive.byu.edu/wnan/vol82/iss1/8]

ANNOUNCEMENTS

Reminder—Renewal Time!

Some of you have received renewal information in your e-mail inbox. If you have not done so, please renew soon. We hope you will continue to support *BRN* for the 2022 volume-year.

Change of Address Requested

Will you be moving in the near future or changing your e-mail address? If so, please **send** your **new postal and e-mail addresses** to Margaret Griffiths (margaret.griffiths01@gmail.com), and include the date on which the change will become effective. Thank you in advance!

Request for News

Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Request for Manuscripts — *Bat Research News*

Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

Back Issues of *Bat Research News*

Many back issues are available on the *Bat Research News* website. The five most recent issues remain available to current subscribers only. To download back issues, click on the "Past Volumes" link found on the home page, and then on the volume you would like to download. I am working on adding more past issues to the site so stay tuned. If you or someone you know need back issues not available on the *BRN* site, please contact the Managing Editor, Margaret Griffiths (margaret.griffiths01@gmail.com).

FUTURE MEETINGS and EVENTS

ALL Professional Meetings and Events

Please check the websites of all professional societies regarding meetings. Given the rapidly changing situation of the COVID-19 pandemic, decisions as to whether professional meetings will be face-to-face, virtual, or hybrid during the year are updated on the respective website.

2022

The Midwest Bat Working Group Hybrid Annual Meeting will be held 4–5 April 2022, Missouri Department of Conservation's Powder Valley Conservation Nature Center, in St. Louis, Missouri. Check the MWBWG website for registration and lodging information and updates — https://www.mwbwg.org/.

The Annual NASBR meeting will be held in conjunction with the International Bat Research Conference (IBRC), 7–12 August 2022, at the Hilton Austin, in Austin, Texas. Check the NASBR website for updates — https://www.nasbr.org/.

2023

The Annual NASBR meeting will be held 11–14 October 2023, at the Fort Garry Hotel, in Winnipeg, Manitoba, Canada. Check the NASBR website for updates — https://www.nasbr.org/.

BAT RESEARCH NEWS

VOLUME 63: NO. 2 SUMMER 2022

BAT RESEARCH NEWS

VOLUME 63: NUMBER 2 **SUMMER 2022**

Table of Contents

Front Cover

Silver-haired Bat (*Lasionycteris noctivagans*). Drawing courtesy of Chester O. Martin. Originally illustrated as a t-shirt design for the 15th Annual Mississippi Bat Working Group Mist Net Event, 2018. Thank you, Chester, for sharing your artwork.

BAT RESEARCH NEWS

Volume 63: Number 2 Summer 2022

Publisher and Managing Editor: Dr. Margaret A. Griffiths, 8594 Berwicke Circle, Bloomington, IL 61705; E-mail: margaret.griffiths01@gmail.com

Editor for Feature Articles: Dr. Allen Kurta, Dept. of Biology, Eastern Michigan University, Ypsilanti MI 48197; E-mail: akurta@emich.edu

Editor for Recent Literature: Dr. Thomas A. Griffiths, 8594 Berwicke Circle, Bloomington, IL 61705; E-mail: thomas.alan.griffiths@gmail.com

Emeritus Editor: Dr. G. Roy Horst

Bat Research News is published four times each year, consisting of one volume of four issues. *Bat Research News* publishes short feature articles and general interest notes that are reviewed by at least two scholars in that field. *Bat Research News* also includes abstracts of presentations at bat conferences around the world, letters to the editors, news submitted by our readers, notices and requests, and announcements of future bat conferences worldwide. In addition, *Bat Research News* provides a listing of recently published bat-related articles. *Bat Research News* is abstracted in several databases (e.g., BIOSIS).

Communications concerning feature articles and "Letters to the Editor" should be addressed to Dr. Al Kurta (akurta@emich.edu), recent literature items to Dr. Tom Griffiths (thomas.alan.griffiths@gmail.com), and all other correspondence (e.g., news, conservation, or education items; subscription information; cover art; back issues) to Dr. Margaret Griffiths (margaret.griffiths01@gmail.com).

The prices for one volume-year (4 issues within a single volume) are:

Institutional/Group subscriptions	US $55.00
Individual subscriptions:	
printed edition (U.S.A.)	US $30.00
printed edition (outside U.S.A)	US $40.00

Subscriptions may be paid by check or money order, payable to "***Bat Research News***." Please include both mailing (postal) and e-mail addresses with your payment, and send to Dr. Margaret Griffiths at the address listed above. To pay by credit card (Visa or MasterCard only) or for further information, please go to the *Bat Research News* website at http://www.batresearchnews.org/ and click on the "Subscription Information" link.

Many **back issues** of *Bat Research News* are available for free download from the *BRN* website at http://batresearchnews.org/. Other back issues may be available by contacting Dr. Margaret Griffiths (margaret.griffiths01@gmail.com). Thank you!

Bat Research News is ISSN # 0005-6227.
Bat Research News is printed and mailed in Bloomington, Illinois, U.S.A.

This issue printed June 24, 2022.

From the Editor: the end of *Bat Research News*?

Greetings to old friends, colleagues, and interested bat researchers from around the world. I hope this finds you doing well. If you are doing field work or in the lab, I hope it goes well. If you are just enjoying summer, good for you and enjoy.

I have been the Publisher and Managing Editor of *Bat Research News* for nearly 20 years and I am ready to retire. I have offered ownership of *BRN* to a professional group of bat researchers who is interested in taking over *BRN* and they have the right of first refusal. But if they decide not to take over *BRN*, I would like to pass it to someone who would continue the publication. If you are interested, or know of someone or a group who is interested, please contact me at margaret.griffiths01@gmail.com. If not, this is the last year I will be able to do this and *Bat Research News* will cease publication at the end of 2022.

As a subscriber, you already know that *Bat Research News* is a quarterly publication available in print and/or online. It publishes short, peer-reviewed original research articles on bats, book reviews of books on bats, bat-related abstracts of papers given at national and international meetings (e.g., NASBR), and news about scientific meetings, recent publications, and other information on bat research. It is read by subscribers in 41 of the 50 states within the United States, and in 31 countries and three territories around the world. It has been continuously published since its founding by Wayne Davis of the University of Kentucky in 1960. Wayne passed *BRN* on to Roy Horst of SUNY Potsdam who published it for a number of years. Roy passed it on to me in 2004.

BRN has a venerable and distinguished history of publishing important short papers. It was, for example, where Karl Koopman first introduced the world of taxonomy to his newly-proposed infraorders Yinochiroptera and Yangochiroptera in 1985. It has always been a perfect place to rapidly publish a short research paper, but in recent years, the proliferation of new journals by Elsevier, Springer, and other publishers that offer rapid online publication has reduced the appeal of publishing in *BRN*. I believe that there is still a "niche" for *Bat Research News* in the world of chiropterology if the ownership can be assumed by the right group of people. Please let me know if you are interested and/or if you'd like more information, or go to: http://www.batresearchnews.org/.

Thank you for your time and consideration. Enjoy your summer, whatever your plans may be or wherever you may travel.

Best wishes,

ANNOUNCEMENTS

Change of Address Requested

Will you be moving in the near future or changing your e-mail address? If so, please **send** your **new postal and e-mail addresses** to Margaret Griffiths (margaret.griffiths01@gmail.com), and include the date on which the change will become effective. Thank you in advance!

Request for News

Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Request for Manuscripts — *Bat Research News*

Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

Back Issues of *Bat Research News*

Many back issues are available on the *Bat Research News* website. The five most recent issues remain available to current subscribers only. To download back issues, click on the "Past Volumes" link found on the home page, and then on the volume you would like to download. I am working on adding more past issues to the site so stay tuned. If you or someone you know need back issues not available on the *BRN* site, please contact the Managing Editor, Margaret Griffiths (margaret.griffiths01@gmail.com).

FUTURE MEETINGS and EVENTS

ALL Professional Meetings and Events

Please check the websites of all professional societies regarding meetings. Given the rapidly changing situation of the COVID-19 pandemic, decisions as to whether professional meetings will be face-to-face, virtual, or hybrid during the year are updated on the respective website.

2022

The 50th Annual NASBR meeting will be held in conjunction with the 19th International Bat Research Conference (IBRC), 7–12 August 2022, at the Hilton Austin, in Austin, Texas. To register for the conference go to: https://www.ibrc.org/.

2023

The Annual NASBR meeting will be held 11–14 October 2023, at the Fort Garry Hotel, in Winnipeg, Manitoba, Canada. Check the NASBR website for updates — https://www.nasbr.org/.

RECENT LITERATURE

Authors are requested to send reprints (PDF files) of their published papers to the Editor for Recent Literature, **Dr. Thomas A. Griffiths**, (e-mail: **thomas.alan.griffiths@gmail.com**) for inclusion in this section. Receipt of reprints is preferred, as it will facilitate complete and correct citation. However, if reprints and/or PDF files are unavailable, please send a complete citation (including complete name of journal and corresponding author e-mailing address) by e-mail. The Recent Literature section is based on several bibliographic sources and for obvious reasons can never be up-to-date. Any error or omission is inadvertent. Voluntary contributions for this section, especially from researchers outside the United States, are most welcome and appreciated.

ANATOMY/HISTOLOGY

Castillo-Figueroa, D. 2022. Exploring a hidden structure in New World bats: the pollex. Tropical Natural History, 22(1): 1–11. [dennis.castillof@gmail.com]

Czaplewski, N. J., and C. G. Baker. 2022. Carnassiform notches improve the functional efficiency of bat molar shearing crests. Acta Palaeontologica Polonica, 67(1): 257–282. [nczaplewski@ou.edu]

De Almeida Pereira, L., S. Marchioro, G. C. Silveira Rocha, and J. M. Deliberador Miranda. 2022. Primer registro de coloración anómala de *Eptesicus taddeii* (Vespertilionidae) en Mata Atlántica, Sur de Brasil. Boletín Científico Centro de Museos, 26(1): 113–118. https://doi.org/10.17151/bccm.2022.26.1.8 [luanabio2014@gmail.com]

El-Nahass, E. E-S., and M. Elwan. 2022. Histology, histochemistry, and ultrastructure of the liver of the Egyptian tomb bat, *Taphozous perforatus*. Egyptian Journal of Histology, https://ejh.journals.ekb.eg/article_233997.html. [emannahass@yahoo.com]

Genelhú, S. M. C., M. H. Simões, M. A. C. Assis, M. S. Ribeiro, and X. Prous. 2022. First report of albinism in a lactating female of the chestnut long-tongued bat *Lionycteris spurrelli* Thomas, 1913 (Chiroptera, Phyllostomidae). Mammalia, 86(3): 257–260. https://doi.org/10.1515/mammalia-2021-0030 [sebastiaogenelhum@gmail.com]

Paksuz, E. P. 2022. Renal adaptation in relation to insectivorous feeding habit in the greater mouse-eared bat, *Myotis myotis* (Chiroptera: Vespertilionidae). The Anatomical Record, pp. 1–11. https://doi.org/10.1002/ar.24946 [epinarpaksuz@trakya.edu.tr]

Snipes, C. C. G., and R. T. Carter. 2022. The hyoid as a sound conducting apparatus in laryngeally echolocating bats. Journal of Anatomy, 240: 1020– 1033. https://doi.org/10.1111/joa.13615 [carterrt@etsu.edu]

Usui, K., E. R. Khannoon, and M. Tokita. 2022. Facial muscle modification associated with chiropteran noseleaf development: Insights into the developmental basis of a movable rostral appendage in mammals. Developmental Dynamics, pp. 1–12.

https://anatomypubs.onlinelibrary.wiley.com/doi/abs/10.1002/dvdy.472
[masayoshi.tokita@sci.toho-u.ac.jp]

A TRIBUTE TO THE LIFE AND WORK OF KUNWAR BHATNAGAR

Smith, T. D. 2022. Vespers and vampires: A lifelong microscopic search for the smallest of things. The Anatomical Record, pp. 1–11. https://doi.org/10.1002/ar.24907
[timothy.smith@sru.edu]

A TRIBUTE TO THE LIFE AND WORK OF GILBERTO SILVA TABOADA

Soto-Centeno, J. A., N. S. Upham, C. A. Mancina, B. K. Lim, and R. M. Timm. 2022. Obituary: Gilberto Silva Taboada (1927–2022). Journal of Mammalogy, 103(3): 745–748. https://doi.org/10.1093/jmammal/gyac030 [btimm@ku.edu]

BATS AND AGRICULTURE

Bhalla, I. S., and R. J. Whittaker. 2022. Batting for rice: the effect of bat exclusion on rice. SSRN. https://ssrn.com/abstract=4109739 or http://dx.doi.org/10.2139/ssrn.4109739
[iqbalbhalla@gmail.com]

Fill, C. T., C. R. Allen, D. Twidwell, and J. F. Benson. 2022. Spatial distribution of bat activity in agricultural fields: implications for ecosystem service estimates. Ecology and Society, 27(2): 11. https://doi.org/10.5751/ES-13170-270211 [christopher.fill@huskers.unl.edu]

BAT BACTERIA MAY MAKE USEFUL BIOLOGICAL MOLECULES

Salazar-Hamm, P. S., J. J. Marshall Hathaway, A. S. Winter, N. A. Caimi, D. C. Buecher, E. W. Valdez, and D. E. Northup. 2022. Great diversity of KSα sequences from bat-associated microbiota suggests novel sources of uncharacterized natural products. FEMS Microbes, 3: xtac012. https://doi.org/10.1093/femsmc/xtac012 [jjm@unm.edu]

BEHAVIOR

Finch, D., H. Schofield, J. A. Firth, and F. Mathews. 2022. Social networks of the greater horseshoe bat during the hibernation season: a landscape-scale case study. Animal Behaviour, 188: 25–34. https://doi.org/10.1016/j.anbehav.2022.03.019 [d.finch@sussex.ac.uk]

Kerth, G. 2022. Long-term field studies in bat research: importance for basic and applied research questions in animal behavior. Behavioral Ecology and Sociobiology, 76: 75. https://doi.org/10.1007/s00265-022-03180-y [gerald.kerth@uni-greifswald.de]

Laverty, T. M., and K. E. Stoner. 2022. In search of bachelorettes: Observations of male *Leptonycteris yerbabuenae* with dorsal patches across its range. Therya, 13(2): 163–170.
[theresalaverty@gmail.com]

BIOGEOGRAPHY

Adams, H., and L. P. McGuire. 2022. Island biogeography theory and the urban landscape: stopover site selection by the silver-haired bat (*Lasionycteris noctivagans*). Canadian Journal of Zoology, 100(4): 243–250. https://doi.org/10.1139/cjz-2021-0214 [liam.mcguire@uwaterloo.ca]

Fichera, G., M. Mucedda, D. Russo, A. Tomassini, A. Kiefer, M. Veith, and L. Ancillotto. 2022. Pantelleria island (Sicily, Italy): a biogeographic crossroad for bats between Africa and Europe. Hystrix, the Italian Journal of Mammalogy, https://doi.org/10.4404/hystrix-00503-2021 [gadfichera@gmail.com]

Gorban, A. A., I. V. Artyushin, A. A. Bannikova, E. Undrakhbayar, and S. V. Kruskop. 2022. Phylogeography of the steppe bat, *Myotis davidii* (Chiroptera; Vespertilionidae) in eastern part of the species range. Doklady Biological Sciences, 502: 21–25. https://doi.org/10.1134/S0012496622010045 [selysius@mail.ru]

Yi, X. and E. K. Latch. 2022. Nuclear phylogeography with strong impacts of gene flow in big brown bats. Journal of Biogeography, 49: 1061– 1074. https://onlinelibrary.wiley.com/doi/10.1111/jbi.14362 [xyi@uwm.edu]

BODY SIZE DISTRIBUTION IN BATS

Gualandi, S., G. Toscani, and E. Vercesi. 2022. A kinetic description of the body size distributions of species. https://doi.org/10.48550/arXiv.2206.00495 [stefano.gualandi@unipv.it]

BOOKS ON BATS

Lausen, C. L., D. W. Nagorsen, R. M. Brigham, and J. Hobbs. 2022. Bats of British Columbia, 2nd Ed. Royal BC Museum Press, Victoria, B.C., 384 pp (paperback), $29.65. [ISBN 978-0772679932]

CONSERVATION

Adam, M. L., L. de Assis Rocha Pessoa, A. R. B. de Lima, and E. Bernard. 2022. DNA damage as indicator of the environmental vulnerability of bats in Brazil's Caatinga drylands. Environmental Monitoring and Assessment, 194: 277. https://link.springer.com/article/10.1007/s10661-022-09906-9 [enrico.bernard@ufpe.br]

Da Silva, D. C., R. M. da Silva, B. C. da Silva Barbosa, and L. A. M. da Silva. 2022. Accidental bat death record (Mammalia: Chiroptera) in barbed wire fence. Research, Society and Development, 11(4): e10911427166. https://rsdjournal.org/index.php/rsd/article/view/27166 [dayannecicera123@gmail.com]

De Oliveira, M. B., and C. Bueno. 2022. Spatial and temporal distribution of bat mortality on a highway in southeast Brazil. Therya, 13(2): 195–203. [cecilia.bueno2020@gmail.com]

Faria, S., P. Barros, E. Bacelar, M. Santos, D. Carvalho, H. Vale-Gonçlaves, L. Braz, P. Travassos, and J. A. Cabral. 2022. A seasonal multi-level trophic approach for bat habitat suitability assessments in peri-urban deciduous forests. European Journal of Wildlife Research, 68, article no.19. https://doi.org/10.1007/s10344-022-01560-3 [pbarros@utad.pt]

Ferreira, D. F., R. Gibb, A. López-Baucells, N. J. Nunes, K. E. Jones, and R. Rocha. 2022. Species-specific responses to land-use change in island insectivorous bats. Journal for Nature Conservation, 67: 126177. https://doi.org/10.1016/j.jnc.2022.126177 [ferreiradfa@cibio.up.pt]

Göttert, T., and N. Starik. 2022. Human–wildlife conflicts across landscapes—general applicability vs. case specificity. Diversity, 14(5): 380. https://doi.org/10.3390/d14050380 [thomas.goettert@hnee.de]

Grimshaw, J. R., D. A. Ray, and R. D. Stevens. 2021. Ecological niche models for bat species of greatest conservation need in Louisiana. Occasional Papers, Museum of Texas Tech University, no. 378, pp. 1–15. [jenna.grimshaw@ttu.edu]

Guimarães Torquetti, C., M. Maciel d'Auriol-Souza, L. Coelho André, A. T. B. Guimarães, and B. Soto-Blanco. 2022. Miniaturized QuEChERS extraction method for the detection of multi-residue pesticides in bat muscle tissue. Scientific Reports, 12: 7164. https://doi.org/10.1038/s41598-022-11352-z [benito@ufmg.br]

Hooker, J., P. Lintott, and E. Stone. 2022. Lighting up our waterways: Impacts of a current mitigation strategy on riparian bats. Environmental Pollution, 307: 119552. https://doi.org/10.1016/j.envpol.2022.119552 [jack.hooker@uwe.ac.uk]

Krings, C. H., K. Darras, A. Hass, P. Batáry, and Y. Fabian. 2022. Not only hedgerows, but also flower fields can enhance bat activity in intensively used agricultural landscapes. Basic and Applied Ecology, 63: 23–35. https://doi.org/10.1016/j.baae.2022.05.002 [celina.herrera.krings@gmail.com]

Kumar, J., A. Kanaujia, and R. Verma. 2021. Various threats to survival of bats in district Lakhimpur-Kheri, Uttar Pradesh, India. Asian Journal of Conservation, 10(2): 337–342. [jkumar4683@gmail.com]

Mo, M., K. Coutts-McClelland, V. Wilson, R. Haering, L. Oliver, L. Bell, and D. Lunney. 2022. Managing the grey-headed flying-fox as a threatened species in New South Wales two decades on: threats and conservation issues. Australian Zoologist, https://doi.org/10.7882/AZ.2022.024 [matthew.mo@environment.nsw.gov.au]

Mo, M., J. Gregory, V. Wilson, K. Robinson, K. Dodds, and L. Bell. 2022. An investment toward non-lethal crop protection measures for a threatened species in New South Wales: the Flying-fox Netting Subsidy Program. Australian Zoologist, https://doi.org/10.7882/AZ.2022.020 [matthew.mo@environment.nsw.gov.au]

Mollier, S., G. Kunstler, J.-L. Dupouey, and L. Bergès. 2022. Historical landscape matters for threatened species in French mountain forests. Biological Conservation, 269: 109544. https://doi.org/10.1016/j.biocon.2022.109544 [sylvain.mollier@inrae.fr]

Nava-Bolaños, A., L. Osorio-Olvera, and J. Soberón. 2022. Estado del arte del conocimiento de biodiversidad de los polinizadores de México (State of the art of knowledge of pollinators biodiversity in Mexico). Revista Mexicana de Biodiversidad, 93: e933948. http://revista.ib.unam.mx/index.php/bio/article/view/3948 [jsoberon@ku.edu]

Noschese, C. S. G., and R. T. Sánchez. 2021. Reserva provincial Aguas Chiquitas: Nueva área de importancia para la conservación de los murciélagos en Argentina. Boletín de la Red Latinoamericana y del Caribe para la Conservación de los Murciélagos, 12(3): 16–18. [rtesanchez@gmail.com]

Pacheco-Figueroa, C. J., J. d. D. Valdez-Leal, F. A. Cervantes, R. d. C. Luna-Ruíz, E. E. Mata-Zayas, and J. C. Saenz. 2022. Documentation of a road-killed spectral bat (*Vampyrum spectrum*) and first report of the species in Tabasco, México. Therya Notes, 3: 98–103. [juan.valdez@ujat.mx]

Pereira, C. G., F. Falcão, and E. Bernard. 2022. One size doesn't fit all: Singularities in bat species richness and activity patterns in wind-energy complexes in Brazil and implications for environmental assessment. Zoologia (Curitiba), 39: e21041. https://doi.org/10.1590/S1984-4689.v39.e21041 [enrico.bernard@ufpe.br]

Rauchenstein, K., K. Ecker, E. Bader, C. Ginzler, C. Düggelin, F. Bontadina, and M. K. Obrist. 2022. LiDAR metrics predict suitable forest foraging areas of endangered mouse-eared bats (*Myotis myotis*). Forest Ecology and Management, 515: 120210. https://doi.org/10.1016/j.foreco.2022.120210 [katja.rauchenstein@swild.ch]

Teshima, N., K. Kawamura, T. Akasaka, S. Yamanaka, and F. Nakamura. 2022. The response of bats to dispersed retention of broad-leaved trees in harvested conifer plantations in Hokkaido, northern Japan. Forest Ecology and Management, 519: 120300. https://doi.org/10.1016/j.foreco.2022.120300 [mail2taq@gmail.com]

Umbrello, L., R. Bullen, R. Shaw, S. McArthur, M. Byrne, S. van Leeuwen, and K. Ottewell. 2022. Extensive gene flow in a threatened bat (*Rhinonicteris aurantia*) in an arid landscape. Global Ecology and Conservation, 37: e02154. https://doi.org/10.1016/j.gecco.2022.e02154 [linette.umbrello@dbca.wa.gov.au]

Van Harten, E., R. Lawrence, L. F. Lumsden, T. Reardon, and T. A. A. Prowse. 2022. Novel passive detection approach reveals low breeding season survival and apparent lactation cost in a critically endangered cave bat. Scientific Reports, 12: 7390. https://doi.org/10.1038/s41598-022-11404-4 [e.vharten@latrobe.edu.au]

Van Harten, E., R. Lawrence, L. F. Lumsden, T. Reardon, A. F. Bennett, and T. A. A. Prowse. 2022. Seasonal population dynamics and movement patterns of a critically endangered, cave-

dwelling bat, *Miniopterus orianae bassanii*. Wildlife Research, https://doi.org/10.1071/WR21088 [e.vharten@latrobe.edu.au]

Wieringa, J. G. 2022. Comparing predictions of IUCN Red List categories from machine learning and other methods for bats. Journal of Mammalogy, 103(3): 528–539. https://doi.org/10.1093/jmammal/gyac005 [wieringa.3@osu.edu]

DISEASE

Esteves, S. B., N. C. Gaeta, J. M. N. Batista, R. A. Dias, and M. B. Heinemann. 2022. *Leptospira* sp. infection in bats: A systematic review and meta-analysis. Transboundary and Emerging Diseases, pp. 1–18. https://doi.org/10.1111/tbed.14589 [marcosbryan@usp.br]

Jara, L., L. M. Delgado, L. L. Vera, and M. C. San Miguel. 2022. Caracterización epidemiológica de agresiones en humanos por murciélagos. Centro Antirrábico Nacional, Paraguay. Período 2018–2021. Anales De La Facultad De Ciencias Médicas, 55(1): 63–74. https://revistascientificas.una.py/index.php/RP/article/view/2494 [msanmiguel@med.una.py]

Jones, S., T. Bell, C. M. Coleman, D. Harris, G. Woodward, L. Worledge, H. Roberts, L. McElhinney, J. Aegerter, E. Ransome, and V. Savolainen. 2022. Testing bats in rehabilitation for SARS-CoV-2 before release into the wild. Conservation Science and Practice, e12707. https://doi.org/10.1111/csp2.12707 [v.savolainen@imperial.ac.uk]

Juergens, K. B., J. Huckabee, and A. L. Greninger. 2022. Two novel iflaviruses discovered in bat samples in Washington State. Viruses, 14(5): 994. https://doi.org/10.3390/v14050994. [agrening@uw.edu]

Jumbo, S. D., R. N. G. Noumedem, R. P. Namegni, L. God-Yang, I. Dah I, C. Mbu'u Mbanwi, and A. Wade. 2022. Rabies in non-canine species: a retrospective study of laboratory detected cases in the Sahelian Zone of Cameroon from 2014 to 2020. Corpus Journal of Dairy and Veterinary Science, 3(2): 1038. [no author email provided: S. D. Jumbo, National Veterinary Laboratory, PO Box 503, Garoua, Cameroon]

Kaňová, M., H. Banďouchová, E. E. E. Abdelsalam, P. Linhart, J. Sedláčková, V. Seidlová, J. Zukal, and J. Pikula. 2022. Torpor/hibernation cycle may enhance the risk of insecticides for bats: an *in vitro* study. Acta Veterinaria Brno, 91(1): 59–68. [bandouchovah@vfu.cz]

Khan, S. A., M. A. Imtiaz, M. M. Islam, A. Z. Tanzin, A. Islam, and M. M. Hassan. 2022. Major bat-borne zoonotic viral epidemics in Asia and Africa: A systematic review and meta-analysis. Veterinary Medicine and Science, pp. 1–15. https://doi.org/10.1002/vms3.835 [miladhasan@yahoo.com]

Latinne, A., and S. Morand. 2022. Climate anomalies and spillover of bat-borne viral diseases in the Asia–Pacific region and the Arabian peninsula. Viruses, 14(5): 1100. https://doi.org/10.3390/v14051100. [alice.latinne@gmail.com]

Pulscher, L. A, A. J. Peel, K. Rose, J. A. Welbergen, M. L. Baker, V. Boyd, S. Low-Choy, D. Edson, C. Todd, A. Dorrestein, J. Hall, S. Todd, C. C. Broder, L. Yan, K. Xu, G. R. Peck, and D. N. Phalen. 2022. Serological evidence of a pararubulavirus and a betacoronavirus in the geographically isolated Christmas Island flying-fox (*Pteropus natalis*). Transboundary and Emerging Diseases, pp. 1–12. https://doi.org/10.1111/tbed.14579 [laura.pulscher@gmail.com]

Ramanantsalama, R. V., S. M. Goodman, M. Dietrich, and C. Lebarbenchon. 2022. Interaction between Old World fruit bats and humans: From large scale ecosystem services to zoonotic diseases. Acta Tropica, 231: 106462. https://doi.org/10.1016/j.actatropica.2022.106462 [riana.ramanantsalama@univ-reunion.fr]

Silva-Ramos, C. R., S. M. Chala-Quintero, Á. A. Faccini-Martínez, M. Hidalgo, A. d. P. Pulido-Villamarín, J. Pérez-Torres, and C. Cuervo. 2022. Pathogenic *Leptospira* species in bats: molecular detection in a Colombian cave. Tropical Medicine and Infectious Disease, 7(6): 84. https://doi.org/10.3390/tropicalmed7060084 [claudia.cuervo@javeriana.edu.co]

Uribe, M., M. E. Rodríguez-Posada, and G. C. Ramirez-Nieto. 2022. Molecular evidence of orthomyxovirus presence in Colombian Neotropical bats. Frontiers in Microbiology, 13: 845546. https://www.frontiersin.org/articles/10.3389/fmicb.2022.845546/full. [gcramirezn@unal.edu.co]

Zhao, K., W. Zhang, B. Li, S.-Z. Xie, F. Yi, R.-D. Jiang, Y. Luo, X.-Y. He, Y-Z. Zhang, Z.-L. Shi, L.-B. Zhang, and X.-L. Yang. 2022. Ecological study of cave nectar bats reveals low risk of direct transmission of bat viruses to humans. Zoological Research, 43(4): 514–522. https://www.zoores.ac.cn/en/article/doi/10.24272/j.issn.2095-8137.2021.480. [zhanglb@giz.gd.cn]

DISTRIBUTION/FAUNAL STUDIES

Abdullah, N.-I., N.-'A. Elias, F. A. A. Khan, J. C.-C. Huang, and L.-S. Lim. 2022. Bat species in the forests reserves of Penang Island after 2010: with two more new records filed. Journal of Sustainability Science and Management, 17(5): 13–22. [nurizzatiabdullah15@gmail.com]

Abreu, M. D. A. A., V. C. Tavares, and L. M. Moras. 2021. Bat diversity from an area of coastal Atlantic Forest in southeastern Brazil. Check List, 17(6): 1731–1743. https://doi.org/10.15560/17.6.1731 [cecella.abreu@gmail.com]

Akmali, V., M. Shahmohamadi, and P. Karami. 2022. Assessing distribution range and suitable habitat patches in the greater mouse-tailed bat *Rhinopoma microphyllum* (Brünnich 1782) (Chiroptera: Rhinopomatidae) using MaxEnt in Iran. Journal of Animal Research (Iranian Journal of Biology), https://animal.ijbio.ir/article_2154.html?lang=en. [v_akmali@yahoo.com]

Ali, A. 2022. Species diversity of bats (Mammalia: Chiroptera) in Assam, Northeast India. Journal of Wildlife and Biodiversity, 6: https://doi.org/10.5281/zenodo.6603976 [azadali58@yahoo.in]

Aninta, S., S. Noerfahmy, S. Wiantoro, and D. Iskandar. 2022. Natural history collections reveal species richness on a small isolated tropical island: The bats of Siberut. Oryx, 1–4. https://doi.org/10.1017/S0030605321001022. [sagitaninta@gmail.com]

Armstrong, M. P., R. A. King, R. A. Niver, J. S. Utrup, V. Kuczynska, E. D. Thorne, J. De La Cruz, S. M. Deeley, K. M. Gorman, A. Silvis, R. E. Russell, and W. M. Ford. 2022. Addendum 2 – An update to the Indiana bat summer survey level of effort trigger and inclusion of minimum recommended effort for northern long-eared bats. U.S. Fish and Wildlife Service, Region 3, Bloomington, MN. 16 pp. https://www.fws.gov/library/collections/range-wide-indiana-bat-and-northern-long-eared-bat-survey-guidelines [no author email provided]

Bakwo Fils, E. M., K. Z. J. Flora, M. D. Ervis, M. M. Aaron, and J. Decher. 2022. New record and update on the geographic distribution of the Egyptian tomb bat *Taphozous perforatus* (E. Geoffroy, 1818) in Cameroon. Journal of Threatened Taxa, 14(5): 21117–21121. https://doi.org/10.11609/jott.6708.14.5.21117-21121 [filsbkw27@gmail.com]

Chacón Pacheco, J. J., G. A. Salcedo-Rivera, and D. A. Zárrate-Charry. 2022. Mamíferos del departamento de Sucre, Colombia. Biota Colombiana, 23(2): e1022. https://doi.org/10.21068/2539200X.1022 [no author email addresses provided]

Cockar, Z. S. 2022. A checklist of the mammals of Rwanda. Journal of East African Natural History, 111(1): 1–17. https://doi.org/10.2982/028.111.0101 [Kenya Professional Safari Guides Association, P.O. Box 63838, Nairobi, Kenya]

Cramer, V. A., K. N. Armstrong, R. D. Bullen, S. L. Cross, L. Gibson, N. Hanrahan, C. G. Knuckey, K. Ottewell, S. Reiffer, L. Ruykys, R. E. Shaw, R. Thavornkanlapachai, S. A. Thompson, S. Wild, and S. van Leeuwen. 2022. Research priorities for the ghost bat (*Macroderma gigas*) in the Pilbara region of Western Australia. Australian Mammalogy, https://doi.org/10.1071/AM21042 [Stephen.Vanleeuwen@curtin.edu.au]

Dahal, D. R., S. Thapa, D. S. Chand, and N. B. Singh. 2022. Distribution records of Dormer's Bat *Scotozous dormeri* (Dobson, 1875) (Mammalia: Chiroptera: Vespertilionidae) in Nepal. Journal of Threatened Taxa, 14(4): 20903–20907. https://doi.org/10.11609/jott.7730.14.4.20903-20907. [dibaywildlifecon@gmail.com]

De Wint, F. C., M. Cornelis, S. Reynaert, P. A. González, N. Bouillard, R. Gyselings, and L. De Bruyn. 2022. New bat species and records for the Adriatic Islands Vis and Biševo (Croatia). Belgian Journal of Zoology, 152: 99–112. https://doi.org/10.26496/bjz.2022.101 [frederikdewint@hotmail.com]. (Editor's note: "New bat species" does not mean newly-named bat species—rather these are newly discovered on the islands)

Estrada-Villegas, S., L. D. Rivas, J. F. Barrera, S. Barrera-Rivas, D. F. Correa, L. S. Argüello-Bernal, A. M. Aldana, L. F. Casas, A. Lozano-Balcázar, V. Gómez-Bahamón, C. Gómez, N. Bayly, A. E. Jahn, A. Quiñones, E. C. Corbett, F. Castro, and P. Stevenson. 2022. Plant, bird, and mammal diversity of the Tomogrande field station, Vichada, Colombia. Biota Colombiana,

23(2): e1027. http://revistas.humboldt.org.co/index.php/biota/article/view/1027/1118 [sergio.estradavillegas@yale.edu]

Garbino, G. S. T., M. V. Brandão, and V. C. Tavares. 2022. First confirmed records of Godman's long-tailed Bat, *Choeroniscus godmani* (Thomas, 1903) (Chiroptera, Phyllostomidae), from Brazil and Panama. Check List, 18(3): 493–499. https://doi.org/10.15560/18.3.493 [val.c.tavares@gmail.com]

Garbino, G. S. T., and C. A. Piñeros. 2022. First record of *Platyrrhinus albericoi* (Chiroptera: Phyllostomidae) roosting in *Ficus americana* (Moraceae). Notas Sobre Mamíferos Sudamericanos, 4. https://doi.org/10.31687/SaremNMS22.4.1 [guilherme.garbino@ufv.br]

Godio, I., R. Toffoli, D. Trombin, and M. Cucco. 2022. Bats (Mammalia, Chiroptera) from a cave area in NW Italy. Revue suisse de Zoologie, 129(1): 137–145. [marco.cucco@uniupo.it]

Idnan, M., S. Mansoor, M. B. Khawar, A. Javid, A. Hussain, M. Imran, and A. Ullah. 2022. Range extension and species confirmation of *Rhyneptesicus nasutus* (*Sind Serotine Bat*) (Mammalia: Chiroptera) from Bajaur Agency, FATA, Pakistan. Molecular Biology Reports, 49: 1791–1797. https://doi.org/10.1007/s11033-021-06989-4 [adnan264@gmail.com]

Kearny, V. M., R. W. Perry, T. S. Risch, and V. Rolland. 2022. Distribution and roost site selection of eastern small-footed bats (*Myotis leibii*) in mountains of west-central Arkansas. Southeastern Naturalist, 21(2): 74–92. https://doi.org/10.1656/058.021.0201 [vrolland@astate.edu]

López-Cuamatzi, I. L., Y. Hortelano-Moncada, J. Ortega, S. M. Ospina-Garcés, G. Zúñiga, and M. C. Mac Swiney G. 2022. Extension of the distribution of Townsend's big-eared bat, *Corynorhinus townsendii* (Cooper, 1837) Chiroptera, Vespertilionidae, to Chiapas, Mexico. Check List, 18(2): 335–339. https://doi.org/10.15560/18.2.335 [cmacswiney @uv.mx]

Pavé, R., and A. I. Gavazza. 2022. Primer registro de *Myotis simus* (Chiroptera: Vespertilionidae) para la provincial de Santa Fe, Argentina. Revista del Museo Argentino de Ciencias Naturales, new series, 24(1): 99–107. [rominaep@gmail.com]

Paes, J. A. S. V., G. S. T. Garbino, F. V. Oliveira, and M. C. do Nascimento. 2022. New records for Brazil and revised distribution of *Lionycteris spurrelli* (Phyllostomidae: Lonchophyllinae), with notes on its morphological diagnosis. Notas sobre Mamíferos Sudamericanos, 4: e22.5.4. https://ojs.sarem.org.ar/index.php/nms/article/view/821 [jasvpaes@gmail.com]

Silva, C. d. A., R. B. Machado, M. Silveira, and L. M. S. Aguiar. 2022. Listening in the dark: acoustics indices reveal bat species diversity in a tropical savannah. Bioacoustics, https://doi.org/10.1080/09524622.2022.2053741. [aguiar.ludmilla@gmail.com]

ECHOLOCATION

Cao, R., J. Li, and D. Koyabu. 2022. A bibliometric analysis of research trends in bat echolocation studies between 1970 and 2021. Ecological Informatics, 69: 101654. https://doi.org/10.1016/j.ecoinf.2022.101654 [dsk8evoluxion@gmail.com]

Ding, J., Y. Zhang, F. Han, T. Jiang, J. Feng, A. Lin, and Y. Liu. 2022. Adaptive temporal patterns of echolocation and flight behaviors used to fly through varied-sized windows by 2 species of high duty cycle bats. Current Zoology, zoac018, https://doi.org/10.1093/cz/zoac018 [liuy252@nenu.edu.cn]

Eitan, O., M. Weinberg, S. Danilovich, Y. Barkai, R. Assa, and Y. Yovel. 2022. Functional daylight echolocation in highly visual bats. Current Biology, 32(7): R309–R310. https://doi.org/10.1016/j.cub.2022.02.075 [ofrieitan@gmail.com]

Finger, N. M., M. Holderied, and D. S. Jacobs. 2022. Detection distances in desert dwelling, high duty cycle echolocators: A test of the foraging habitat hypothesis. PLoS ONE, 17(5): e0268138. https://doi.org/10.1371/journal.pone.0268138 [david.jacobs@uct.ac.za]

Halley, A. C., M. K. L. Baldwin, D. F. Cooke, M. Englund, C. R. Pineda, T. Schmid, M. M. Yartsev, and L. Krubitzer. 2022. Coevolution of motor cortex and behavioral specializations associated with flight and echolocation in bats. Current Biology, https://doi.org/10.1016/j.cub.2022.04.094 [lakrubitzer@ucdavis.edu]

Kohyt J., A. E. Pierzchła, A. Koza, And K. Piksa. 2022. Resting frequency of echolocation calls within a lesser horseshoe bat population (southern Poland) and its relation to body size, condition and mass. Folia Biologica (Kraków), 70: 33–42. [Joanna.Kohyt@Us.Edu.Pl]

Lara-Nuñez, A. C., J. A. Guerrero, and A. Rizo-Aguilar. 2022. Effect of anthropogenic noise on the echolocation pulses of the bats *Molossus sinaloae* and *Mormoops megalophylla*. Therya, 13(2): 235–243. [areli.rizo@uaem.mx]

Pedersen, M. B., A. S. Uebel, K. Beedholm, I. Foskolos, L. Stidsholt, and P. T. Madsen. 2022. Echolocating Daubenton's bats call louder, but show no spectral jamming avoidance in response to bands of masking noise during a landing task. Journal of Experimental Biology. 225(7): jeb243917. https://doi.org/10.1242/jeb.243917 [michael.pedersen@bio.au.dk]

Rodríguez, J. D., and F. Sánchez. 2022. Physical clutter affects the use of artificial ponds by the lesser bulldog bat *Noctilio albiventris* (Chiroptera: Noctilionidae). Papéis Avulsos de Zoologia, 62: e202262019. https://doi.org/10.11606/1807-0205/2022.62.019 [asbos@gmail.com]

Rubin, J. J. 2022. Darwin's hawkmoth (*Xanthopan praedicta*) responds to bat ultrasound at sonar-jamming rates. Biotropica, 54: 571– 575. https://doi.org/10.1111/btp.13093 [juliettejrubin@gmail.com]

Salles, A. 2022. Bats: Vision or echolocation, why not both? Current Biology, 32(7): R318–R320. https://doi.org/10.1016/j.cub.2022.02.049 [salles@uic.edu]

Teshima, Y., Y. Hasegawa, T. Tsuchiya, R. Moriyama, S. Genda, T. Kawamura, and S. Hiryu. 2022. Reconstruction of echoes reaching bats in flight from arbitrary targets by acoustic simulation. Journal of the Acoustical Society of America, 151(3): 2127–2134. https://doi.org/10.1121/10.0009916 [yuteshima18@gmail.com]

Teshima, Y., Y. Yamada, T. Tsuchiya, O. Heim, and S. Hiryu. 2022. Analysis of echolocation behavior of bats in "echo space" using acoustic simulation. BMC Biology, 20: (Article 59). https://doi.org/10.1186/s12915-022-01253-y [yuteshima18@gmail.com]

ECOLOGY

Aguilar-Rodríguez, P. A., A. Méndez-Rodríguez, S. M. Ospina-Garcés, M. C. MacSwiney G., and Y. Yovel. 2022. Free-ranging Van Gelder's bat *Bauerus dubiaquercus* (Chiroptera: Vespertilionidae) preying on dung beetles in southern Mexico. Mammalia, 86(3): 252–256. https://doi.org/10.1515/mammalia-2021-0060 [ospinagarcess@gmail.com]

Ancillotto, L., D. Pafundi, F. Cappa, G. Chaverri, M. Gamba, R. Cervo, and D. Russo. 2022. Bats mimic hymenopteran insect sounds to deter predators. Current Biology, 32(9): R408–R409. https://doi.org/10.1016/j.cub.2022.03.052 [danrusso@unina.it]

Andersen, B. R., L. P. McGuire, T. B. Wigley, D. A. Miller, and R. D. Stevens. 2022. Habitat associations of overwintering bats in managed pine forest landscapes. Forests, 13(5): 803. https://doi.org/10.3390/f13050803 [brandersen1992@gmail.com]

Barreda, S. 2022. Uso del espacio de los murciélagos insectívoros en un campus universitario en el desierto del Pacífico de Perú. Mammalogy Notes, 7(1): 195. [valerysue.bo@gmail.com]

Castillo-Figueroa, D. 2022. Does Bergmann's rule apply in bats? Evidence from two neotropical [*sic*] species. Neotropical Biodiversity, 8(1): 200–221. https://doi.org/10.1080/23766808.2022.2075530 [dennis.castillof@gmail.com]

Castillo-Figueroa, D., B. A. Tarrá-Jaramillo, M. M. Peñuela-Salgado, C. A. Giraldo-Martínez, and C. H. Rodríguez-León. 2022. First evidence of frugivory in *Gardnerycteris crenulatum* (Chiroptera: Phyllostomidae). Acta Amazonica, 52: 38–41. http://dx.doi.org/10.1590/1809-4392202102151 [dennis.castillof@gmail.com]

De La Cruz, J. L., M. C. True, H. Taylor, D. C. Brown, and W. M. Ford. 2022. Unique land cover classification to assess day-roost habitat selection of northern long-eared bats on the coastal plain of North Carolina, USA. Forests, 13(5): 792. https://doi.org/10.3390/f13050792 [delacruz@vt.edu]

De Oliveira, M. B., H. S. F. de Andrade, J. L.P. Cordeiro, and L. F. B. de Oliveira. 2022. Potential feeding event of *Priodontes maximus* (Cingulata: Dasypodidae) by *Desmodus rotundus* (Chiroptera: Desmodontinae) in the Cerrado, Western Brazil. Notas Sobre Mamíferos Sudamericanos, 4: 10 pp. https://doi.org/10.31687/SaremNMS22.5.1 [oliveira01marcione@gmail.com]

Gorman, K. M., E. L. Barr, T. Nocera, and W. M. Ford. 2022. Characteristics of day-roosts used by northern long-eared bats (*Myotis septentrionalis*) in coastal New York. Northeastern Naturalist, 29(2): 153–170. [no author email provided—Gorman: Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, 149 Cheatham Hall, 310 West Campus Drive, Blacksburg, VA 24061]

Guo, Q., J. Wang, Y. Yang, G. Zhang, W. Liu, H. Niu, and Y. Bu. 2022. Roost selection and ecology of *Hipposideros pomona* in China. Animal Biology, https://brill.com/view/journals/ab/aop/article-10.1163-15707563-bja10081/article-10.1163-15707563-bja10081.xml?ebody=article%20details [no author email provided—Guo: College of Life Science, Henan Normal University, Xinxiang 453007, China]

Humaña, A. M., C. E. Valdivia, A. Jiménez, and R. M. Barahona-Segovia. 2021. *Browningia candelaris* (Meyen) Britton & Rose, un cactus autoincompatible polinizado por colibríes e insectos en el Desierto de Atacama. Gayana. Botánica, 78(2): 131-140. https://dx.doi.org/10.4067/S0717-66432021000200131 [carlos.valdivia@ulagos.cl]. (Editor's note: how a cactus that is elsewhere pollinated by *Platalina genovensium* fares in the absence of that pollinator)

Hurme, E., J. Fahr, B. F. Eric, C. T. Hash, M. T. O'Mara, H. Richter, I. Tanshi, P. W. Webala, N. Weber, M. Wikelski, and D. K. N. Dechmann. 2022. Fruit bat migration matches green wave in seasonal landscapes. Functional Ecology. https://doi.org/10.1111/1365-2435.14097 [ehurme@ab.mpg.de]

Kearny, V. M., R. W. Perry, T. S. Risch, and V. Rolland. 2022. Distribution and roost site selection of eastern small-footed bats (*Myotis leibii*) in mountains of west-central Arkansas. Southeastern Naturalist, 21(2): 74–92. [vrolland@astate.edu]

Lance, R. F., X. Guan, J. F. Swift, C. E. Edwards, D. L. Lindsay. and E. R. Britzke. 2022. Multifaceted DNA metabarcoding of guano to uncover multiple classes of ecological data in two different bat communities. Evolutionary Applications, https://doi.org/10.1111/eva.13425. [richard.f.lance@erdc.dren.mil]

Lin, J., L. S. Harris, M. L. Truan, A. Engilis, Jr., and D. A. Kelt. 2022. Spatiotemporal patterns of riparian bat assemblages in a novel riparian ecosystem. Journal of Mammalogy, 103(3): 512–527. https://doi.org/10.1093/jmammal/gyab170 [dakelt@ucdavis.edu]

Madala, M. F., C. Guna, A. Pradeepan, and A. K. Chalil. 2022. Roost tree characteristics of *Pteropus medius* (Chiroptera: Pteropodidae) in the midland laterite hillocks of northern Kerala, India. Journal of Asia-Pacific Biodiversity, https://doi.org/10.1016/j.japb.2022.04.011. [malikfasil.m@kau.in]

Medina-Bello, K. I., E. Vázquez-Rueda, and J. Ayala-Berdón. 2022. Ecological interaction between *Artibeus jamaicensis* and *Microdesmia arborea* in a deciduous forest of central México. Therya Notes, 3: 115–118. https://doi.org/10.12933/therya_notes-22-81 [jorgeayalaberdon@gmail.com]

Meierhofer, M. B., S. J. Leivers, B. L. Pierce, G. W. Powers, J. W. Evans, and M. L. Morrison. 2022. Structural and environmental predictors of tricolored bat presence and abundance in Texas caves. Journal of Mammalogy, 103(2): 407–414. https://doi.org/10.1093/jmammal/gyab143 [melissa.meierhofer@ag.tamu.edu]

Nava-Bolaños, A., L. Osorio-Olvera, and J. Soberón. 2022. Estado del arte del conocimiento de biodiversidad de los polinizadores de México. Revista Mexicana de Biodiversidad, 93: e933948. [jsoberon@ku.edu]. (Editor's note: almost entirely about insect pollinators)

Pellón, J. J. 2022. Fruits consumed by phyllostomid bats in a Peruvian Yungas forest: new dietary items for *Chiroderma salvini* and *Lonchophylla handleyi*. Mammalia, 86(3): 261–265. https://doi.org/10.1515/mammalia-2021-0121 [juanpe2104@gmail.com]

Presley, S. J., and M. R. Willig. 2022. From island biogeography to landscape and metacommunity ecology: A macroecological perspective of bat communities. Annals of the New York Academy of Sciences, 1–19. https://doi.org/10.1111/nyas.14785 [steven.presley@uconn.edu]

Sazima, I., and M. Sazima. 2022. Two in one: the little bat that pollinates and disperses plants at an urban site in southeastern Brazil. Biota Neotropica [online], 22(2): e20211290. https://doi.org/10.1590/1676-0611-BN-2021-1290 [isazima@gmail.com]

Sucre, S., E. Griffith, M. Castillo, and Á. Sosa-Bartuano. 2022. Predation of a mouse-eared bat, *Myotis* sp. (Chiroptera: Vespertilionidae), by a juvenile mangrove treeboa, *Corallus ruschenbergerii* (Cope 1875) (Squamata: Boidae), in Darién, Panamá. Reptiles & Amphibians, 29: 262–263. [asosa2983@gmail.com]

Villalobos-Chaves, D. and S. E. Santana. 2022. Craniodental traits predict feeding performance and dietary hardness in a community of Neotropical free-tailed bats (Chiroptera: Molossidae). Functional Ecology, pp. 1–10. https://doi.org/10.1111/1365-2435.14063 [dvchaves@uw.edu]

Vivas-Toro, I., and J. A. Mendivil-Nieto. 2022. Daytime diet of the lesser sac-winged bat (*Saccopteryx leptura*) in a Colombian Pacific Island. Therya, 13(2): 153–161. https://www.revistas-conacyt.unam.mx/therya/index.php/THERYA/article/view/2099/html_502 [isavivas94@gmail.com]

EVOLUTION

Cornman, R. S., and P. M. Cryan. 2022. Positively selected genes in the hoary bat (*Lasiurus cinereus*) lineage: prominence of thymus expression, immune and metabolic function, and regions of ancient synteny. PeerJ, 10: e13130. https://doi.org/10.7717/peerj.13130 [rcornman@usgs.gov]

Imlau-Cardoso, R., R. Maestri, L. Duarte, and M. J. R. Pereira. 2022. Diversification of South American Vespertilionidae (Chiroptera) is not constrained by evolutionary priority effects. Biological Journal of the Linnean Society, 136(2): 334–345. https://doi.org/10.1093/biolinnean/blac037 [rafa.i.cardoso@hotmail.com]

López-Aguirre, C., S. J. Hand, N. B. Simmons, and M. T. Silcox. 2022. Untangling the ecological signal in the dental morphology in the bat superfamily Noctilionoidea. Journal of Mammalian Evolution, https://doi.org/10.1007/s10914-022-09606-8. [c.lopezaguirre@utoronto.ca]

Rojas, D., M. A. Borrero-Ospina, and Ó. E. Murillo-García. 2022. Coevolution of brain and palate during the diversification of specialized frugivorous bats. Biological Journal of the Linnean Society, 136(2): 346–353. https://doi.org/10.1093/biolinnean/blac042 [rojasmartin.cu@gmail.com]

Santana, S. E., D. M. Grossnickle, A. Sadier, E. Patterson, and K. E. Sears. 2022. Bat dentitions: a model system for studies at the interface of development, biomechanics, and evolution, integrative and comparative biology. Integrative and Comparative Biology, icac042, https://doi.org/10.1093/icb/icac042. [ssantana@uw.edu]

Vannatta, J. M., and B. D. Carver. 2022. Sexual size dimorphism and geographic variation in forearm length of Rafinesque's big-eared bat (*Corynorhinus rafinesquii*) and southeastern myotis (*Myotis austroriparius*). Mammalia, 86(3): 280–286. https://doi.org/10.1515/mammalia-2021-0033 [jessiwest1@outlook.com]

GENETICS

Chen, W., and X. Mao. 2022. Impacts of seasonality on gene expression in the Chinese horseshoe bat. Ecology and Evolution, 12: e8923. https://onlinelibrary.wiley.com/doi/full/10.1002/ece3.8923 [xgmao@sklec.ecnu.edu.cn]

HIBERNATION

Boyles, J. G., E. M. Johnson, N. W. Fuller, K. A. Silas, L. Hou, W. F. Frick, and L. P. McGuire. 2022. Behavioural microclimate selection and physiological responses to environmental conditions in a hibernating bat. Canadian Journal of Zoology, 100(3): 233–238. https://doi.org/10.1139/cjz-2021-0193 [jgboyles.lab@gmail.com]

McGuire, L. P., N. W. Fuller, C. G. Haase, K. A. Silas, and S. H. Olson. 2022. Lean mass dynamics in hibernating bats and implications for energy and water budgets. Physiological and Biochemical Zoology, 95(4): 317–325. [liam.mcguire@uwaterloo.ca]

Meier, F., L. Grosche, C. Reusch, V. Runkel, J. van Schaik, and G. Kerth. 2022. Long-term individualized monitoring of sympatric bat species reveals distinct species- and demographic differences in hibernation phenology. BMC Ecology and Evolution, 22(7), https://doi.org/10.1186/s12862-022-01962-6 [frauke.meier@icloud.com]

Stachyra, P., M. Piskorski, M. Tchórzewski, K. Łopuszyńska-Stachyra, and R. W. Mysłajek. 2022. Importance of anthropogenic winter roosts for endangered hibernating bats. Journal of Vertebrate Biology, 71(21071): 21071.1–7. [no author email address provided— Mysłajek: Department of Ecology, Institute of Functional Biology and Ecology, Faculty of Biology, University of Warsaw, Biological and Chemical Research Centre, Warszawa, Poland]

HISTORY OF BAT BIOLOGY

Griffiths, T. A. 2022. '*Shout hurrah!*' New thoughts on the origin and meaning of the bat species name *Ia io*, created in 1902 by Oldfield Thomas FRS. Notes and Records—The Royal Society Journal of the History of Science, pp. 1–14. http://doi.org/10.1098/rsnr.2022.0006 [thomas.alan.griffiths@gmail.com]

MIGRATION AND NAVIGATION OF BATS IN FLIGHT

Liberti, W. A., T. A. Schmid, A. Forli, M. Snyder, and M. M. Yartsev. 2022. A stable hippocampal code in freely flying bats. Nature**,** 604: 98–103. https://doi.org/10.1038/s41586-022-04560-0 [myartsev@berkeley.edu]

NATURAL HISTORY

Bellizzi, I. S., S. S. P. da Silva, P. G. Guedes, and J. C. de Almeida. 2022. The natural history of the Stenodermatinae *Chiroderma doriae vizottoi* Taddei and Lim 2010 (Chiroptera, Phyllostomidae) in a semiarid region from Brazil. Mammalia, 86(3): 247–251. https://doi.org/10.1515/mammalia-2021-0022 [pgguedes@gmail.com]

PALEONTOLOGY

Czaplewski, N. J., G. S. Morgan, R. J. Emry, P. M. Gignac, and H. D. O'Brien. 2022. Three new Early Middle Eocene bats (Mammalia: Chiroptera) from Elderberry Canyon, Nevada, USA. Smithsonian Contributions to Paleobiology, no. 106, viii + 26 pages, 11 figures, 3 tables. [nczaplewski@ou.edu]

Kottkamp, S., V. L. Santucci, J. S. Tweet, R. D. Horrocks, and G. S. Morgan. 2022. Pleistocene vertebrates from Carlsbad Caverns National Park, New Mexico. New Mexico Museum of Natural History and Science Bulletin, 88: 267–290. [gary.morgan1@state.nm.us]

Parparousi, E.-M. A. 2022. The Villafranchian mammal fauna of Aghia Kyriaki, Aetoloakarnania, Greece: taxonomy and taphonomy. *Προ/Μεταπτυχιακές Διατριβές στη Βιβλιοθήκη Θεόφραστος του Τμήματος Γεωλογίας του ΑΠΘ*. [no author email provided]

Piñero, P., J. Agustí, C. Laborda, M. Duval, J.-X. Zhao, H.-A. Blain, M. Furió, C. Laplana, A. Rosas, and P. Sevilla. 2022. Quibas-Sima: A unique 1 ma-old vertebrate succession in southern Iberian Peninsula. Quaternary Science Reviews, 283: 107469. https://doi.org/10.1016/j.quascirev.2022.107469 [ppinero@iphes.cat]

Rosina, V., and M. Pickford. 2021. The new small emballonurid (Emballonuridae, Chiroptera, Mammalia) from the Miocene of Africa: its phylogenetic and palaeogeographic implications. Historical Biology, https://doi.org/10.1080/08912963.2021.1973451. [rossina@mail.ru]

PARASITOLOGY

De Araújo, G. R., É. M. de Mello, V. N. G. M. de Oliveira, T. R. dos Santos, R. V. Nunes, H. M. de Andrade, L. F. V. Furtado, and É. M. L. Rabelo. 2022. Bats as hosts of *Leishmania* (*Leishmania*) *infantum* in Minas Gerais, an endemic area for visceral leishmaniasis. Veterinary

Parasitology: Regional Studies and Reports, 32: 100740. https://doi.org/10.1016/j.vprsr.2022.100740 [luis.furtado@uemg.br]

Fernandes, T. F., F. T. de Vasconcelos Melo, and J. N. dos Santos. 2022. The natural interaction between *Myotis nigricans* (Schinz, 1821) and its trematodes: A histopathological analysis. International Journal for Parasitology: Parasites and Wildlife, 18: 112–118. https://doi.org/10.1016/j.ijppaw.2022.04.012 [thayane.fernandes@icb.ufpa.br]

Kirillova, N. Y., S. V. Shchenkov, A. A. Kirillov, and A. B. Ruchin. 2022. Trematodes of genera *Gyrabascus* and *Parabascus* from bats in European Russia: Morphology and molecular phylogeny. Biology, 11(6): 878. https://doi.org/10.3390/biology11060878 [ruchin.alexander@gmail.com]

Stekolnikov, A. 2022. A new genus and species of bat chiggers (Acariformes: Trombiculidae) from Kenya. Acarologia, 62(2): 418–425. https://doi.org/10.1080/08912963.2021.1973451 [no author email provided: Laboratory of Parasitic Arthropods, Zoological Institute of the Russian Academy of Sciences, Universitetskaya embankment 1, St. Petersburg 199034, Russia]

Zamora-Mejías, D., R.-E. Trejo-Salazar, L. E. Eguiarte, M. Ojeda, B. Rodríguez-Herrera, J. B. Morales-Malacara, and R. A. Medellín. 2022. Traveler mites: population genetic structure of the wing mites *Periglischrus paracaligus* (Acari: Mesostigmata: Spinturnicidae). Journal of Medical Entomology, tjac059, https://doi.org/10.1093/jme/tjac059 [dazamoram@gmail.com]

Zamora-Mejías, D., M. Ojeda, R. A. Medellín, B. Rodríguez-Herrera, and J. B. Morales-Malacara. 2022. Morphological variation in the wing mite *Periglischrus paracaligus* (Acari: Spinturnicidae) associated with different moving strategies of the host *Leptonycteris yerbabuenae* (Chiroptera: Phyllostomidae). Journal of Medical Entomology, tjac058, https://doi.org/10.1093/jme/tjac058 [morales.malacara@gmail.com]

PHYSIOLOGY

Fjelldal, M. A., R. Sørås, and C. Stawski. 2022. Universality of torpor expression in bats. Physiological and Biochemical Zoology, 95(4): 326–339. [mari.a.fjelldal@ntnu.no]

Rummel, A. D., S. M. Swartz, R. L. Marsh, and P. A. Faure. 2022. A comparison of thermal sensitivities of wing muscle contractile properties from a temperate and tropical bat species. Journal of Experimental Biology, jeb.243987. https://doi.org/10.1242/jeb.243987 [arummel@princeton.edu]

REPRODUCTION

Kazeem, E. O., O. G. Samuel, and O. O. Bankole. 2022. Reproductive cycle in the male African fruit bat (*Epomops franqueti*). Journal of Entomology and Zoology Studies, 10(1): 395-402. https://doi.org/10.22271/j.ento.2022.v10.i1e.8959 [No author email provided—Kazeem: Department of Veterinary Anatomy, University of Benin, Benin city, Edo state, Nigeria]

Orr, T. J., T. Lukitsch, T. P. Eiting, and P. L. R Brennan. 2022. Testing morphological relationships between female and male copulatory structures in bats. Integrative and Comparative Biology, icac040. https://doi.org/10.1093/icb/icac040 [TeriOrr@nmsu.edu]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Abduriyim, S., T. Kasimu, J.-K. Lan, Z.-L. Pu, J.-L. Bai, and Y.-C. Wang. 2022. Morphological and molecular confirmation of the common pipistrelle bat, *Pipistrellus pipistrellus* Schreber, 1774 (Vespertilionidae: Chiroptera), in Xinjiang, China. Mammalia, 86(3): 298–302. https://doi.org/10.1515/mammalia-2021-0045 [shamshidin@shzu.edu.cn]

Czaplewski, N. J., G. S. Morgan, R. J. Emry, P. M. Gignac, and H. D. O'Brien. 2022. See full citation under **PALEONTOLOGY**. (Editor's note: two new fossil genera and three new fossil species, and a major range extension for species within the fossil genus *Palaeochiropteryx*.)

Jargalsaikhan, A., B. Ariunbold, M. Dalannast, E. Purevee, W. K. Paek, K. Tsagaan, and O. Ganbold. 2022. Molecular phylogenetic analysis of bats in the family Vespertilionidae (Order: Superfamily) [*sic*] in Mongolia. Journal of Asia-Pacific Biodiversity, https://doi.org/10.1016/j.japb.2022.04.006 [f.naumanni13@gmail.com]

Jenkins, P. D., and S. G. Sealy. 2022. The problems of resolving historical specimen data, focusing on a specimen of *Myotis austroriparius* (Mammalia, Chiroptera, Vespertilionidae) collected by Thomas Drummond. Canadian Journal of Zoology, 100(5): 281–295. https://doi.org/10.1139/cjz-2021-0211 [p.jenkins@nhm.ac.uk]

Luo, P.-F., W.-F. Wang, X.-L. Wang, Y.-L. Wang, S.-W. Wang, S.-S. Yan, Q.-Q. He, and J. Zhou. 2022. The complete mitochondrial genome of the great evening bat *Ia io* (Chiroptera: Vespertiilionidae) from karst area, Southwestern China. Mitochondrial DNA Part B, 7(4): 587–589. https://doi.org/10.1080/23802359.2022.2057247 [zhoujiang@ioz.ac.cn]

Novaes, R. L. M., V. C Cláudio, C. Carrión-Bonilla, E. F. Abreu, D. E. Wilson, J. E. Maldonado, and M. Weksler. 2022. Variation in the *Myotis keaysi* complex (Chiroptera, Vespertilionidae), with description of a new species from Ecuador. Journal of Mammalogy, 103(3): 540–559. https://doi.org/10.1093/jmammal/gyab139 [robertoleonan@gmail.com]

Novaes, R. L. M., R. K. LaVal, D. E. Wilson, and R. Moratelli. 2022. Redescription of *Myotis atacamensis* (Chiroptera, Vespertilionidae) with neotype designation. Zoologia (Curitiba) 39, e21026. https://doi.org/10.1590/S1984-4689.v39.e21026 [robertoleonan@gmail.com]

Pietsch, T. W., and B. Marx. 2021. Charles Plumier's (1646–1704) *Vespertilio maximus ex insula Sancti Vincentii*: a previously unpublished description and drawings of the greater bulldog bat, *Noctilio leporinus* (Linnaeus, 1758). Proceedings of the Biological Society of Washington, 134(1): 29-41. https://doi.org/10.2988/006-324X-134.1.yy [twp@uw.edu]

Saha, A., K. Vogt, M. M. Feeroz, and Md. K. Hasan. 2022. A re-discovery of *Coelops frithii* (Chiroptera, Hipposideridae) from its type locality after one and a half century. Mammalia, 86(3): 271-275. https://doi.org/10.1515/mammalia-2021-0092 [aniksaha0090@gmail.com]

Smith, P., and P. Teta. 2022. Confused identities: the case of the chauve–souris septième or chauve–souris brun–blanchâtre of Azara (1801). Therya Notes, 3: 104–109. https://doi.org/10.12933/therya_notes-22-79 [faunaparaguay@gmail.com]

Yu, W., C. Lin, Z. Huang, S. Liu, Q. Wang, R. Quan, S. Li, and Y. Wu. 2022. Discovery of *Kerivoula kachinensis* and a validity of *K. titania* (Chiroptera: Vespertilionidae) in China. Mammalia, 86(3): 303–308. https://doi.org/10.1515/mammalia-2021-0102 [wuyizhouq@263.net]

TEACHING USING BATS

Armour, M. T. 2022. Cladistic analysis lesson using bats. QUBES Educational Resources, https://qubeshub.org/publications/3281/?v=1 [marmour@bridgew.edu]

Morales, K. I. C. M., and M. G. C. Viña. 2022. Conservación de los murciélagos del jardín botánico San Jorge basado en un modelo de educación ambiental: Conservation of the bats of the San Jorge botanical garden based on an environmental education model. Latin American Journal of Development, 4(3): 1023–1033. https://doi.org/10.46814/lajdv4n3-030 [Katerinca07@hotmail.com]

TECHNIQUES FOR STUDYING BATS

Aylen, O., P. J. Bishop, R. bin Hj Abd Wahab, and T. U. Grafe. 2022. Effectiveness of acoustic lures for increasing tropical forest understory bat captures. Ecology and Evolution, 12: e8775. https://doi.org/10.1002/ece3.8775 [o.aylen@unsw.edu.au]

Baumgardt, J. A., M. L. Morrison, L. A. Brennan, H. T. Davis, R. R. Fern, J. M. Szewczak, and T. A. Campbell. 2022. Monitoring occupancy of bats with acoustic data: power and sample size recommendations. Western North American Naturalist, 82(1): 36–49. https://doi.org/10.3398/064.082.0104 [jeremy.baumgardt@tamuk.edu]

Prakash, S., and C. D. Markfort. 2022. A Monte-Carlo based 3-D ballistics model for guiding bat carcass surveys using environmental and turbine operational data. Ecological Modelling, 470: 110029. https://doi.org/10.1016/j.ecolmodel.2022.110029 [corey-markfort@uiowa.edu]

Rydell, J., D. Russo, P. Sewell, E. C. J. Seamark, C. M. Francis, S. L. Fenton, and M. B. Fenton. 2022. Bat selfies: photographic surveys of flying bats. Mammalian Biology, https://doi.org/10.1007/s42991-022-00233-7 [bfenton@uwo.ca]

Taylor, H., K. E. Powers, and E. M. Hallermamn. 2022. Development of a bat guano and acoustic sampling testing protocol to identify species occupying Virginia Department of Transportation bridges. Report Number: FHWA/VTRC 22-R20 https://rosap.ntl.bts.gov/view/dot/61053 http://www.virginiadot.org/vtrc/main/online_reports/pdf/22-r20.pdf

Zadeh, A. T., M. Diyap, J. Moll, and V. Krozer. 2022. Towards localization and classification of birds and bats in windparks using multiple FMCW-radars at Ka-Band. Progress in Electromagnetic Research M, 109: 1–12. [ashkan.taremi@gmail.com]

WHITE-NOSE SYNDROME

Frick, W. F., E. Johnson, T. L. Cheng, J. S. Lankton, R. Warne, J. Dallas, K. L. Parise, J. T. Foster, J. G. Boyles, and L. P. McGuire. 2022. Experimental inoculation trial to determine the effects of temperature and humidity on white-nose syndrome in hibernating bats. Science Reports, 12: 971. https://doi.org/10.1038/s41598-022-04965-x [wfrick@batcon.org]

Jackson, R. T., E. V. Willcox, and R. F. Bernard. 2022. Winter torpor expression varies in four bat species with differential susceptibility to white-nose syndrome. Scientific Reports, 12: 5688. https://doi.org/10.1038/s41598-022-09692-x [rtj006@uark.edu]

Lutsch, K. E., A. G. McDonald, K. T. Gabriel, and C. T. Cornelison. 2022. Roadway-associated culverts may serve as a transmission corridor for *Pseudogymnoascus destructans* and white-nose syndrome in the coastal plains and coastal region of Georgia, USA. Journal of Wildlife Diseases, 58(2): 322–332. https://doi.org/10.7589/JWD-D-21-00069 [ccornel5@kennesaw.edu]

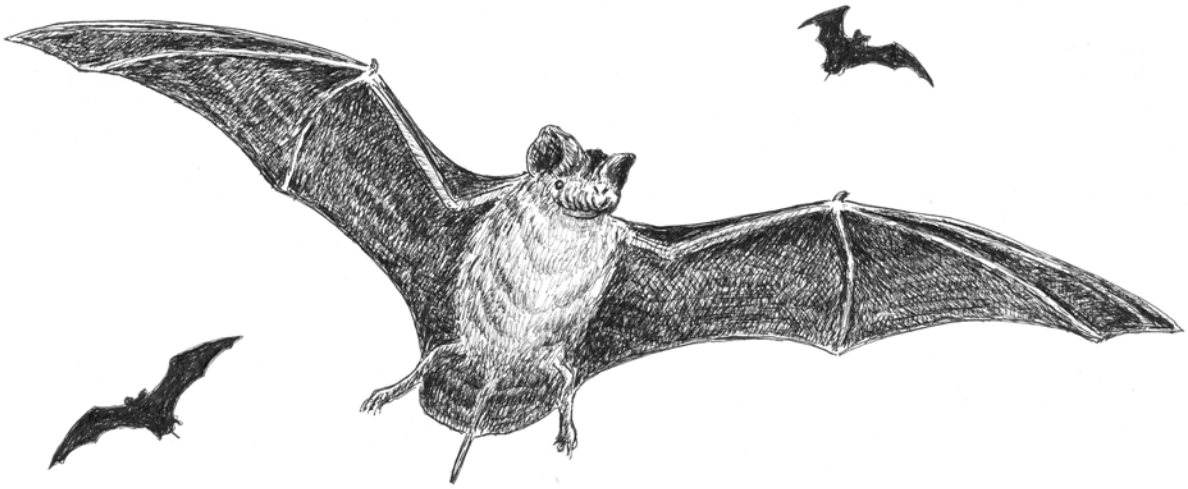
Meteyer, C. U., J. Y. Dutheil, M. K. Keel, J. G. Boyles, and E. H. Stukenbrock. 2022. Plant pathogens provide clues to the potential origin of bat white-nose syndrome *Pseudogymnoascus destructans*. Virulence, https://doi.org/10.1080/21505594.2022.2082139. [meteyerc@gmail.com]

Thapa, V., N. P. Keller, and M. J. Roossinck. 2022. Evaluation of virus-free and wild-type isolates of *Pseudogymnoascus destructans* using a porcine ear model. mSphere, 7(2): 1–10. https://doi.org/10.1128/msphere.01022-21 [no author email provided—Thapa: Department of Plant Pathology and Environmental Microbiology, Center for Infectious Disease Dynamics, Pennsylvania State University, University Park, Pennsylvania, USA]

Wolf, L. K., M. B. Meierhofer, M. L. Morrison, D. M. Cairns, and T. E. Lacher, Jr. 2022. Modeling the suitability of Texas karst regions for infection by *Pseudogymnoascus destructans* in bats. Journal of Mammalogy, 103(3): 503–511. https://doi.org/10.1093/jmammal/gyac017 [lilianna4@gmail.com]

Wray, A. K., C. Gratton, M. A. Jusino, J. J. Wang, J. M. Kochanski, J. M. Palmer, M. T. Banik, D. L. Lindner, and M. Z. Peery. 2022. Disease-related population declines in bats demonstrate non-exchangeability in generalist predators. Ecology and Evolution, 12: e8978. https://doi.org/10.1002/ece3.8978 [amykwray7@gmail.com]

BAT RESEARCH NEWS



VOLUME 63: NO. 3 **FALL 2022**

BAT RESEARCH NEWS

VOLUME 63: NUMBER 3 **FALL 2022**

Table of Contents

Front Cover

Brazilian Free-tailed Bat (*Tadarida brasiliensis*). Drawing courtesy of Chester O. Martin. Originally illustrated as a t-shirt design for the 17th Annual Mississippi Bat working Group Mist Net Event, 2019. Thank you, Chester, for sharing your artwork once again!

RECENT LITERATURE

Authors are requested to send reprints (PDF files) of their published papers to the Editor for Recent Literature, **Dr. Thomas A. Griffiths**, (e-mail: **thomas.alan.griffiths@gmail.com**) for inclusion in this section. Receipt of reprints is preferred, as it will facilitate complete and correct citation. However, if reprints and/or PDF files are unavailable, please send a complete citation (including complete name of journal and corresponding author e-mailing address) by e-mail. The Recent Literature section is based on several bibliographic sources and for obvious reasons can never be up-to-date. Any error or omission is inadvertent. Voluntary contributions for this section, especially from researchers outside the United States, are most welcome and appreciated.

ANATOMY/HISTOLOGY

Alves, J. G. M., M. B. Freitas, J. S. Cruz, and A. Paglia. 2022. O coração de um mamífero voador: características únicas e compartilhadas da anatomia cardíaca do morcego frugívoro *Artibeus lituratus*. (The heart of a flying mammal: unique and shared features of the cardiac anatomy of the fruit bat *Artibeus lituratus*.) Brazilian Journal of Mammalogy, 91: e91202246. https://doi.org/10.32673/bjm.vi91.46 [no author email address provided]

Gaudioso, P. J., M. J. Pérez, R. M. Barquez, J. Arroyo-Cabrales, and M. M. Díaz. 2022. Morphology of the hand skeleton of bats of the genus *Noctilio* (Chiroptera: Noctilionidae). Zoologischer Anzeiger, 300: 65–74. [mariju_perez@hotmail.com]

Geronimo, E., P. M. Favetta, G. C. Palin, W. A. Trindade, G. F. Serenini, L. A. Martins, L. K. Otutumi, and R. M. Germano. 2022. Morphological aspects of the digestive tract of insectivorous bats of the species *Molossus rufus* (E. Geoffroy, 1805). Acta Zoologica, pp. 1–9. https://doi.org/10.1111/azo.12432 [germano@prof.unipar.br]

Pätz, C., L. Console-Meyer, and F. Felmy. 2022. Structural arrangement of auditory brainstem nuclei in the bats *Phyllostomus discolor* and *Carollia perspicillata*. Journal of Comparative Neurology, 530: 2762– 2781. https://doi.org/10.1002/cne.25355 [felix.felmy@tiho-hannover.de]

Smith, T. D., V. B. DeLeon, T. P. Eiting, H. M. Corbin, K. P. Bhatnagar, and S. E. Santana. 2022. Venous networks in the upper airways of bats: A histological and diceCT study. The Anatomical Record, 305(8): 1871–1891. https://doi.org/10.1002/ar.24762 [timothy.smith@sru.edu]

Torrent, L., G. Apoznański, T. Kokurewicz, C. Mitrus, M. De Maegdt, and J. Juste. 2022. First record of polydactyly for a European bat, *Myotis daubentonii* (Chiroptera, Vespertilionidae). Mammalia, 86(5): 501–504. https://doi.org/10.1515/mammalia-2022-0015 [arual.torrent@gmail.com]

Van Engelshoven, M. C., K. C. Brito, A. M. Calouro, and R. S. Verde. 2022. Dorsal hair morphology of some species of bats of southwestern Amazonia (Mammalia: Chiroptera): new

descriptions of the cuticular pattern of guard hairs. Notas Sobre Mamíferos Sudamericanos, 4: https://doi.org/10.31687/SaremNMS22.8.4 [rair.verde@gmail.com]

BATS AND AGRICULTURE

Ancillotto, L., R. Rummo, G. Agostinetto, N. Tommasi, A. P. Garonna, F. de Benedetta, U. Bernardo, A. Galimberti, and D. Russo. 2022. Bats as suppressors of agroforestry pests in beech forests. Forest Ecology and Management, 522: 120467. https://doi.org/10.1016/j.foreco.2022.120467 [danrusso@unina.it]

Harahap, H. A., and Yonariza. 2022. Assessing local farmer's perspectives on the role of bat [sic] in providing ecosystem services in the Batang Toru ecosystem, North Sumatra, Indonesia. Biodiversitas, 23: 4322–4328. https://www.researchgate.net/publication/362925521_Assessing_local_farmer%27s_perspectives_on_the_role_of_bat_in_providing_ecosystem_services_in_the_Batang_Toru_ecosystem_North_Sumatra_Indonesia [yonariza@agr.unand.ac.id]

BAT FLIGHT DESCRIBED IN POETRY

Ionescu, A., and H. A. Al-Khalaf. 2022. A twitch, a twitter, an elastic shudder in flight: kinesthetic empathy in D. H. Lawrence's bat poems. SubStance (Johns Hopkins University Press), 51(2): 21–37. Project MUSE, https://muse.jhu.edu/article/862520.

BEHAVIOR

Bakker, A., B. Jackson, and E. Polla. 2022. Breeding and post-breeding behavior of the ghost bat (*Macroderma gigas*) at Perth Zoo. Journal of Bat Research & Conservation, 15(1): 1–10. https://secemu.org/wp-content/uploads/2022/07/Bakker_et_al_2022.pdf. [aundrealauren11@gmail.com]

Dixon, M. M., P. L. Jones, M. J. Ryan, G. G. Carter, and R. A. Page. 2022. Long-term memory in frog-eating bats. Current Biology, 32(12): R557–R558. https://doi.org/10.1016/j.cub.2022.05.031 [mmdixon@utexas.edu]

Edwards, M. J., C. R. Stanley, C. A. Hosie, S. Richdon, E. Price, D. Wormell, and T. E. Smith. 2022. Social roles influence cortisol levels in captive Livingstone's fruit bats (*Pteropus livingstonii*). Hormones and Behavior, 144: 105228. https://doi.org/10.1016/j.yhbeh.2022.105228 [1821362@chester.ac.uk]

Hanrahan, N., A. H. Dalziell, C. Turbill, K. N. Armstrong, and J. A. Welbergen. 2022. Ethogram of ghost bat (*Macroderma gigas*) behaviours and associated social vocalisations. Acta Chiropterologica, 24(1): 195–208. https://doi.org/10.3161/15081109ACC2022.24.1.016 [nicola.hanrahan@hotmail.com]

Kernan, C. E., A. N. Yiambilis, Z. E. Searcy, R. M. Pulica, R. A. Page, and M. S. Caldwell. 2022. Mid-flight prey switching in the fringed-lipped bat (*Trachops cirrhosus*). The Science of Nature, 109: 43. https://doi.org/10.1007/s00114-022-01813-w [mcaldwel@gettysburg.edu]

BOOKS ON BATS

Bat Rock Habitat Key. 2021. Bat roosts in rock: a guide to identification and assessment for climbers, cavers and ecology professionals. Pelagic Publishing, Exeter, United Kingdom. ISBN 978-1-784-27261-6, 312 pp (paperback). $49.00.

BUMBLEBEE BAT POOP—USED CORRECTLY—IS PRETTY GOOD FERTILIZER

Musa A., M. L. Abu, A. B. Lawal, and A. Uthman. 2022. Soil amendment with graded levels of *Craseonycteris thonglongyai* compost on the concentrations of some phytotoxins in the leaf of *Cnidoscolus aconitifolius* (tree spinach). Tropical Journal of Natural Product Research, 6(2): 265–269. https://tjnpr.org/viewarticle.aspx?articleid=2200 [musaamanabo@gmail.com]

CONSERVATION

Allegrini, C., C. Korine, and B. R. Krasnov. 2022. Insectivorous bats in eastern Mediterranean planted pine forests—Effects of forest structure on foraging activity, diversity, and implications for management practices. Forests, 13(9): 1411. https://doi.org/10.3390/f13091411 [allegrin@post.bgu.ac.il]

Aronson, J. 2022. Current state of knowledge of wind energy impacts on bats in South Africa. Acta Chiropterologica, 24(1): 221–238. https://doi.org/10.3161/15081109ACC2022.24.1.018 [jonathan@camissaconsulting.com]

Ayivor, J. S., E. T. Lawson, F. Ohemeng, and Y. Ntiamoa-Baidu. 2022. Conservation perspectives and perception of bats as reservoirs of zoonotic diseases in Ghana. Human Dimensions of Wildlife, https://www.tandfonline.com/doi/abs/10.1080/10871209.2022.2120650 [jsayivor@staff.ug.edu.gh]

Bach, P., C. C. Voigt, M. Göttsche, L. Bach, V. Brust, R. Hill, O. Hüppop, S. Lagerveld, H. Schmaljohann, and A. Seebens-Hoyer. 2022. Offshore and coastline migration of radio-tagged Nathusius' pipistrelles. Conservation Science and Practice, e12783. https://doi.org/10.1111/csp2.12783 [antje.seebens-hoyer@nabu-mv.de]

Beattie, I., D. Schofer, G. McGregor, M. J. Lee, L. K. F. Lee, C. G. Himsworth, and K. A. Byers. 2022. An investigation of bat mortality in British Columbia, Canada. Canadian Journal of Zoology, 100(7): 464–473. https://doi.org/10.1139/cjz-2021-0230 [kaylee.byers@ubc.ca]

Bolliger, J., J. Haller, B. Wermelinger, S. Blum, and M. K. Obrist. 2022. Contrasting impacts of street light shapes and LED color temperatures on nocturnal insects and bats. Basic and Applied Ecology, https://doi.org/10.1016/j.baae.2022.07.002 [janine.bolliger@wsl.ch]

Brooks, A. C., J. H. Nopper, A. Blakey, M. Ebeling, M. Foudoulakis, and A. Weyers. 2022. Predicted dermal and dietary exposure of bats to pesticides. Environmental Toxicology and Chemistry, 00(00): 1–8. https://pubmed.ncbi.nlm.nih.gov/35866471/ [no author email address provided]

Chiverton, L., R. Cromie, and R. Kock. 2022. European mammal exposure to lead from ammunition and fishing weight sources. Heliyon, 8(8): e10014. https://doi.org/10.1016/j.heliyon.2022.e10014 [louchiv@gmail.com]

Colombo, G. T., R. Di Ponzio, M. Benchimol, C. A. Peres, and P. E. D. Bobrowiec. 2022. Functional diversity and trait filtering of insectivorous bats on forest islands created by an Amazonian mega dam. Functional Ecology, pp. 1–13. https://doi.org/10.1111/1365-2435.14118 [guthiericolombo@gmail.com]

Cú-Vizcarra, J. D., F. Villalobos, M. C. MacSwiney G., V. J. Sosa, and B. Bolívar-Cimé. 2022. The agony of choice: species richness and range size in the determination of hotspots for the conservation of phyllostomid bats. Perspectives in Ecology and Conservation, https://pubag.nal.usda.gov/catalog/7914352 [no author email address provided]

Diengdoh, V. L., S. Ondei, M. Hunt, and B. W. Brook. 2022. Predicted impacts of climate change and extreme temperature events on the future distribution of fruit bat species in Australia. Global Ecology and Conservation, 37: e02181. https://doi.org/10.1016/j.gecco.2022.e02181 [vishesh.diengdoh@utas.edu.au]

Festa, F., L. Ancillotto, L. Santini, M. Pacifici, R. Rocha, N. Toshkova, F. Amorim, A. Benítez-López, A. Domer, D. Hamidović, S. Kramer-Schadt, F. Mathews, V. Radchuk, H. Rebelo, I. Ruczynski, E. Solem, A. Tsoar, D. Russo, and O. Razgour. 2022. Bat responses to climate change: a systematic review. Biological Reviews, https://doi.org/10.1111/brv.12893 [danrusso@unina.it]

Ganesh, T., A. Saravanan, and M. Mathivanan. 2022. Temples and bats in a homogeneous agriculture landscape: Importance of microhabitat availability, disturbance and land use for bat conservation. PLoS One, 17(7): e0251771. https://doi.org/10.1371/journal.pone.0251771 [tganesh@atree.org]

Gregorin, R., A. Tahara, M. Mancini, K. Lobão, L. Oliveira, and V. Tavares. 2022. Mixed sampling methods reveal elevated bat richness in a semideciduous Atlantic Forest remnant. Acta Chiropterologica, 24(1): 139–150. https://doi.org/10.3161/15081109ACC2022.24.1.011 [rgregorin@ufla.br]

Griffiths, S. R., P. E. Lentini, K. Semmens, and K. A. Robert. 2022. "Set and forget" does not work when it comes to fissure roosts carved into live trees for bats. Restoration Ecology, e13751. https://doi.org/10.1111/rec.13751 [s.griffiths@latrobe.edu.au]

Genelhú, S. M. C., A. S. Tahara, L. L. de Oliveira, and R. Gregorin. 2022. Karstic limestone outcrops harbor high bat diversity in a deeply anthropized landscape in southeastern Brazil. Acta Chiropterologica, 24(1): 127–138. https://doi.org/10.3161/15081109ACC2022.24.1.010 [sebastiaogenelhum@gmail.com]

Khandal, D., I. Dhar, D.L. Bohra and S.S. Talmale. 2022. Natural history notes on three bat species. Journal of Threatened Taxa, 14(8): 21501–21507. https://doi.org/10.11609/jott.7995.14.8.21501-21507 [dhar.ishan@gmail.com]

Martin-Regalado, C. N., S. C. Pedersen, and M. C. Lavariega. 2022. Alopecia in bats. Acta Chiropterologica, 24(1): 209–219. https://doi.org/10.3161/15081109ACC2022.24.1.017 [scott.pedersen@sdstate.edu]

Oliveira, H. F. M., G. Fandos, P. L. Zangrandi, H. D. N. Bendini, D. C. Silva, R. L. Muylaert, J. S. Marinho-Filho, L. M. G. Fonseca, P. Rufin, M. Schwieder, and F. M. C. B. Domingos. 2022. Crops, caves, and bats: deforestation and mining threaten an endemic and endangered bat species (Lonchophylla: Phyllostomidae) in the Neotropical savannas. Hystrix, the Italian Journal of Mammalogy, http://www.italian-journal-of-mammalogy.it/Topic-Conservation+and+management/3777 [oliveiradebioh@gmail.com]

Oliveira, J. M., S. S. Condessa, A. L. F. Destro, G. D. A. Lima, M. do Carmo Cupertino, S. A. Cardoso, M. B. Freitas, and L. L. de Oliveira. 2022. Morphophysiological alterations in fruit-eating bats after oral exposure to deltamethrin. International Journal of Experimental Pathology, https://doi.org/10.1111/iep.12455. [leandro.licursi@ufv.br]

Pretorius M., and M. Keith. 2022. The shortfall of using locality records in the conservation planning of South African cavernicolous bats: the Natal long-fingered bat as a case study. African Journal of Wildlife Research, 52: 83–89. https://doi.org/10.3957/056.052.0083 [mark.keith@up.ac.za]

Sangermano, F. 2022. Acoustic diversity of forested landscapes: Relationships to habitat structure and anthropogenic pressure. Landscape and Urban Planning, 226: 104508. https://doi.org/10.1016/j.landurbplan.2022.104508 [fsangermano@clarku.edu]

Schanzer, S., M. Koch, A. Kiefer, T. Jentke, M. Veith, F. Bracher, J. Bracher, and C. Müller. 2022. Analysis of pesticide and persistent organic pollutant residues in German bats. Chemosphere, 305: 135342. https://doi.org/10.1016/j.chemosphere.2022.135342 [christoph.mueller@cup.uni-muenchen.de]

Silva, J. S., N. P. da Silva, E. E. C. Santana, F. A. G. de Andrade, E. da Costa Fraga, M. C. Barros, and A. P. M. Olímpio. 2022. Percepciones populares sobre los murciélagos que obstaculan la acción de conservación en Maranhão, Norte de Brasil. Revista Etnobiologia, 20(2): 270–281. [mbdene@yahoo.com.br]

Sotero, D. F., M. Benvindo-Souza, R. P. de Freitas, and D. de Melo e Silva. 2022. Bats and pollution: Genetic approaches in ecotoxicology. Chemosphere, 307(2): 135934. https://doi.org/10.1016/j.chemosphere.2022.135934 [daianyfolador@discente.ufg.br]

Sritongchuay, T., B. Dalsgaard, K. Wayo, Y. Zou, P. Simla, K. C. Tanalgo, M. C. Orr, and A. C. Hughes. 2022. Landscape-level effects on pollination networks and fruit-set of crops in tropical

small-holder agroecosystems. Agriculture, Ecosystems & Environment, 339: 108112. https://doi.org/10.1016/j.agee.2022.108112 [t.sritongchuay@gmail.com]

Takeda, K., K. Manago, A. Morita, Y. K. Kawai, N. Yasuo, M. Sekijima, Y. Ikenaka, T. Hashimoto, R. Minato, Y. Oyamada, K. Horikoshi, H. Suzuki, M. Ishizuka, S. M.M. Nakayama. 2022. Toxicokinetic analysis of the anticoagulant rodenticides warfarin & diphacinone in Egyptian fruit bats (*Rousettus aegyptiacus*) as a comparative sensitivity assessment for Bonin fruit bats (*Pteropus pselaphon*). Ecotoxicology and Environmental Safety, 243: 113971. https://doi.org/10.1016/j.ecoenv.2022.113971 [shouta-nakayama@vetmed.hokudai.ac.jp]

Wang, W., H. Gao, C. Li, Y. Deng, D. Zhou, Y. Li, W. Zhou, B. Luo, H. Liang, W. Liu, P. Wu, W. Jing, and J. Feng. 2022. Airport noise disturbs foraging behavior of Japanese pipistrelle bats. Ecology and Evolution, 12: e8976. https://doi.org/10.1002/ece3.8976 [fengj@nenu.edu.cn]

Wolf, J. M., J. M. Jeschke, C. C. Voigt, and Y. Itescu. 2022. Urban affinity and its associated traits: A global analysis of bats. Global Change Biology, 28: 5667–5682. https://doi.org/10.1111/gcb.16320 [janis.wolf@uni-greifswald.de]

Wright, P. G. R., T. Kitching, R. Hanniffy, M. B. Palacios, K. McAney, and H. Schofield. 2022. Effect of roost management on populations [sic] trends of *Rhinolophus hipposideros* and *Rhinolophus ferrumequinum* in Britain and Ireland. Conservation Evidence Journal, 19: 21–26. [patrickwright@vwt.org.uk]

DEVELOPMENTAL BIOLOGY/ONTOGENY

Eastick, D. L., S. R. Griffiths, J. D. L. Yen, and K. A. Robert. 2022. Size at birth, postnatal growth, and reproductive timing in an Australian microbat. Integrative Organismal Biology, 4(1): obac030, https://doi.org/10.1093/iob/obac030 [d.eastick@latrobe.edu.au]

DISEASE

Abreu, W. U., L. R. R. Rodrigues, A. C. da Costa, V. dos Santos Morais, A. C. de Paula, and E. A. Barreiros. 2022. Retroviral sequences of interest in veterinary medicine identified in urban bats from the Amazon. Research, Society and Development, 11(10): e394111032993. https://doi.org/10.33448/rsd-v11i10.32993 [uchoa_vet@yahoo.com.br]

Barrón-Rodríguez, R. J., R. Parra-Laca, E. Rojas-Anaya, J. Á. I. Romero-Espinoza, J. T. Ayala-Sumuano, J. A. Vázquez-Pérez, G. García-Espinosa, and E. Loza-Rubio. 2022. Evidence of viral communities in three species of bats from rural environment in Mexico. Acta Chiropterologica, 24(1): 249–264. https://doi.org/10.3161/15081109ACC2022.24.1.020 [eli_rubio33@hotmail.com]

Bueno, L. M., L. S. Rizotto, A. de O. Viana, L. M. N. Silva, M. V. dos S. de Moraes, J. C. Benassi, G. P. Scagion, E. G. Dorlass, B. L. T. Lopes, I. N. Cunha, R. Melinski, I. F. de Alvarenga, G. L. Leitão, R. C. Rodrigues, I. M. da S. Pereira, L. D. N. dos Santos, F. Fisch, A. D. Rocha, D. Port, G. S. Pereira, A. Greatti, A. C. de S. Barnabé, J. Tsukamoto, E. Hingst-Zaher,

S. M. de Azevedo, Jr., W. R. Telino, Jr., J. O. Branco, T. Ometto, J. de Araujo, C. W. Arns, H. L. Ferreira, and E. L. Durigon. 2022. High genetic diversity of alphacoronaviruses in bat species (Mammalia: Chiroptera) from the Atlantic Forest in Brazil. Transboundary and Emerging Diseases, pp. 1–13. https://doi.org/10.1111/tbed.14636 [hlage@usp.br]

Cupertino, M. do C., T. de S. Bayão, M. F. Xisto, S. O. Paula, S. P. Ribeiro, S. S. P. Montenegro, M. B. Freitas, A. P. Gomes, and R. Siqueira-Batista. 2022. Yellow fever virus investigation in tissues of vampire bats *Desmodus rotundus* during a wild yellow fever outbreak in Brazilian Atlantic Forest. Comparative Immunology, Microbiology and Infectious Diseases, 101869. https://doi.org/10.1016/j.cimid.2022.101869 [marlicuppertino@gmail.com]

Fountain, K., A. Barbon, M. J. Gibbon, D. H. Lloyd, A. Loeffler, and E. J. Feil. 2022. *Staphylococcus aureus* lineages associated with a free-ranging population of the fruit bat *Pteropus livingstonii* retained over 25 years in captivity. Scientific Reports, 12: 13457. https://doi.org/10.1038/s41598-022-17835-3 [kay.fountain21@gmail.com]

Gonzalez, V., and A. Banerjee. 2022. Molecular, ecological, and behavioral drivers of the bat-virus relationship. iScience, 25(8): 104779. https://doi.org/10.1016/j.isci.2022.104779 [No author email address provided]

Mantovan, K. B., B. D. Menozzi, L. M. Paiz, A. P. Sevá, P. E. Brandão, and H. Langoni. 2022. Geographic distribution of common vampire bat *Desmodus rotundus* (Chiroptera: Phyllostomidae) shelters: Implications for the spread of rabies virus to cattle in southeastern Brazil. Pathogens, 11(8): 942. https://doi.org/10.3390/pathogens11080942 [karine.bott@unesp.br]

Weinberg, M., and Y. Yovel. 2022. Revising the paradigm: Are bats really pathogen reservoirs or do they possess an efficient immune system? iScience, 25(8):104782. https://doi.org/10.1016/j.isci.2022.104782 [mayababa@gmail.com]

Murakami, S., T. Kitamura, H. Matsugo, T. Yamamoto, K. Mineshita, M. Sakuyama, R. Sasaki, A. Takenaka-Uema, and T. Horimoto. 2022. Detection and genetic characterization of bat MERS-related coronaviruses in Japan. Transboundary and Emerging Diseases, https://doi.org/10.1111/tbed.14695 [shin-murakami@g.ecc.u-tokyo.ac.jp]

Rêgo, A. G. de O. do., D. dos S. Rodrigues, C. K. da S. Farias, A. M. Vieira, L. de O. Franco, R. de C. C. Maia, and L. C. Alves. 2022. Epidemiological profile of anti-rabies post-exposure care from wild animals' aggressions in Pernambuco, Brazil. Research, Society and Development, *[S. l.]*, 11(10): e200111032593. https://rsdjournal.org/index.php/rsd/article/view/32593 [anagabyolive@yahoo.com.br]

Sánchez, C. A., H. Li, K. L. Phelps, C. Zambrana-Torrelio, L.-F. Wang, P. Zhou, Z.-L. Shi, K. J. Olival, and P. Daszak. 2022. A strategy to assess spillover risk of bat SARS-related coronaviruses in Southeast Asia. Nature Communications, 13: 4380. https://doi.org/10.1038/s41467-022-31860-w [daszak@ecohealthalliance.org]

Soupé-Gilbert, M. -E., M. Oedin, M. Kainiu, D. Girault, O. Figuet, F. Brescia, and C. Goarant. 2022. Original *Leptospira* spp. in island's native terrestrial mammals: A case study in *Pteropus* spp. bats of New Caledonia. Transboundary and Emerging Diseases, pp. 1–11. https://doi.org/10.1111/tbed.14635 [msoupe@pasteur.nc]

DISTRIBUTION/FAUNAL STUDIES

Ali, A. 2022. Species diversity of bats (Mammalia: Chiroptera) in Assam, Northeast India. Journal of Wildlife and Biodiversity, 6(3): 115–125. https://doi.org/10.5281/zenodo.6603976 [azadali58@yahoo.in]

Andersen, B. R., and K. Geluso. 2022. Roost characteristics of bats in the Pine Ridge region of Nebraska. Northwestern Naturalist, 103(1): 30–41. https://doi.org/10.1898/1051-1733-103.1.30 [no author email address provided]

Bendjeddou, M. L., I. Bouam, S. Aulagnier, S. E. Abdelaziz, K. Etayeb, A. D. Mihalca, and A. D. Sándor. 2022. First record of the lesser horseshoe bat, *Rhinolophus hipposideros* (Borkhausen, 1797), in Libya and potential distribution in North Africa. Mammalia, 86(4): 328–332. https://doi.org/10.1515/mammalia-2021-0130 [mohammedlaminebendjeddou@gmail.com]

Dahal, D. R., S. Thapa, S. Baral, T. B. Thapa, and N. B. Singh. 2022. First record of East Asian tailless leaf-nosed bat (*Coelops frithii*) from Nepal and extension of its global range. Mammalia, 86(5): 521–523. https://doi.org/10.1515/mammalia-2021-0075 [dibyawildlifecon@gmail.com]

Godlevska, L., S. Rebrov, P. Vorobei, M. Savchenko, and P. Panchenko. 2022. Bats of central Ukraine: a synopsis. Zoodiversity, 56(3): https://doi.org/10.15407/zoo2022.03.203 [lgodlevska@izan.kiev.ua]

Karataş, A., Ş. Bulut, A. Sefali, F. Toprak, M. K. Şahin, and Ş. Ö. Özkurt. 2022. Contributions on the southern distribution of *Vespertilio murinus* Linnaeus, 1758 (Chiroptera: Vespertilionidae) from Türkiye. Turkish Journal of Zoology, 46: https://journals.tubitak.gov.tr/zoology/vol46/iss5/5/. [safak82@gmail.com]

Kobayashi, S., K. Maeda, H. Tamura, and M. Izawa. 2022. First record of the black-bearded tomb bat *Taphozous melanopogon* Temminck, 1841 (Chiroptera: Emballonuridae) from Japan. Mammal Study, 47(4): 1–5. https://doi.org/10.3106/ms2022-0007 [kobashun@sci.u-ryukyu.ac.jp]

Lewis, M. A., E. A. Ferrall, J. S. Johnson, K. M. Morris, N. W. Sharp, J. M. Stober, K. E. Torrey, and A. J. Edelman. Extralimital occurrences of southeastern Myotis in Alabama and Georgia. Southeastern Naturalist, 21(3): 211–219. https://doi.org/10.1656/058.021.0304 [ml574318@ohio.edu]

Mahyudin, A., S. S. Sukiman, S. V. Kumar, and M. Z. Hoque. 2022. Research notes on bats' species assemblage in Madai Cave of Segama Valley, Sabah, Malaysia. Tropical Forestry, 1053: https://iopscience.iop.org/article/10.1088/1755-1315/1053/1/012017 [azniza@ums.edu.my]

Massaad, M., R. da S. Bueno, I. Bentaleb, and T. La Mantia. 2022. Priorities and gaps in Mediterranean bat research evidence: a systematic review for the early twenty-first century. Hystrix, the Italian Journal of Mammalogy, 0. http://www.italian-journal-of-mammalogy.it/Topic-Conservation+and+management/3777. [rafael.dasilveirabueno@unipa.it]

Montgomery, C. B., and A. S. Hogue. 2022. The first confirmed occurrence of *Myotis septentrionalis* (northern long-eared bat) on the Delmarva Peninsula. Northeastern Naturalist, 29(2): N35–N39. https://doi.org/10.1656/045.029.0210 [cjnarang@gmail.com]

Nivelo-Villavicencio, C., F. Sánchez-Karste, D. C. Siddons, and J. F. de Córdova. 2022. Unusual record for greater bulldog bat *Noctilio leporinus* Linnaeus, 1758 (Chiroptera: Noctilionidae) in the southern Andes of Ecuador. ACI: Avances en Ciencias e Ingenieras, 11(19): 34–39. [cvillavicencio@uazuay.edu.ec]

Osorio-Rodriguez, A. N., A. Juárez-Agis, C. Castro-Flores, M. R. González, J. Z. Torres, L. A. G. Lopez, and G. Hernández-Canchola. 2022. Northwesternmost records of *Vampyressa thyone* Thomas, 1909 (Chiroptera, Phyllosrtomidae) from Sierrs de Atoyac, Guerrero, México. Checklist, 18(4): 821–827. [giovani@ciencias.unam.mx]

Paes, J. A. S. V., G. S. T. Garbino, F. V. Oliveira, and M. C. do Nascimento. 2022. New records for Brazil and revised distribution of *Lionycteris spurrelli* (Phyllostomidae: Lonchophyllinae), with notes on its morphological diagnosis. Notas Sobre Mamíferos Sudamericanos, 4:e22.5.4. [jasvpaes@gmail.com]

Palacios-Mosquera, L., V. D. Palacios-Mayoral, Y. del C. Copete-Mosquera, A. M. Jimenez-Ortega, H. Mantilla-Meluk, and P. M. Velazco. 2022. Extensión del rango y mapa de distribución actualizado de *Hsunycteris cadenai* (Chiroptera: Phyllostomidae). Revista De La Academia Colombiana De Ciencias Exactas, Físicas Y Naturales. Recuperado a partir de https://raccefyn.co/index.php/raccefyn/article/view/range-extension-and-distribution-update-of-sunycteris-cadenai-ch [lepamo8@gmail.com]

Pavé, R., A. I. Gavazza, M. E. Rodríguez, S. Ulman, and A. R. Giraudo. 2022. *Cynomops planirostris* (Peters, 1866) y *Myotis albescens* (É. Geoffroy Saint-Hilaire, 1806), nuevas especies de murciélagos para la provincia de Santa Fe, República Argentina. Notas Sobre Mamíferos Sudamericanos, 4: https://doi.org/10.31687/SaremNMS22.8.3 [rominaep@gmail.com]

Portugal-Zegarra, G., G. Calizaya-Mamani, P. Sánchez-Vendizú, M. Flores-Quispe, and J. Ugarte-Núñez. 2022. Distribution extension of *Lasiurus arequipae* Málaga, Díaz, Arias & Medina, 2020 (Chiroptera, Vespertilionidae) and contributions to its natural history. Check List, 18(4): 907–918. https://doi.org/10.15560/18.4.907 [gandalpz182@gmail.com]

Pulido, J. A. B., J. H. Peñuela, M. Franco, H. Villarroel, J. Álvarez, J. García, E. Colón, C. Rabascall, and M. E. Álvarez. 2022. Aportes al conocimiento de los mamíferos, reptiles y anfibios continentales de Araya, Península de Araya, Estado Sucre, Venezuela. (=Contributions to the knowledge of mammals, reptiles and continental amphibians of Araya, Araya Peninsula,

Sucre State, Venezuela). Saber, Universidad de Oriente, Venezuela, 32: 243–260. https://doi.org/10.5281/zenodo.5297241 [jesusantoniobello@gmail.com]

Rodríguez-San Pedro, A., J. A. Ugarte-Núñez, C. Beltrán, and J. L. Allendes. 2022. First record of the Peale's free-tailed bat *Nyctinomops aurispinosus* (Peale, 1848) (Chiroptera, Molossidae) from Chile revealed by acoustic surveys, with notes on ecology and distribution. Mammalia, 86(4): 321–327. https://doi.org/10.1515/mammalia-2021-0123 [arodriguezs@santotomas.cl]

Slough, B. G., C. L. Lausen, B. Paterson, I. J. Hansen, J. P. Thomas, P. M. Kukka, T. S. Jung, J. Rae, and D. van de Wetering. 2022. New records about the diversity, distribution, and seasonal activity patterns by bats in Yukon and northwestern British Columbia. Northwestern Naturalist, 103(2): 162–182. https://doi.org/10.1898/NWN21-10 [no author email address provided]

Smirnov, D., N. Kirillova, A. Kirillov, A. Ruchin, and V. Vekhnik. 2022. New records of *Nyctalus leisleri* (Kuhl, 1817) and *Myotis nattereri* (Kuhl, 1817) (Mammalia: Chiroptera: Vespertilionidae) from National Park "Smolny" and its surroundings, Republic of Mordovia. Journal of Threatened Taxa, 14(8): 21553–21560. https://doi.org/10.11609/jott.6919.14.8.21553-21560 [parasitolog@yandex.ru]

Soni, P. 2022. New roosting site of microbat (*Rhinopoma microphyllum kinneri*) in Khed, Balotra, India. International Journal of Research Publication and Reviews, 3(3): 644–646. [drpreetisoni29@gmail.com]

Valdez-Leal, J. de D., E. S. Hernández-Morales, C. J. Pacheco-Figueroa, F. J. Hernández-Sánchez, and E. J. Moguel-Ordoñez. 2022. Bat community structure in the Tabasco Plain wetlands. Agro Productividad, 15(6): 93–101. https://doi.org/10.32854/agrop.v14i6.2200 [pachecoral@yahoo.com.mx]

Thong, V. D., H. Limbert, and D. Limbert. 2022. First records of bats (Mammalia: Chiroptera) from the world's largest cave in Vietnam. Diversity, 14(7): 534. https://doi.org/10.3390/d14070534 [thongvudinh@gmail.com]

ECHOLOCATION

Kuc, R. 2022. Brain-inspired sensorimotor echolocation system for confident landmark recognition. The Journal of the Acoustical Society of America, 152(1272): https://doi.org/101121/10.0013853 [roman.kuc@yale.edu]

Michaelsen, T. C., J. Rydell, R. Bååth, and K. H. Jensen. 2022. Uncertainty and ignored information in the analysis of bat ultrasound: Bayesian approximation to the rescue. Ecological Informatics, 70: 101721. https://doi.org/10.1016/j.ecoinf.2022.101721 [michaelsen@biometrika.no]

Simmons, A. M., A. Tuninetti, B. M. Yeoh, and J. A. Simmons. 2022. Non-invasive auditory brainstem responses to FM sweeps in awake big brown bats. Journal of Comparative Physiology A, 208: 505–516. https://doi.org/10.1007/s00359-022-01559-w [Andrea_Simmons@brown.edu]

ECOLOGY

Alencastre-Santos, A. B., L. L. Correia, L. M. Sousa, C. R. Silva, and T. B. Vieira. 2022. Opportunistic predation of *Carollia brevicauda* (Schinz, 1821) (Chiroptera: Phylostomidae) by *Marmosa demerarae* (Thomas, 1905) (Marsupialia: Didelphidae) in the Brazilian Amazon. Mammalia, 86(4): 347–350. https://doi.org/10.1515/mammalia-2021-0083 [ana.alencastre.aba@gmail.com]

Amponsah-Mensah, K., A. A. Cunningham, J. L. N. Wood, and Y. Ntiamoa-Baidu. 2022. Roosting behavior and roost selection by *Epomophorus gambianus* (Pteropodidae) in a west African rural landscape. Biotropica, 54: 1030–1041. https://doi.org/10.1111/btp.13127 [mak2kofi@gmail.com]

Andrews, P. T., M. M. Andrews, T. P. McOwat, P. Culyer, R. J. Haycock, A. N. Haycock, D. J. Harries, N. P. Andrews, and R. E. Stebbings. 2022. Foraging time and temperature affected birth timing of *Rhinolophus ferrumequinum* and predicted year-to-year changes for 25 years in a population in West Wales, U.K. Acta Chiropterologica, 24(1): 65–81. https://doi.org/10.3161/15081109ACC2022.24.1.005 [m.m.andrews@ljmu.ac.uk]

Askaripour, N., S. Ashrafi, S. R. Ara, and B. Naimi. 2022. Understanding the summer roosting habitat selection of the greater mouse-tailed bat (*Rhinopoma microphyllum*) and the small mouse-tailed bat (*Rhinopoma muscatellum*) in Iran. Mammal Research, 67: 483–497. https://doi.org/10.1007/s13364-022-00644-4 [sohrab.ashrafi@ut.ac.ir]

Bell, C. P. 2022. Daily, seasonal and inter-annual variation in activity within a common pipistrelle swarming site and hibernaculum. Acta Chiropterologica, 24(1): 103–114. ttps://doi.org/10.3161/15081109ACC2022.24.1.008 [mail@cpbell.co.uk]

Borray-Escalante, N. A., J. Pérez-Torres, and M. E. Castro-Benitez. 2022. Nutritional ecology of *Carollia perspicillata* (Chiroptera: Phyllostomidae): Relationship between the preference and the nutritional content of fruits. Acta Chiropterologica, 24(1): 177–185. https://doi.org/10.3161/15081109ACC2022.24.1.014 [nborray@javeriana.edu.co]

Castillo-Figueroa, D. 2022. Does Bergmann's rule apply in bats? Evidence from two neotropical [sic] species. Neotropical Biodiversity, 8(1): 200–221. https://doi.org/10.1080/23766808.2022.2075530 [dennis.castillof@gmail.com]

Cvecko, P., S. D. Brändel, T. Hiller, A. Rose, J. P. Bechler, R. A. Page, and M. Tschapka. 2022. New architecture of leaf-tents in American oil palms (*Elaeis oleifera*) used by Pacific tent-making bat (*Uroderma convexum*) in Panama. Mammalia, 86(4): 355–358. https://doi.org/10.1515/mammalia-2021-0058 [Patrick.Cvecko@alumni.uni-ulm.de]

Didorenko, S. I., A. D. Botvinkin, and V. V. Takhteev. 2022. *Myotis petax* (Chiroptera, Vespertilionidae) preys on pelagic amphipoda (Crustacea, Gammaroidea) of Lake Baikal. Acta Chiropterologica, 24(1): 187–194. https://doi.org/10.3161/15081109ACC2022.24.1.015 [botvinkin_ismu@mail.ru]

Diggins, C. A., and W. M. Ford. 2022. Seasonal activity patterns of bats in high-elevation conifer sky islands. Acta Chiropterologica, 24(1): 91–101. https://doi.org/10.3161/15081109ACC2022.24.1.007 [cordie1@vt.edu]

Divoll, T. J., V. A. Brown, G. F. McCracken, and J. M. O'Keefe. 2022. Prey size is more representative than prey taxa when measuring dietary overlap in sympatric forest bats. Environmental DNA, pp. 1–13. https://doi.org/10.1002/edn3.354 [timothy.divoll@gmail.com]

Gong, L., Y. Geng, Z. Wang, A. Lin, H. Wu, L. Feng, Z. Huang, H. Wu, J. Feng, and T. Jiang. 2022. Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. iScience, 25(9): 104973. https://doi.org/10.1016/j.isci.2022.104973 [jiangtl730@nenu.edu.cn]

Owen, R. D., C. López-González, and G. G. de Weston. 2022. Sharing the space: variation in morphometric, ecoregional, migratory and reproductive patterns of three sympatric *Artibeus* species. Acta Chiropterologica, 24(1): 51–64. https://doi.org/10.3161/15081109ACC2022.24.1.004 [rowen@pla.net.py]

O'Rourke, D., N. P. Rouillard, K. L. Parise, and J. T. Foster. 2022. Spatial and temporal variation in New Hampshire bat diets. Scientific Reports, 12: 14334. https://doi.org/10.1038/s41598-022-17631-z [devon@outermostlab.com]

Pineda-Lizano, W., and G. Chaverri. 2022. Bat assemblages along an elevational gradient in Costa Rica. Acta Chiropterologica, 24(1): 151–165. https://doi.org/10.3161/15081109ACC2022.24.1.012 [williepineda@gmail.com]

Santos-Moreno, A., and I. Hernández-Aguilar. 2022. Movements of three mormoopid bat species (Chiroptera, Mormoopidae) among three underground roosts in southeastern Mexico. Mammalia, 86(5): 474–482. https://doi.org/10.1515/mammalia-2021-0103 [itandehui0901@gmail.com]

Scherman, S. J., T. S. Risch, and V. Rolland. 2021. Fall and winter activity of two bat species in response to winter flooding and decreasing temperature. Global Ecology and Conservation, 38: e02276. https://doi.org/10.1016/j.gecco.2022.e02276 [SScherman@scprt.com]

Solick, D. I., and R. M. R. Barclay. 2022. Coat color of western long-eared bats (*Myotis evotis*) living in different environments: a test of Gloger's Rule. Northwestern Naturalist, 103(2): 183–189. https://doi.org/10.1898/NWN21-14 [no author email address provided]

Vieira, T. B., L. C. da Silva, M. Oprea, P. Mendes, V. T. Pimenta, D. Brito, C. E. L. Esbérard, L. M. de Souza Aguiar, and A. D. Ditchfield. 2022. Species composition of bats in Brazilian Restingas: Testing environmental versus geographical hypotheses for community composition. Acta Chiropterologica, 24(1): 115–126. https://doi.org/10.3161/15081109ACC2022.24.1.009 [liriannens@gmail.com]

Waag, A. G., J. J. Treanor, J. N. Kropczynski, and J. S. Johnson. 2022. Population sizes and activity patterns of little brown myotis in Yellowstone National Park. Journal of Mammalogy, 103(4): 805–813. https://doi.org/10.1093/jmammal/gyac019 [jjohnson@ohio.edu]

Weissflog, A., L. Markesteijn, A. Aiello, J. Healey, and I. Geipel. 2022. Do prey shape, time of day, and plant trichomes affect the predation rate on plasticine prey in tropical rainforests? Biotropica, pp. 1–11. https://doi.org/10.1111/btp.13150 [anita.weissflog@bangor.ac.uk]

Wibowo, A. A., A. Basukriadi, E. Nurdin, and G. Benhard. 2022. Ecology and microhabitat model of long-tongued fruit bat *Macroglossus minimus* (Chiroptera: Pteropididae) in karst ecosystem of Klapanunggal, Bogor, West Java, Indonesia. International Journal of Tropical Drylands, 6: 11–15. [awbio2021@gmail.com]

EVOLUTION

Frank, H. K., D. Enard, and S. D. Boyd. 2022. Exceptional diversity and selection pressure on coronavirus host receptors in bats compared to other mammals. Proceedings of the Royal Society B. Biological Sciences, 289(1979): http://doi.org/10.1098/rspb.2022.0193 [hkfrank@tulane.edu]

Ospina-Garcés, S. M., and L. León-Paniagua. 2022. The influence of geography in the cranial diversification of the bulldog bats of the genus *Noctilio* (Noctilionidae: Chiroptera). Organisms Diversity & Evolution, https://doi.org/10.1007/s13127-022-00567-7 [llp@ciencias.unam.mx]

Tanshi, I., B. C. Obitte, A. Monadjem, S. J. Rossiter, M. Fisher-Phelps, and T. Kingston. 2022. Multiple dimensions of biodiversity in paleotropical hotspots reveal comparable bat diversity. Biotropica, pp. 1–12. https://doi.org/10.1111/btp.13143 [iroro.tanshi@smacon-africa.org]

Wu, J., L. Zhang, C. Shen, S. Y. W. Sin, C. Lei, and H. Zhao. 2022. Comparative transcriptome analysis reveals molecular adaptations underlying distinct immunity and inverted resting posture in bats. Integrative Zoology, https://doi.org/10.1111/1749-4877.12676 [huabinzhao@whu.edu.cn]

Yohe, L. R., M. Fabbri, D. Lee, K. T. J. Davies, T. P. Yohe, M. K. R. Sánchez, E. M. Rengifo, R. P. Hall, G. Mutumi, B. P. Hedrick, A. Sadier, N. B. Simmons, K. E. Sears, E. Dumont, S. J. Rossiter, B. -A. S. Bhullar, and L. M. Dávalos. 2022. Ecological constraints on highly evolvable olfactory receptor genes and morphology in neotropical [sic] bats. Evolution, https://doi.org/10.1111/evo.14591 [laurel.yohe@yale.edu]

FLIGHT

Cheney, J. A., J. C. Rehm, S. M. Swartz, and K. S. Breuer. 2022. Bats actively modulate membrane compliance to control camber and reduce drag. Journal of Experimental Biology, 225(14): jeb243974. https://doi.org/10.1242/jeb.243974 [jcheney@rvc.ac.uk]

Knight, K. 2022. Membrane muscles tension bat wings for faster flight. Journal of Experimental Biology, 225(14): jeb244731. https://doi.org/10.1242/jeb.244731 [kathryn.knight@biologists.com]

Rahman, A., P. Windes, and D. Tafti. 2022. Turning-ascending flight of a *Hipposideros pratti* bat. Royal Society Open Science, 9: 211788. http://doi.org/10.1098/rsos.211788 [dtafti@exchange.vt.edu]

GENE EXPRESSION

Li, Q., W. Chen, and X. Mao. 2022. Characterization of microRNA and gene expression in the cochlea of an echolocating bat (*Rhinolophus affinis*). Ecology and Evolution, 12: e9025. https://doi.org/10.1002/ece3.9025 [xgmao@sklec.ecnu.edu.cn]

HIBERNATION

Chenery, M., F. Geiser, and C. Stawski. 2022. Thermal biology and roost selection of free-ranging male little forest bats, *Vespadelus vulturnus*, during winter. Journal of Mammalogy, 103(4): 826–834. https://doi.org/10.1093/jmammal/gyac022 [clare.stawski@ntnu.no]

Dzięciołowski, R., G. Wojtaszyn, K. Laskowska-Dzięciołowska, W. Stephan, T. Rutkowski, and G. Lesiński. 2022. Changes in bat abundance in winter roosts close to the Polish-German border in the years 2000-2019: Are the increasing trends continued in central Europe? Acta Zoologica Bulgarica, 74(2): 227–233. http://www.acta-zoologica-bulgarica.eu/2021/002584 [grzegorz_lesinski@sggw.edu.pl]

Kłys, G., Z. Ziembik, and J. Makuchowska-Fryc. 2022. Physical parameters beneficial for grouping of western barbastelle bats into clusters during hibernation. Biogeosciences, https://doi.org/10.5194/bg-2022-159 [no author email address provided]

Muise, K. A. 2022. Hibernating bats may use protein stores for water balance. Journal of Experimental Biology, 225(13): JEB243492. https://doi.org/10.1242/jeb.243492 [kristinamuise@gmail.com]

Sullivan, I. R., D. M. Adams, L. J. S. Greville, P. A. Faure, and G. S. Wilkinson. 2022. Big brown bats experience slower epigenetic ageing during hibernation. Proceedings of the Royal Society B, 289(1980): http://doi.org/10.1098/rspb.2022.0635 [wilkinso@umd.edu]

IMMUNOLOGY

Barr, J., V. Boyd, S. Todd, I. Smith, D. Prada, M. O'Dea, B. Jackson, L. Pearce, T. E. Adams, E. Vanderduys, D. Westcott, A. McKeown, M. L. Baker, and G. A. Marsh. 2022. Detection of filovirus-reactive antibodies in Australian bat species. Journal of General Virology, 103: 001785. https://pubmed.ncbi.nlm.nih.gov/35972225/ [jennifer.barr@csiro.au]

Friedrichs, V., C. Toussaint, A. Schäfer, M. Rissmann, O. Dietrich, T. C. Mettenleiter, G. Pei, A. Balkema-Buschmann, A.-E. Saliba, and A. Dorhoi. 2022. Landscape and age dynamics of

immune cells in the Egyptian rousette bat. Cell Reports, 40(10): 111305. https://doi.org/10.1016/j.celrep.2022.111305 [emmanuel.saliba@helmholtz-hiri.de]

LONGEVITY

Christiansen, J. J. A., D. M. Green, D. J. Bender, D. L. Gummer, M. C. Kalcounis-Rueppell, and R. M. Brigham. 2022. A male little brown myotis (*Myotis lucifugus*) recaptured after 28 years at the same site in southwest Saskatchewan, Canada. The Canadian Field-Naturalist, 136(1): 13–16. [Mark.Brigham@uregina.ca]

MIGRATION

Haddaway, L., and L. P. McGuire. 2022. Seasonal and nightly activity patterns of migrating silver-haired bats (*Lasionycteris noctivagans*) compared to non-migrating big brown bats (*Eptesicus fuscus*) at a fall migration stopover site. Acta Chiropterologica, 24(1): 83–90. https://doi.org/10.3161/15081109ACC2022.24.1.006 [liam.mcguire@uwaterloo.ca]

Vasenkov, D., J.-F. Desmet, I. Popov, and N. Sidorchuk. 2022. Bats can migrate farther than it was previously known: a new longest migration record by Nathusius' pipistrelle *Pipistrellus nathusii* (Chiroptera: Vespertilionidae). Mammalia, 86(5): 524–526. https://doi.org/10.1515/mammalia-2021-0139 [jfdesmet@orange.fr]

NATURAL HISTORY

Khandal, D., I. Dhar, D. L. Bohra, and S. S. Talmale. 2022 . Natural history notes on three bat species. Journal of Threatened Taxa, 14(8): 21501–21507. https://doi.org/10.11609/jott.7995.14.8.21501-21507 [dhar.ishan@gmail.com]. (Editor's note: three species from Rajasthan, India)

Trujillo, L. A., J. G. Martínez-Fonseca, J. Hernández, J. O. Cajas-Castillo, L. Girón-Galván, A. Medina-Fitoria, M. E. Rodríguez, and R. Barahona-Fong. 2022. Notes on the life history of *Centurio senex* (Chiroptera: Phyllostomidae) from northern Central America. Mammalia, 86(5): 468–473. https://doi.org/10.1515/mammalia-2021-0178 [trujillososaluis@gmail.com]

NEUROPHYSIOLOGY

García-Rosales, F., L. López-Jury, E. González-Palomares, J. Wetekam, Y. Cabral-Calderín, A. Kiai, M. Kössl, and J. C. Hechavarría. 2022. Echolocation-related reversal of information flow in a cortical vocalization network. Nature Communications, 13: 3642. https://doi.org/10.1038/s41467-022-31230-6 [francisco.garcia-rosales@esi-frankfurt.de]

López-Jury, L., F. García-Rosales, E. González-Palomares, J. Wetekam, and J. C. Hechavarria. 2022. A neuron model with unbalanced synaptic weights explains asymmetric effects of ketamine in auditory cortex. bioRxiv, https://doi.org/10.1101/2022.06.12.495822 [lopezjury@bio.uni-frankfurt.de]

Macias, S., K. Bakshi, T. Troyer, and M. Smotherman. 2022. The prefrontal cortex of the Mexican free-tailed bat is more selective to communication calls than primary auditory cortex.

Journal of Neurophysiology, 128(3): 634–648. https://doi.org/10.1152/jn.00436.2021 [smacias@bio.tamu.edu]

Pastyrik, J. D., and U. Firzlaff. 2022. Object-specific adaptation in the auditory cortex of bats. Journal of Neurophysiology, 128(3): 556–567. https://doi.org/10.1152/jn.00151.2022 [jan.pastyrik@tum.de]

Sarel, A., S. Palgi, D. Blum, J. Aljadeff, L. Las, and N. Ulanovsky. 2022. Natural switches in behaviour rapidly modulate hippocampal coding. Nature, 609: 119–127. https://doi.org/10.1038/s41586-022-05112-2 [nachum.ulanovsky@weizmann.ac.il]

PALEONTOLOGY

García, J. G., S. Bañuls-Cardona, G. Cuenca-Bescós, and J. M. Vergès. 2022. Understanding the biogeography of Western European bats: the latest Pleistocene to Middle Holocene assemblage of El Mirador site (Sierra de Atapuerca, Spain). Historical Biology, https://doi.org/10.1080/08912963.2022.2107430 [julia.galan@ehu.eus]

PARASITOLOGY

Carvajal-Agudelo, J. D., H. E. Ramírez-Chaves, P. A. Ossa-López, and F. A. Rivera-Páez. 2022. Bacteria related to tick-borne pathogen assemblages in *Ornithodoros* cf. *hasei* (Acari: Argasidae) and blood of the wild mammal hosts in the Orinoquia region, Colombia. Experimental and Applied Acarology, 87: 253–271. https://doi.org/10.1007/s10493-022-00724-9 [fredy.rivera@ucaldas.edu.co]

Couso-Pérez, S., X. Pardavila, E. Ares-Mazás, and H. Gómez-Couso. 2022. Molecular identification of *Eimeria* species in Spanish bats. Parasitology International, 91: 102621. https://doi.org/10.1016/j.parint.2022.102621 [hipolito.gomez@usc.es]

Dolabela Falcão, L. A., W. S. Araújo, L. O. Leite, M. Fagundes, M. M. Espírito-Santo, M. A. Zazá-Borges, P. Vasconcelos, G. W. Fernandes, and A. Paglia. 2022. Network structure of bat-ectoparasitic interactions in tropical dry forests at two different regions in Brazil. Acta Chiropterologica, 24(1): 239–248. https://doi.org/10.3161/15081109ACC2022.24.1.019 [luizdolabelafalcao@gmail.com]

Fajri, S. R., and S. Armiani. 2022. Identification of ectoparasitic bats in Buwun Cave. Jurnal Biologi Tropis, 22(3): 740–745. https://doi.org/10.29303/jbt.v22i3.3702 [sitirabiatulfajri@undikma.ac.id]

Ivanova-Aleksandrova, N., H. Dundarova, B. Neov, R. Emilova, I. Georgieva, R. Antova, K. Kirov, J. Pikula, K. Zukalová, and J. Zukal. 2022. Ectoparasites of cave-dwelling bat species in Bulgaria. Proceedings of the Zoological Society, https://doi.org/10.1007/s12595-022-00451-4 [heliana.dundarova@iber.bas.bg]

Kamani, J., Y. J. Atuman, D. A. Oche, A. Shekaro, O. Werb, I. Ejotre, and J. Schaer. 2022. Molecular detection of *Trypanosoma* spp. and *Hepatocystis* parasite infections of bats in

northern Nigeria. Parasitology, 1–8. https://pubmed.ncbi.nlm.nih.gov/35822266/ [schaerju@hu-berlin.de]

Ramos, L. G. S. M., V. A. Costa, N. M. Louzeiro, C. C. A. Carvalho, R. de Maria Seabra Nogueira, M. A. Speranca, A. D. Cabral, F. B. Costa, M. C. Barros, E. da Costa Fraga, A. Marcili, and A. P. da Costa. 2022. Chiropterans as a potential hosts of *Leishmania* spp. in endemic areas for leishmaniasis in northeastern Brazil. Zoonoses and Public Health, pp. 1– 6. https://doi.org/10.1111/zph.12997 [andrea.costa@professor.uema.br]

Rosyadi, I., H. Shimoda, A. Takano, T. Yanagida, and H. Sato. 2022. Isolation and molecular characterization of *Polychromophilus* spp. (Haemosporida: Plasmodiidae) from the Asian long-fingered bat (*Miniopterus fuliginosus*) and Japanese large-footed bat (*Myotis macrodactylus*) in Japan. Parasitology Research, 121: 2547–2559. https://doi.org/10.1007/s00436-022-07592-7 [sato7dp4@yamaguchi-u.ac.jp]

Speer, K. A., T. S. M. Teixeira, A. M. Brown, S. L. Perkins, K. Dittmar, M. R. Ingala, C. Wultsch, K. Krampis, C. W. Dick, S. C. Galen, N. B. Simmons, and E. L. Claire. 2022. Cascading effects of habitat loss on ectoparasite-associated bacterial microbiomes. ISME Communications, 2: 67. https://doi.org/10.1038/s43705-022-00153-0 [speerk@si.edu]

Toshkova, N., B. Zlatkov, A. Fakirova, V. Zhelyazkova, and N. Simov. 2022. First record of *Psorergatoides* Fain, 1959 (Acari, Cheyletoidea, Psorergatidae) for the Balkan Peninsula with description of the cutaneous lesions on the wing membrane of its hosts *Myotis myotis* (Borkhausen, 1797) and *Myotis blythii* (Tomes, 1857) (Chiroptera, Vespertilionidae). Biodiversity Data Journal, 10: e89514. https://doi.org/10.3897/BDJ.10.e89514 [nia.toshkova@iber.bas.bg]

Urbieta, G. L., G. Graciolli, and V. da Cunha Tavares. 2022. Review of studies about bat-fly interactions inside roosts, with observations on partnership patterns for publications. Parasitology Research, https://doi.org/10.1007/s00436-022-07635-z [gustavo.cx@hotmail.com]

PHYSIOLOGY

Balzer, E. W., A. D. Grottoli, L. E. Burns, and H. G. Broders. 2022. Active season body mass patterns of little brown and northern myotis bats. Ecology and Evolution, 12: e9230. https://doi.org/10.1002/ece3.9230 [hugh.broders@uwaterloo.ca]

Hornok, S., R. Berkecz, E. Sós, A. D. Sándor, T. Körmöczi, N. Solymosi, J. Kontschán, and A. Hunyadi. 2022. Arthropod moulting hormones (ecdysteroids) are present in the blood of insectivorous bats. Mammal Review, 52: 317–321. https://doi.org/10.1111/mam.12283 [hornok.sandor@univet.hu]

Montiani-Ferreira, F., C. E. Plummer, and E. Adkins. 2022. Ophthalmology of Chiroptera: Bats. *In* F. Montiani-Ferreira, B. A. Moore, and G. Ben-Shlomo, Eds. Wild and Exotic Animal Ophthalmology. Springer, https://doi.org/10.1007/978-3-030-81273-7_15 [montiani@ufpr.br]

POPULATION GENETICS

Gutiérrez, E. G., B. Rodríguez-Herrera, J. A. Baeza, Ma. I. Salazar, and J. Ortega. Genetic analyses reveal high connectivity among populations of the Honduran white bat *Ectophylla alba* in the Caribbean lowlands of central eastern Costa Rica. Acta Chiropterologica, 24(1): 41–50. https://doi.org/10.3161/15081109ACC2022.24.1.003 [artibeus2@aol.com]

REPRODUCTION

Pretorius, M., H. Broders, G. Hall, and M. Keith. 2022. Reproductive status affects isotopic niches of *Miniopterus natalensis* in northeastern South Africa. Journal of Mammalogy, 103(4): 795–804. https://doi.org/10.1093/jmammal/gyac049 [mark.keith@up.ac.za]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Curran, M., M. Kopp, M. Ruedi, and J. Bayliss. 2022. A new species of horseshoe bat (Chiroptera: Rhinolophidae) from Mount Namuli, Mozambique. Acta Chiropterologica, 24(1): 19–40. https://doi.org/10.3161/15081109ACC2022.24.1.002 [michael.curran@fibl.org]

Kusuminda, T., A. Mannakkara, K. D. B. Ukuwela, S. V. Kruskop, C. J. Amarasinghe, U. Saikia, P. Venugopal, M. Karunarathna, R. Gamage, M. Ruedi, G. Csorba, W. B. Yapa, and B. D. Patterson. 2022. DNA barcoding and morphological analyses reveal a cryptic species of *Miniopterus* from India and Sri Lanka. Acta Chiropterologica, 24(1): 1–17. https://doi.org/10.3161/15081109ACC2022.24.1.001 [t.kusuminda@gmail.com]

Novaes, R. L. M., D. E. Wilson, and R. Moratelli. 2022. Catalogue of primary types of Neotropical *Myotis* (Chiroptera, Vespertilionidae). ZooKeys, 1105: 127–164. https://doi.org/10.3897/zookeys.1105.85055 [robertoleonan@gmail.com]

Ruelas, D., and V. Pacheco. 2022. Variación intraespecífica de *Carollia brevicaudum* y *Carollia perspicillata* (Phyllostomidae: Chiroptera) de Perú y Ecuador. Neotropical Biodiversity, 8(1): 253–266. https://doi.org/10.1080/23766808.2022.2093816 [druelasp@unmsm.edu.pe]

Saikia, S., M. Ruedi, and G. Csorba. 2022. Out of southeast Asia: A new species of thick-thumbed bat (Chiroptera: Vespertilionidae: *Glischropus*) from Meghalaya, north-eastern India. Zootaxa, https://pubmed.ncbi.nlm.nih.gov/36095616/ [no author email provided]

Soisook, P., and P. J. J. Bates. 2022. Replacement name (nomen novum) for *Rhinolophus monticolus* Soisook et al., 2016. Mammalia, 86(5) 539–539. https://doi.org/10.1515/mammalia-2022-0012 [pipat66@gmail.com]

Souza, J. K. de, R.F. de Sousa, J. M. da Silva, and K. de C. Faria. 2022. Citogenética e morfometria com morcegos dos gêneros *Phyllostomus* e *Phylloderma*. (Cytogenetics and morphometry with bats of the genera *Phyllostomus* and *Phylloderma*.) Brazilian Journal of Development, 8(8): 55392–55411. https://doi.org/10.34117/bjdv8n8-046 [jasciene.kraemer@unemat.br]

Yi, X., and E. K. Latch. 2022. Systematics of the New World bats *Eptesicus* and *Histiotus* suggest *trans*-marine dispersal followed by Neotropical cryptic diversification. Molecular Phylogenetics and Evolution, 175: 107582. https://doi.org/10.1016/j.ympev.2022.107582 [xyi@uwm.edu]

TECHNIQUES FOR STUDYING BATS

Bellafkir, H., M. Vogelbacher, J. Gottwald, M. Mühling, N. Korfhage, P. Lampe, N. Frieß, T. Nauss, and B. Freisleben. 2022. Bat echolocation call detection and species recognition by transformers with self-attention. *In*: Bennour, A., Ensari, T., Kessentini, Y., Eom, S. (eds) Intelligent Systems and Pattern Recognition. ISPR 2022. Communications in Computer and Information Science, vol 1589. Springer, Cham. https://doi.org/10.1007/978-3-031-08277-1_16 [bellafkir@informatik.uni-marburg.de]

De Lavor, C. S., F. dos S. Queiroz, P. S. Bacelar, A. T. M. Rosa, and M. C. Diniz. 2022. Prospecção tecnológica sobre estudos bioacústicos em morcegos. (Technological prospecting on bioacoustic studies in bats.). Journal of Biotechnology and Biodiversity, 10(2): 137–143. https://doi.org/10.20873/jbb.uft.cemaf.v10n2.lavor [cristine.vanzb@gmail.com]

Görföl, T., J. C.-C. Huang, G. Csorba, D. Győrössy, P. Estók, T. Kingston, K. L. Szabadi, E. McArthur, J. Senawi, N. M. Furey, V. T. Tu, V. D. Thong, F. A. A. Khan, E. R. Jinggong, M. Donnelly, J. V. Kumaran, J.-N. Liu, S.-F. Chen, M.-N. Tuanmu, Y.-Y. Ho, H.-C. Chang, N.-A. Elias, N. I. Abdullah, L.-S. Lim, C. D. Squire, and S. Zsebfik. 2022. ChiroVox: a public library of bat calls. PeerJ, 10: e12445. http://doi.org/10.7717/peerj.12445 [tamas@gorfol.eu]

Khalighifar, A., B. S. Gotthold, E. Adams, J. Barnett, L. O. Beard, E. R. Britzke, P. A. Burger, K. Chase, Z. Cordes, P. M. Cryan, E. Ferrall, C. T. Fill, S. E. Gibson, G. S. Haulton, K. M. Irvine, L. S. Katz, W. L. Kendall, C. A. Long, O. Mac Aodha, T. McBurney, S. McCarthy, M. W. McKown, J. O'Keefe, L. D. Patterson, K. A. Pitcher, M. Rustand, J. L. Segers, K. Seppanen, J. L. Siemers, C. Stratton, B. R. Straw, T. J. Weller, and B. E. Reichert. 2022. *NABat ML*: Utilizing deep learning to enable crowdsourced development of automated, scalable solutions for documenting North American bat populations. Journal of Applied Ecology, https://doi.org/10.1111/1365-2664.14280 [a.khalighifar@colostate.edu]

Luciano, B. F. L., G. A. Elias, J. J. Zocche, E. M. Costa Neto, and F. Carvalho. 2022. The scientific literature on bats (chiroptera) in Brazil: a scientometric analysis from 1954 – 2018. Anais da Academia Brasileira de Ciências, 94(4): e20211621. https://pubmed.ncbi.nlm.nih.gov/35830073/ [beatrizfll@unesc.net]

McCarthy, E. D., J. M. Martin, M. M. Boer, and J. A. Welbergen. 2022. Ground-based counting methods underestimate true numbers of a threatened colonial mammal: an evaluation using drone-based thermal surveys as a reference. Wildlife Research, https://doi.org/10.1071/WR21120 [eliane.mccarthy@sydney.edu.au]

Schorr, R. A., M. D. Matthews, and B. A. Hoover. 2022. Finding bat roosts along cliffs: using rock climbing surveys to identify roosting habitat of bats. Acta Chiropterologica, 24(1): 167–176. https://doi.org/10.3161/15081109ACC2022.24.1.013 [robert.schorr@colostate.edu]

Silva, B., F. Mestre, S. Barreiro, P. J. Alves, and J. M. Herrera. 2022. SoundClass: An automatic sound classification tool for biodiversity monitoring using machine learning. Methods in Ecology and Evolution, pp. 1–7. https://doi.org/10.1111/2041-210X.13964 [bmsasilva@gmail.com]

WHITE-NOSE SYNDROME

Forsythe, A., N. Fontaine, J. Bissonnette, B. Hayashi, C. Insuk, S. Ghosh, G. Kam, A. Wong, C. Lausen, J. Xu, and N. Cheeptham. 2022. Microbial isolates with anti-*Pseudogymnoascus destructans* activities from western Canadian bat wings. Scientific Reports, 12: 9895. https://doi.org/10.1038/s41598-022-14223-9 [clausen@wcs.org]

Grider, J., W. E. Thogmartin, E. H. C. Grant, R. F. Bernard, and R. E. Russell. 2022. Early treatment of white-nose syndrome is necessary to stop population decline. Journal of Applied Ecology, pp. 1–11. https://doi.org/10.1111/1365-2664.14254 [jfgrider@colostate.edu]

Jackson, R. T., E. V. Willcox, J. M. Zobel, and R. F. Bernard. 2022. Emergence activity at hibernacula differs among four bat species affected by white-nose syndrome. Ecology and Evolution, 12: e9113. https://doi.org/10.1002/ece3.9113 [rtj006@uark.edu]

Kalen, N. J., M. S. Muthersbaugh, J. B. Johnson, A. Silvis, and W. M. Ford. 2022. Northern long-eared bats in the central Appalachians following white-nose syndrome: Failed maternity colonies? Journal of the Southeastern Association of Fish and Wildlife Agencies, 9: 159–167. [nickkalen@gmail.com]

Lewis, M. A., G. G. Turner, M. R. Scafini, and J. S. Johnson. 2022. Seasonal roost selection and activity of a remnant population of northern myotis in Pennsylvania. PLoS One, 17(7): e0270478. https://doi.org/10.1371/journal.pone.0270478 [joseph.johnson@uc.edu]

Loeb, S. C., and E. A. Winters. 2022. Changes in hibernating tricolored bat (*Perimyotis subflavus*) roosting behavior in response to white-nose syndrome. Ecology and Evolution, 12: e9045. https://doi.org/10.1002/ece3.9045 [susan.loeb@usda.gov]

Niessen, L., M. Fritze, G. Wibbelt, and S. J. Puechmaille. 2022. Development and application of loop-mediated isothermal amplification (LAMP) assays for rapid diagnosis of the bat white-nose disease fungus *Pseudogymnoascus destructans*. Mycopathologia, https://doi.org/10.1007/s11046-022-00650-9 [niessen@mytum.de]

Perea, S., J. A. Yearout, E. A. Ferrall, K. M. Morris, J. T. Pynne, and S. B. Castleberry. 2022. Seven-year impact of white-nose syndrome on tri-colored bat (*Perimyotis subflavus*) populations in Georgia, USA. Endangered Species Research, 48: 99–106. https://doi.org/10.3354/esr01189 [scastle@uga.edu]

Perry, R. W., and P. N. Jordan. 2022. Changes in the forest bat community after arrival of white-nose syndrome in the Ouachita Mountains of Arkansas. Southeastern Naturalist, 21(2): 107–115. [rperry03@fs.fed.us]

ANNOUNCEMENTS

Change of Address Requested

Will you be moving in the near future or changing your e-mail address? If so, please **send** your **new postal and e-mail addresses** to Margaret Griffiths (margaret.griffiths01@gmail.com), and include the date on which the change will become effective. Thank you in advance!

Request for News

Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Request for Manuscripts — *Bat Research News*

Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

Back Issues of *Bat Research News*

Many back issues are available on the *Bat Research News* website. The five most recent issues remain available to current subscribers only. To download back issues, click on the "Past Volumes" link found on the home page, and then on the volume you would like to download. I am working on adding more past issues to the site so stay tuned. If you or someone you know need back issues not available on the *BRN* site, please contact the Managing Editor, Margaret Griffiths (margaret.griffiths01@gmail.com).

FUTURE MEETINGS and EVENTS

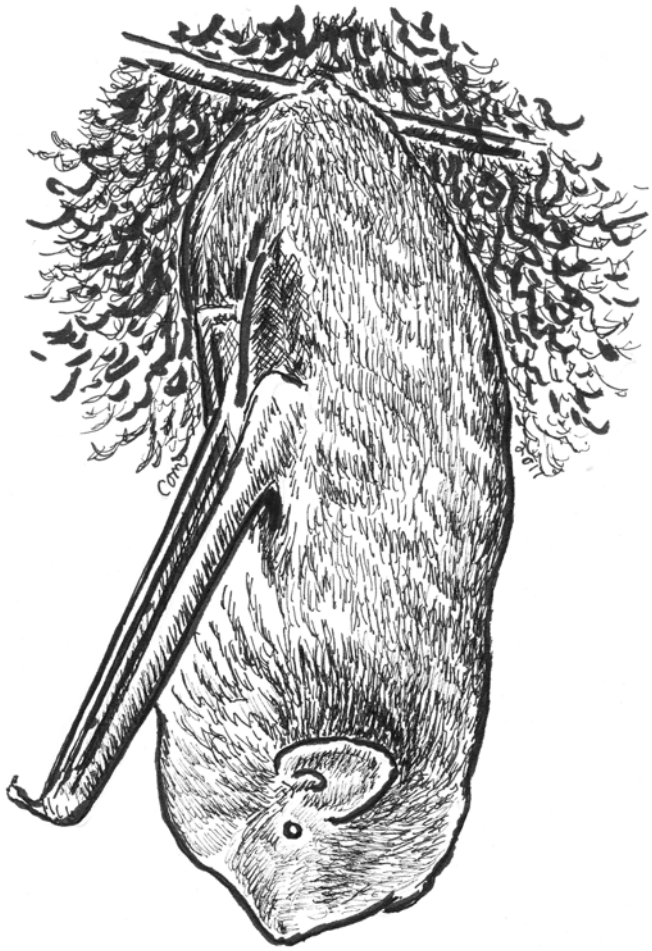
ALL Professional Meetings and Events

Please check the websites of all professional societies regarding meetings. Given the rapidly changing situation of the COVID-19 pandemic, decisions as to whether professional meetings will be face-to-face, virtual, or hybrid during the year are updated on the respective website.

2023

The Annual NASBR meeting will be held 11–14 October 2023, at the Fort Garry Hotel, in Winnipeg, Manitoba, Canada. Check the NASBR website for updates — https://www.nasbr.org/.

BAT RESEARCH NEWS



VOLUME 63: NO. 4 WINTER 2022

BAT RESEARCH NEWS

VOLUME 63: NUMBER 4 **WINTER 2022**

Table of Contents

Front Cover

Seminole Bat (*Lasiurus seminolus*). Drawing courtesy of Chester O. Martin. Originally illustrated as a t-shirt design for the 14th Annual Mississippi Bat Working Group Mist Net Event, 2017. Thank you, Chester, for sharing your artwork once again!

Observations of an Infundibular Recess in Vampire Bats

Kunwar P. Bhatnagar[1, †] and Timothy D. Smith[2]

[1]*Department of Anatomical Sciences and Neurobiology, University of Louisville, Louisville, Kentucky 40241*; *and*
[2]*School of Physical Therapy, Slippery Rock University, Slippery Rock, PA 16057*
[†] *Deceased*

E-mail: timothy.smith@sru.edu

The infundibular recess (IR) is an extension of the third ventricle that projects into the infundibular stalk of the posterior lobe of the pituitary but not into the pars nervosa itself. Like the ventricles, the IR is filled with cerebrospinal fluid (CSF) and brings the cerebroventricular passages closer to the hypophyseal portal system (Caraty and Skinner, 2008). The portal system transports blood from the median eminence of the hypothalamus to the anterior pituitary. The median eminence is home to neurons that secrete hypothalamic hormones, such as gonadotropin-releasing hormone, which can be released into either the blood of the portal system or into the CSF (Caraty and Skinner, 2008; Yin and Gore, 2010). Thus, the IR may be part of an endocrine pathway by which the hypothalamus sends signals to the anterior pituitary gland or to other regions of the brain (Yin and Gore, 2010).

A persisting embryonal IR is a rare anomaly in adult humans (e.g., Belotti et al., 2021; Steno et al., 2009), and the structure may also be reduced in great apes. Fujita et al. (1959:273), for example, describe the IR as "shallow" in the chimpanzee (*Pan troglodytes*). Nevertheless, the IR persists in many other mammals and has been especially well studied in rodents (e.g., Ugrumov et al., 1986). To our knowledge, the recess has only been described in one bat; Anthony et al. (1992) indicated that the passageway deeply penetrates the infundibular stalk in the little brown bat (*Myotis lucifugus*). Here, we present a brief report on the IR in two species of phyllostomid bats—the common vampire (*Desmodus rotundus*) and the white-winged vampire (*Diaemus youngii*)—to extend knowledge of this anatomical space to another group of mammals.

Two adult bats, one of each species, were studied. Both were part of a collection of histologically sectioned bats that were mostly prepared by the first author and currently housed in the laboratory of the second author. The specimens were serially sectioned through the snout and most of the cranial cavity, after the whole head was decalcified and then processed for paraffin histology. The specimen of *Diaemus*, collected in Trinidad, was previously sectioned (Cooper and Bhatnagar, 1976).

The *Desmodus*, which was originally collected in Veracruz, Mexico, was newly prepared for this study. Although this specimen and others were first used to produce a cytoarchitectural atlas of the brain of *Desmodus* (Bhatnagar, 2008), the remaining parts of the head were decalcified and embedded in paraffin for later examination. In the present study, we serially sectioned the posterior half of this head in the coronal plane at 10 µm and alternately stained the slides with Gomori trichrome or hematoxylin and eosin. The specimens were viewed and photographed using a camera (Axiocam MRc 5 Firewire, Zeiss, Oberkochen, Germany) attached to a photomicroscope (Leica DMLB, Leica

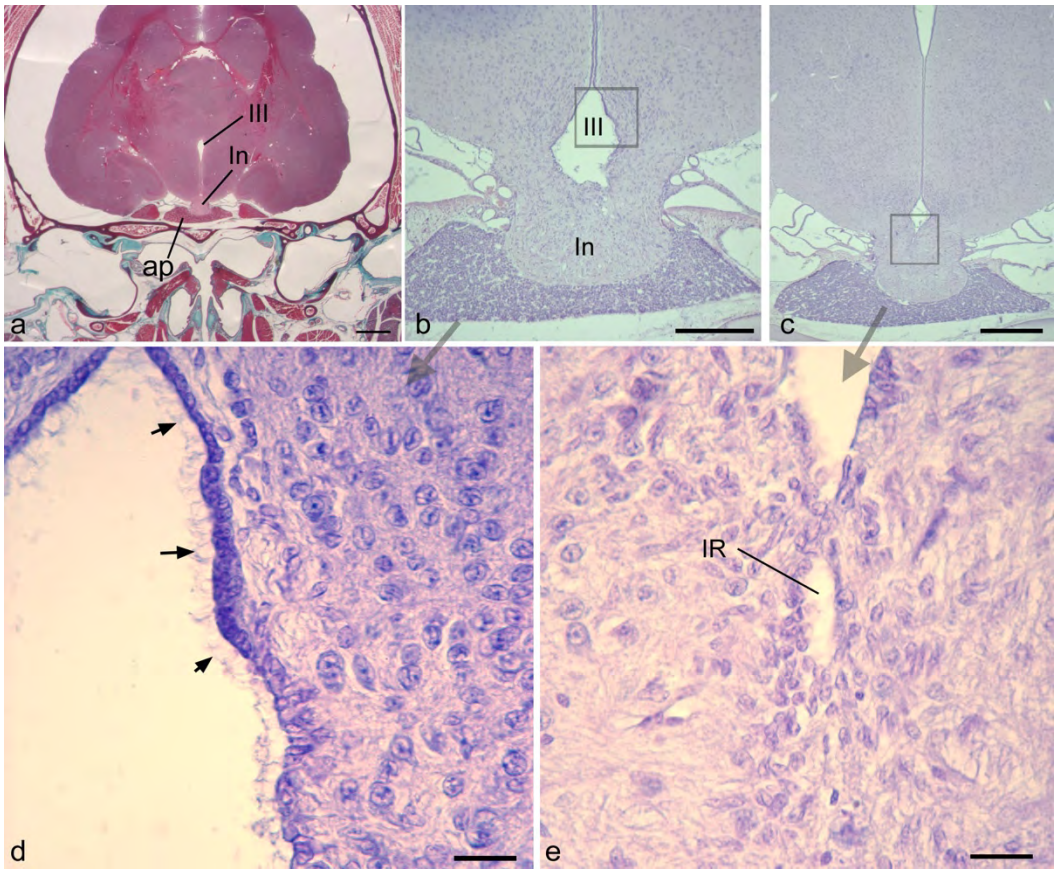


Figure 1. Pituitary gland with infundibular recess in an adult *Desmodus rotundus*. a) Low-magnification view of a coronal section through the hypophysis at the level of the infundibular stalk (In). Also shown is the anterior pituitary (ap) and the third ventricle (III). b) A nearby section, enlarged, showing the third ventricle. c) A section slightly posterior to b, showing an extension of the third ventricle toward the infundibulum. d) An enlargement of the boxed area in b, showing the ependymal lining of the third ventricle, and the apical cell processes (arrows) extending into the lumen. e) An enlargement of the boxed area in c, showing extension of the third ventricle, communicating with a small infundibular recess (IR), which penetrates the infundibulum. Scale bars: a, 1 mm; b, 250 µm; c, 400 µm; and d, 20 µm.

Microsystems, Wetzlar, Germany) for high-magnification views (25–630 x) and a second camera (Axiocam MRc 150 Firewire, Zeiss) attached to a stereomicroscope (Stemi, Zeiss) for low-magnification views (0.64–1.6 x).

Both adult bats possess an extension of the third ventricle into the infundibulum. In *Desmodus*, the third ventricle has a large lumen superior to the infundibulum (Figs. 1a, b). From the ventricle, a small IR (lumen < 10 µm in diameter) penetrates the infundibulum but does not extend far through the remainder of the stalk (Fig. 1c). The ventricle has numerous apical projections of ependymal cells that jut into the lumen (Fig. 1d), and these projections (cilia) are important to the flow of cerebrospinal fluid (Eichele et al., 2020). However, the ependymal lining of the IR lacks visible apical projections (Fig. 1e).

The IR of *Diaemus*, in contrast, extends throughout most of the length of the infundibulum (Fig. 2a, b). The lumen is wider than in the *Desmodus*, approximately 80 µm in greatest diameter (Fig. 2c). However, the recess ends before the infundibulum connects to the pars nervosa of the posterior pituitary (Fig. 2d).

Although the pituitary gland has been studied previously in bats (e.g., Bhatnagar et

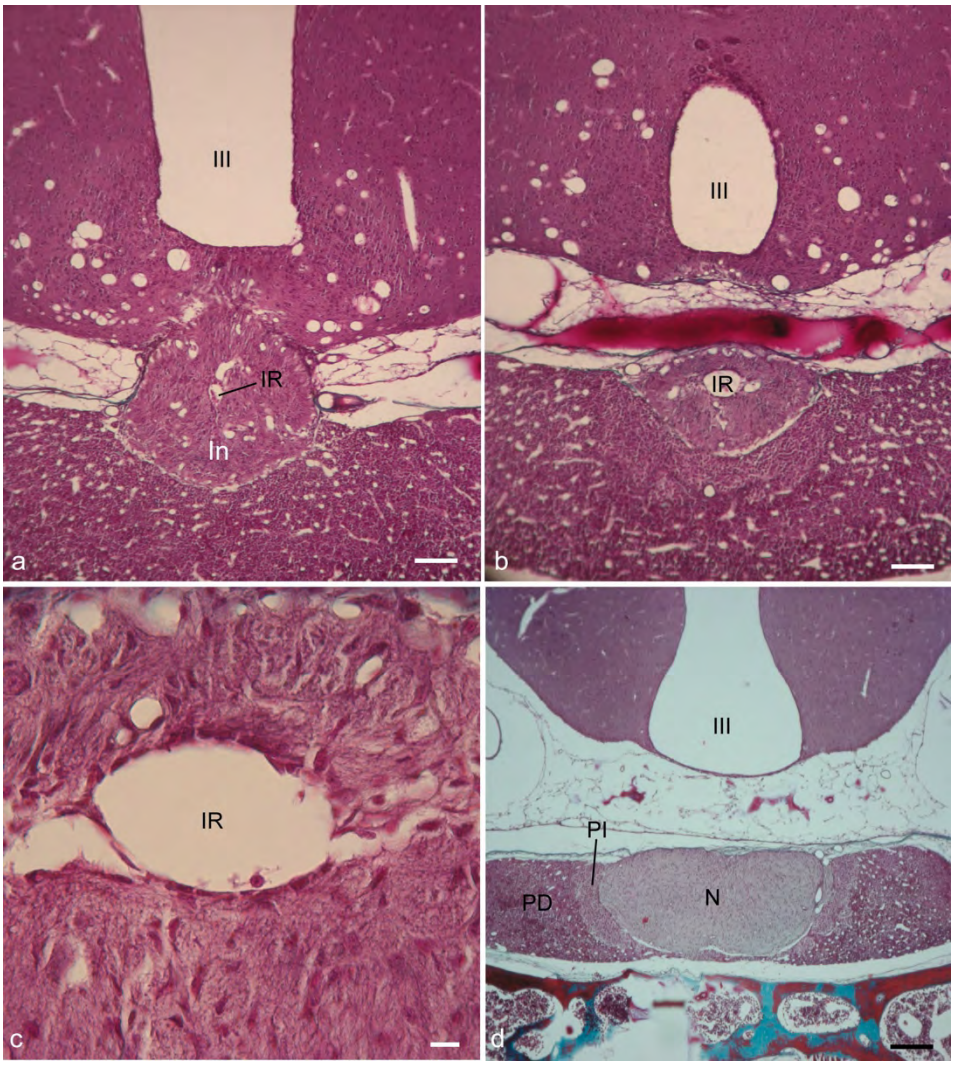


Figure 2. Pituitary gland with infundibular recess (IR) in an adult *Diaemus youngii*. a, b) Sections through an anterior level (a) and midlength (b) of the infundibular recess. III represents the third ventricle. c) A magnified view of the recess. A thin lining of ependymal cells borders the recess. d) More posteriorly, the infundibulum leads to the pars nervosa (N) of the posterior pituitary, and the recess ends anterior to this structure. PD and PI indicate the pars distalis and pars intermedia, respectively, of the anterior pituitary. Scale bars: a and b, 100 µm; c, 10 µm; and d, 200 µm.

al., 2016; Reyes-Amaya and Flores, 2019), the IR mostly has been ignored (e.g., Anthony et al., 1992). This passageway is continuous with the third ventricle, and the ependymal lining of the recess may be an important source of gonadotropin-releasing hormone found in cerebrospinal fluid (Caraty and Skinner, 2008). Given the importance of pituitary hormone delivery for reproduction, the IR should be ubiquitous in mammals, and indeed, it has been described in numerous species, such as the nine-banded armadillo (*Dasypus novemicinatus*), one bat, multiple rodents, and sheep (Anthony et al., 1992; Caraty and Skinner, 2008; Ives and McArthur, 1979; Umgrumov et al., 1986), although humans, which lack the recess as adults, appear unusual. Nonetheless, our brief examination of two vampire bats suggests that the size and extent of the recess may be variable among species of bats. A broader survey of the Chiroptera may reveal

patterns of IR morphology, which, in turn, might be correlated with the diverse reproductive strategies of bats (e.g., Anthony, 2000; McCracken and Wilkinson, 2000).

Literature Cited

Anthony, E. L. P. 2000. Endocrinology of reproduction in bats: central control. Pp.1–26 *in* Reproductive biology of bats (E. C. G. Crichton and P. H. Krutzsch, eds.). Academic Press, New York.

Anthony, E. L. P., K. Neel, and M. E. Cicione. 1992. Fine structural characteristics of the zone of contact between the lower infundibular stem and the pituitary pars distalis in the little brown bat, *Myotis lucifugus*. Anatomical Record, 234:116–128.

Belotti, F., L. Lupi, M. Cosottini, C. Ambrosi, R. Gasparotti, F. Bogazzi, M. M. Fontanella, and F. Doglietto. 2018. Persisting embryonal infundibular recess (PEIR): two case reports and systematic literature review. Journal of Clinical Endocrinology and Metabolism, 103:2424–2429.

Bhatnagar, K. P. 2008. The brain of the common vampire bat, *Desmodus rotundus murinus* (Wagner, 1840): a cytoarchitectural atlas. Brazilian Journal of Biology, 68:583–599.

Bhatnagar, K. P., T. D. Smith, S. N. Rai, and H. D. Frahm. 2016. The chiropteran brain database: volumetric survey of the hypophysis in 165 species. Anatomical Record, 299:492–510.

Caraty, A., and D. C. Skinner. 2008. Gonadotropin-releasing hormone in third ventricular cerebrospinal fluid: endogenous distribution and exogenous uptake. Endocrinology, 149:5227–5234.

Cooper, J. G., and K. P. Bhatnagar. 1976. Comparative anatomy of the vomeronasal organ complex in bats. Journal of Anatomy, 122:571–601.

Eichele, G., E. Bodenschatz, Z. Ditte, A.-K. Günther, S. Kapoor, Y. Wang, and C. Westendorf. 2020. Cilia-driven flows in the brain third ventricle. Philosophical Transactions of the Royal Society B, 375(1792): 20190154.

Fujita, H., Y. Hirakawa, and M. Oka. 1959. Histological observations on the hypothalamo-hypophysial system of a chimpanzee (one case report). Contributions to the comparative histology of the hypothalamo-hypophysial system. 40th report. Archivum Histologicum Japonicum, 16:273–278.

Ives, P. J., and N. H. McArthur. 1979. Transventricular blood vessels in the third ventricle of the armadillo brain. Anatomical Record, 194:181–185.

McCracken, G. F., and G. S. Wilkinson. 2000. Bat mating systems. Pp. 321–362 *in* Reproductive biology of bats (E. C. G. Crichton and P. H Krutzsch, eds.). Academic Press, New York.

Reyes-Amaya, N., and D. Flores. 2019. Hypophysis size evolution in Chiroptera. Acta Chiropterologica, 21:65–74.

Steno, A., A. J. Popp, S. Wolfsburger, V. Belan, and J. Steno. 2009. Persisting embryonal infundibular recess. Journal of Neurosurgery, 110:359–362.

Ugrumov, M. V., M. S. Mitskevich, B. Halász, J. Kiss, and N. A. Borisova. 1986. Ependymal lining of infundibular recess in perinatal rats: relationships with portal capillaries and permeability. International Journal of Developmental Neuroscience, 4:101–111.

RECENT LITERATURE

~~Authors are requested to send reprints (PDF files) of their published papers to the Editor for Recent Literature, **Dr. Thomas A. Griffiths**, (e-mail: **thomas.alan.griffiths@gmail.com**) for inclusion in this section. Receipt of reprints is preferred, as it will facilitate complete and correct citation. However, if reprints and/or PDF files are unavailable, please send a complete citation (including complete name of journal and corresponding author e-mailing address) by e-mail~~.

The Recent Literature section is based on several bibliographic sources and for obvious reasons can never be up-to-date. Any error or omission is inadvertent.

~~Voluntary contributions for this section, especially from researchers outside the United States, are most welcome and appreciated.~~

This is the final issue of *Bat Research News* for which I will serve as Editor for Recent Literature. In fact, this may very well be the last issue and number of *Bat Research News* that will ever be published. For several years now, Dr. Margaret Griffiths—the Editor, Publisher, and Owner of this journal (and my wife)—has been seeking an individual or group who would be willing to take over the publication and ownership of *Bat Research News*. So far, no one has stepped forward to assume those duties. As the current Editorial staff prepares this final issue of Volume 63, Margaret and I have each decided that whether a replacement group comes along or not, we will not continue beyond Vol 63(4). **For that reason, I must ask that authors NO LONGER send reprints (PDF files) or complete citations of their published papers to me for inclusion in this section.**

My sincerest thanks to all of you who have helped me produce this section of *Bat Research News* through the years. My tenure as an Editor of *BRN* goes back to the early 1980's when then-publisher G. Roy Horst asked me to become Editor for Recent Literature and then (briefly) Managing Editor for him. Finding citations of bat-related papers in those ancient days involved many tedious hours of me poring over hundreds of printed journal pages in the old Biological Sciences Library (in Burrill Hall) at the University of Illinois in Champaign-Urbana. Today the job has become infinitely easier and quicker with the invention of online searching on the internet. But ironically, it is my strong belief that despite the ease of conducting searches on the internet today, the need for a Recent Literature section in a journal like *BRN* has never been greater. What modern bat researcher has the time to conduct comprehensive searches that encompass ALL of bat biology and deliver citations in a neat package (both electronically and in print) on a quarterly basis directly to him/her? After 63 years of publication, it is a pity that this convenient service will no longer continue.

Very best wishes to you all and—one last time—thanks for reading. TAG.

ANATOMY/HISTOLOGY

Bravo-Salinas, R., and J. A. Salas. 2022. Registro de desorden cromático en *Trachops cirrhosus* (Spix, 1823) (Chiroptera: Phyllostomidae) en la Amazonia del Ecuador. (=Chromatic disorder in *Trachops cirrhosus* (Spix, 1823) (Chiroptera: Phyllotomidae) on Ecuadorian Amazon.) Revista Peruana de Biología, 29(4): e23598. https://doi.org/10.15381/rpb.v29i4.23598 [jaime.salasz@ug.edu.ec]

Cahyadi, D. D., N. Nurhidayat, S. Supratikno, S. Novelina, H. Setijanto, and S. Agungpriyono. 2022. Musculoskeletal structure of the shoulder and arm in large flying fox (*Pteropus*

vampyrus). Biodiversitas Journal of Biological Diversity, 23(11): 5902–5913. DOI: 10.13057/biodiv/d231144 [nhdayat@apps.ipb.ac.id]

Llaven-Macías, V., Y. Rico, E. J. Naranjo, and L. Ruíz-Montoya. 2022. Variación estacional de la morfología del ala y la masa corporal de la colonia de *Tadarida brasiliensis* (Chiroptera: Molossidae) en su refugio más sureño de México. (=Seasonal variation of the wing morphology and the body mass of the colony of *Tadarida brasiliensis* (Chiroptera: Molossidae), in its southernmost refuge in Mexico). Mastozoologia Neotropical, 29(2): https://doi.org/10.31687/saremMN.22.29.2.06.e0785 [vllaven-m@hotmail.com]

Mora, J. M., and R. Sánchez. 2022. First case of piebaldism in *Eumops auripendulus* in Costa Rica. Therya Notes, 3: 164–167. https://doi.org/10.12933/therya_notes-22-90 [josemora07@gmail.com]

Nuriliani, A., R. Wulandari, and L. Nurhididayat. 2022. Tongue structure of *Rhinolophus pusillus* and *Miniopterus schreibersii*. Acta Veterinaria Indonesiana, 10(3): 211–219. http://www.journal.ipb.ac.id/indeks.php/actavetindones [ardaning@ugm.ac.id]

Rabenstein, R., and D. Stiefel. 2022. Rare dental anomalies in two sympatric European bat species (Pipistrellus spp.). Bulletin of the International Association for Paleodontology, 16(2): 284–291. https://hrcak.srce.hr/288337 [renate.rabenstein@senckenberg.de]

BATS AND AGRICULTURE

Ancillotto, L., C. Scaramella, F. Dartora, A. Migliozzi, and D. Russo. 2023. Organic farming sustains bats in Mediterranean farmland. Agriculture, Ecosystems & Environment, 342: 108230. https://doi.org/10.1016/j.agee.2022.108230 [danrusso@unina.it]

Boonchuay, P., and S. Bumrungsri. 2022. Activity of insectivorous bats in organic rice fields is higher than in conventional rice fields: A preliminary study. Journal of Tropical Forest Research, 6(1): 19–28. [sara.b@psu.ac.th]

Da Silva, L .P., D. Oliveira, and V. A. Mata. 2022. Can bats help paper industry? An evaluation of eucalypt insect-related predation by bats. Mammalian Biology, pp.1–4. https://doi.org/10.1007/s42991-022-00333-4 [lfpascoals@gmail.com]

Schäckermann J., E. J. Morris, A. Alberdi, O. Razgour, and C. Korine. 2022. The contribution of desert-dwelling bats to pest control in hyper-arid date agriculture. Diversity, 14(12): 1034. https://doi.org/10.3390/d14121034 [mopres@rd.ardom.co.il]

Tortosa, A., B. Giffard, L. Barbaro, J. S. P. Froidevaux, S. Ladet, J. Delhommel, and A. Vialatte. 2023. Diverse agricultural landscapes increase bat activity and diversity: Implications for biological pest control. Agriculture, Ecosystems & Environment, 345: 108318. https://doi.org/10.1016/j.agee.2022.108318 [axelle.tortosa@inrae.fr]

BAT ECHOLOCATION SOUNDS—PRODUCED ARTIFICIALLY—CAN BE USED TO DRIVE AWAY INSECT PESTS

Nakano, R., A. Ito, and S. Tokumaru. 2022. Sustainable pest control inspired by prey-predator ultrasound interactions. Proceedings of the National Academy of Sciences, 119(43): e2211007119. https://doi.org/10.1073/pnas.2211007119 [rnakano@affrc.go.jp]

BEHAVIOR

Bakker, A., B. Jackson, and E. Polla. 2022. Breeding and post-breeding behavior of the ghost bat (*Macroderma gigas*) at Perth Zoo. Bat Research & Conservation, 15(1): 2–10. DOI: https://doi.org/10.14709/BarbJ.15.1.2022.01 [aundrealauren11@gmail.com]

Håkansson J., C. Mikkelsen, L. Jakobsen, and C. P. H. Elemans. 2022. Bats expand their vocal range by recruiting different laryngeal structures for echolocation and social communication. PLoS Biology, 20(11): e3001881. https://doi.org/10.1371/journal.pbio.3001881 [jhaakans@uccs.edu]

Murugavel, B., A. Rathinakumar, S. Baskaran, G. Marimuthu, A. Kelber, and H. Somanathan. 2022. Effect of artificial light on activity in frugivorous bats (Pteropodidae). Journal of Ethology, https://doi.org/10.1007/s10164-022-00771-0 [baheerathanm15@iisertvm.ac.in]

Richdon, S., E. Price, D. Wormell, G. Jones, and G. McCabe. 2022. Predictors of dominance rank and agonistic interactions in captive Livingstone's fruit bats. Current Zoology: zoac091. https://doi.org/10.1093/cz/zoac091 [srichdon@gmail.com]

Salganek, S., T. J. Weller, and J. M. Szewczak. 2022. Autumn roost-site selection by male hoary bats (*Lasiurus cinereus*) in northern California. Journal of Mammalogy, 103(5): 1103–1111. https://doi.org/10.1093/jmammal/gyac055 [skye@humboldt.edu]

Sunga, J., M. R. Q. Webber, J. Humber, B. Rodrigues, and H. G. Broders. 2022. Roost fidelity partially explains maternity roosting association patterns in *Myotis lucifugus*. Animal Behaviour, 194: 67–78. https://doi.org/10.1016/j.anbehav.2022.09.008 [hugh.broders@uwaterloo.ca]

Tan, X., A. Lin, K. Sun, L. Jin, and J. Feng. 2022. Greater horseshoe bats recognize the sex and individual identity of conspecifics from their echolocation calls. Animals, 12(24): 3490. https://doi.org/10.3390/ani12243490 [fengj@nenu.edu.cn]

Yantén, A. V., A. Cruz-Roa, and F. A. Sánchez. 2022. Traffic noise affects foraging behavior and echolocation in the lesser bulldog bat, *Noctilio albiventris* (Chiroptera: Noctilionidae). Behavioural Processes, 203: 104775. https://doi.org/10.1016/j.beproc.2022.104775 [angelica.yanten@unillanos.edu.co]

BIOGEOGRAPHY

Carvalho, W. D., I. E. Fluck, I. J. de Castro, R. R. Hilário, A. C. M. Martins, J. J. de Toledo, B. da Silva Xavier, C. Dambros, and P. E. D. Bobrowiec. 2022. Elevation drives taxonomic,

functional and phylogenetic β-diversity of phyllostomid bats in the Amazon biome. Journal of Biogeography, pp. 1–16. https://doi.org/10.1111/jbi.14533 [william.mustin@uam.es]

Fichera, G., M. Mucedda, D. Russo, A. Tomassini, A. Kiefer, M. Veith, and L. Ancillotto. 2022. Pantelleria Island (Sicily, Italy): a biogeographic crossroad for bats between Africa and Europe. Hystrix, the Italian Journal of Mammalogy, https://doi.org/10.4404/hystrix-00503-2021 [gadfichera@gmail.com]

Hernández-Mazariegos, W. C., C. M. Ibáñez, and R. E. Palma. 2022. An updated biogeographic evaluation of endemism and conservation of small mammals from Chile. Journal of Mammalogy, 2022;, gyac104. https://doi.org/10.1093/jmammal/gyac104 [wendychm7@gmail.com]

BOOKS ON BATS

Fenton, M. B., and J. Rydell. 2023. A Miscellany of Bats. Pelagic Publishing, Exeter, United Kingdom, 256 pp. Available in paperback or as an e-book. [https://pelagicpublishing.com/products/a-miscellany-of-bats]

BROCK FENTON, TRIBUTE TO

Clare, E. L., and B. Lim. 2022. Interpretation and application of bat diversity and phylogeny. Canadian Journal of Zoology, https://doi.org/10.1139/cjz-2022-0103 [eclare@yorku.ca]

CONSERVATION

Anderson, A. M., C. B. Jardine, J. R. Zimmerling, E. F. Baerwald, and C. M. Davy. 2022. Effects of turbine height and cut-in speed on bat and swallow fatalities at wind energy facilities. FACETS, 7: 1281–1297. https://doi.org/10.1139/facets-2022-0105 [aande763@gmail.com]

Brasileiro, L. A. M., R. B. Machado, and L. M. S. Aguiar. 2022. Ecosystems services provided by bats are at risk in Brazil. Froniers in Ecology and Evolution, 10:852177. doi: 10.3389/fevo.2022.852177 [laisbioufc@gmail.com]

Brack Jr, V., D. W. Sparks, and S. Kennedy. 2022. Case study: upland ponds provide on-site mitigation for bat habitat along American Electric Power's 765-kV powerline ROW in the Appalachian Mountains, USA. In" L. Hufnagel, Ed. New Insights into Protected Area Management and Conservation Biology. DOI: 10.5772/intechopen.109061 [vbrack@envsi.com]

Buys, J. C., E. A. Jansen, and J. S. van Zweden. 2022. Hibernating bats in fortifications of the New Dutch Waterline 1980-2020: The ups and downs of a dynamic co-existence of natural and cultural heritage. Lutra, 65(1): 63–82. https://www.Zoogdier vereniging.nl/ publicaties/2022/lutra-65-1-2022 [jan@buys-van-nature.nl]

Cronin, M. R., L. A. de Wit, and L. Martínez-Estévez. 2022. Aligning conservation and public health goals to tackle unsustainable trade of mammals. Conservation Science and Practice, 4(11): e12818. https://doi.org/10.1111/csp2.12818 [mecronin@ucsc.edu]

Cú-Vizcarra, J. D., F. Villalobos, M. C. MacSwiney G., V. J. Sosa, and B. Bolívar-Cimé. 2022. The agony of choice: Species richness and range size in the determination of hotspots for the conservation of phyllostomid bats. Perspectives in Ecology and Conservation, 20(4): 360–368. https://doi.org/10.1016/j.pecon.2022.08.005 [jcvizcarra104@gmail.com]

Da Silva Lima, A. C. and S. B. Mendes. 2022. Desmitificando os morcegos: uma análise da percepção de discentes do Ensino Fundamental II e práticas de Educação Ambiental. (=Demystifying bats: An analysis of the perception of students of Ensino Fundamental II and practices of environmental education.) Revista Brasileira de Educação Ambiental, 17(6): 458–477. https://doi.org/10.34024/revbea.2022.v17.13678 [amanda01cristiny@outlook.com]

Fialas, P. C., L. R. V. Gilmour, S. Vickress, E. Underwood, C. A. Williams, H. Miller, and P. R. Lintott. 2022. Sexual segregation occurs in bats within fragmented remnant woodlands in an agricultural landscape. Ecology and Evolution, 12: e9350. https://doi.org/10.1002/ece3.9350 [pf313@exeter.ac.uk]

Gaultier, S. P., T. M. Lilley, E. J. Vesterinen, and J. E. Brommer. 2023. The presence of wind turbines repels bats in boreal forests. Landscape and Urban Planning, 231: 104636. https://doi.org/10.1016/j.landurbplan.2022.104636 [simon.s.gaultier@utu.fi]

Giuntini, S., L. Ancillotto, M. Falaschi, A. Viviano, E. Palagi, and E. Mori. 2022. Alien parakeets as a potential threat to the common noctule *Nyctalus noctula*. Biodiversity and Conservation, 31: 3075–3092. https://doi.org/10.1007/s10531-022-02476-9 [emiliano.mori@cnr.it]

Hayes, M. A., S. R. Lindsay, D. I. Solick, and C. M. Newman. 2022. Simulating the influences of bat curtailment on power production at wind energy facilities. Wildlife Society Bulletin, p.e1399. https://doi.org/10.1002/wsb.1399 [mark_hayes@fws.gov]

Iannella, M., F. Cerasoli, M. Di Musciano, and M. Biondi. 2022. Assessing future shifts in habitat suitability and connectivity to old-growth forests to support the conservation of the endangered giant noctule. PeerJ, 10: p.e14446. https://doi.org/10.7717/peerj.14446 [francesco.cerasoli@univaq.it]

Kunberger, J. M., and A. M. Long. 2022. The influence of forest management practices on seasonal bat species occurrence and activity at the Kisatchie National Forest in Louisiana, USA. Forest Ecology and Management, 526: 120579. https://doi.org/10.1016/j.foreco.2022.120579 [janemkunberger@gmail.com]

Lajeunesse, A., and Y. Fourcade. 2022. Temporal analysis of GBIF data reveals the restructuring of communities following climate change. Journal of Animal Ecology, https://doi.org/10.1111/1365-2656.13854 [yoan.fourcade@u-pec.fr]

Mariton, L., I. Le Viol, Y. Bas, and C. Kerbiriou. 2023. Characterising diel activity patterns to design conservation measures: Case study of European bat species. Biological Conservation, 277: 109852. https://doi.org/10.1016/j.biocon.2022.109852 [lea.mariton@mnhn.fr]

Massaad, M., R. Da Silveira Bueno, I. Bentaleb, and T. La Mantia. 2022. Priorities and gaps in Mediterranean bat research evidence: a systematic review for the early twenty-first century. Hystrix, the Italian Journal of Mammalogy, https://doi.org/10.4404/hystrix-00534-2022 [rafael.dasilveirabueno@unipa.it]

Mo, M., S. Cross, and K. Boyd. 2022. Post-release survivorship of 18 years in a hand-reared grey-headed flying-fox (*Pteropus poliocephalus*) revealed by a metal identification band. Australian Mammalogy, https://doi.org/10.1071/AM22021 [matthew.mo@environment.nsw.gov.au]

Mondragon, K. Y. R., E. Aguirre-Planter, J. Gasca-Pineda, A. Klimova, R.-E. Trejo-Salazar, M. A. R. Guerra, R. A. Medellin, D. Piñero, R. Lira, and L. E. Eguiarte. 2022. Conservation genomics of *Agave tequilana* Weber var. azul: Low genetic differentiation and heterozygote excess in the tequila agave from Jalisco, Mexico. PeerJ, 10: e14398 [eaplanter@gmail.com]

Monteiro-Alves, P. S., E. L. Captivo, R. O. Meire, and H. de G. Bergallo. 2022. Banned persistent organic pollutants: A quantitative and qualitative systematic review on bats (Mammalia: Chiroptera). Research Square, pp 1–22. DOI: https://doi.org/10.21203/rs.3.rs-2284525/v1 [prism.alves@gmail.com]

Oliveira, H. F. M., G. Fandos, P. L. Zangrandi, H. D. N. Bendini, D. C. Silva, R. L. Muylaert, J. S. Marinho-Filho, L. M. G. Fonseca, P. Rufin, M. Schwieder, and F. M. C. B. Domingos. 2022. Crops, caves, and bats: deforestation and mining threaten an endemic and endangered bat species (Lonchophylla: Phyllostomidae) in the Neotropical savannas. Hystrix, the Italian Journal of Mammalogy, https://doi.org/10.4404/hystrix-00541-2022 [oliveiradebioh@gmail.com]

Raman, S., T. T. Shameer, U. Pooja, and A. C. Hughes. 2022. Identifying priority areas for bat conservation in the Western Ghats mountain range, peninsular India. Journal of Mammalogy, gyac060. https://doi.org/10.1093/jmammal/gyac060 [ach_conservation2@hotmail.com]

Saltus, C. L., and E. R. Britzke. 2022. Literature Review: Microhabitat metrics to identify presence of Chiroptera on the landscape in the United States. Ecosystem Management and Restoration Research Program (EMRRP), pp. i-v + 1–29. [ERDC-EL SR-22-8.pdf]

Summers, J. L., J. P. White, H. M. Kaarakka, S. E. Hygnstrom, B. S. Sedinger, J. Riddle, T. Van Deelen, and C. Yahnke. 2022. Influence of underground mining with explosives on a hibernating bat population. Conservation Science and Practice, p.e12849. https://doi.org/10.1111/csp2.12849 [jsummers@uwsp.edu]

Tanshi, I., B. C. Obitte, A. Monadjem, S. J. Rossiter, M. Fisher-Phelps, and T. Kingston. 2022. Multiple dimensions of biodiversity in paleotropical hotspots reveal comparable bat diversity. Biotropica, 54: 1205–1216. https://doi.org/10.1111/btp.13143 [iroro.tanshi@smacon-africa.org]

Vakaciriwaqa, S., O. Seniucidromo, D. L. Waldien, and S. Tikoca. 2022. Discovery of new cave-roosts of the endangered Pacific sheath-tailed bat on Ovalau Island, Fiji. Pacific Conservation Biology, https://doi.org/10.1071/PC21063 [semaema@naturefiji.org]

Vlaschenko, A., K. Kravchenko, Y. Yatsiuk, V. Hukov, S. Kramer-Schadt, and V. Radchuk. 2022. Bat assemblages are shaped by land cover types and forest age: A case study from eastern Ukraine. Forests, 13: 1732. https://doi.org/10.3390/f13101732 [anton.vlaschenko@gmail.com]

DISEASE

Agbomola, J. O., and A. C. Loyinmi. 2022. Modelling the impact of some control strategies on the transmission dynamics of Ebola virus in human-bat population: An optimal control analysis. Heliyon, p.e12121. https://doi.org/10.1016/j.heliyon.2022.e12121 [loyinmiac@tasued.edu.ng]

Bueno, L. M., D. M. Melo, R. D. Azevedo, W. M. de Souza, and L. T. M. Figueiredo. 2022. Serological evidence of hantavirus infection in neotropical [sic] bats in an urban area of São Paulo State, Brazil. Transactions of The Royal Society of Tropical Medicine and Hygiene, trac111, https://doi.org/10.1093/trstmh/trac111 [buenolm@usp.br]

Caraballo, D. A., M. S. Sabio, V. C. Colombo, M. G. Piccirilli, L. Vico, S. M. H. Riade, J. Campos, G. Martínez, F. Beltrán, E. Baumeister, D. M. Cisterna, B. He and Y. Peng. 2022. The role of Molossidae and Vespertilionidae in shaping the diversity of alphacoronaviruses in the Americas. Microbiology Spectrum, e03143-22. https://doi.org/10.1128/spectrum.03143-22 [no author e-mail provided]

Chaitanya, K. R. and V. R. S. Anusha. 2022. Recapitulation of Nipah virus disease: Multiple strategies for future therapeutics. Research Journal of Pharmacy and Technology, 15(9): 4048–4054. DOI: 10.52711/0974-360X.2022.00679 [koppala526@gmail.com]

Chan, L. L. Y., A. M. Gamage, C. W. Tan, K. S. Tan, J. Liu, D. J. W. Tay, R. J. H. Foo, L. Rénia, D. Y. Wang, and L.-F. Wang. 2022. Generation of self-replicating airway organoids from the cave nectar bat *Eonycteris spelaea* as a model system for studying host-pathogen interactions in the bat airway epithelium. Emerging Microbes & Infections, DOI: 10.1080/22221751.2022.2148561 [linfa.wang@duke-nus.edu.sg]

Ch'ng, L., S. M. Tsang, Z. A. Ong, D. H. W. Low, S. Wiantoro, I. L. Smith, N. B. Simmons, Y. C. F. Su, D. J. Lohman, G. J. D. Smith, and I. H. Mendenhall. 2022. Co-circulation of alpha- and beta- coronaviruses in *Pteropus vampyrus* flying foxes from Indonesia. Transboundary and Emerging Diseases. https://doi.org/10.1111/tbed.14762 [gavin.smith@duke-nus.edu.sg]

Eby, P., A. J. Peel, A. Hoegh, W. Madden, J. R. Giles, P. J. Hudson, and R. K. Plowright. 2022. Pathogen spillover driven by rapid changes in bat ecology. Nature, https://doi.org/10.1038/s41586-022-05506-2 [raina.plowright@cornell.edu]

Gamage, A. M., W. O.Y. Chan, F. Zhu, Y. T. Lim, S. Long, M. Ahn, C. W. Tan, R. J. H. Foo, W. R. Sia, X. F. Lim, H. He, W. Zhai, D. E. Anderson, R. M. Sobota, C.-A. Dutertre, and L.-F. Wang. 2022. Single-cell transcriptome analysis of the in vivo response to viral infection in the cave nectar bat *Eonycteris spelaea*. Immunity, 55(11): 2187–2205.e5. https://doi.org/10.1016/j.immuni.2022.10.008 [linfa.wang@duke-nus.edu.sg]

Gonzalez, V., and A. Banerjee. 2022. Molecular, ecological, and behavioral drivers of the bat-virus relationship. iScience, 25(8): 104779. https://doi.org/10.1016/j.isci.2022.104779 [arinjay.banerjee@usask.ca]

Huang, Y., Y. Sun, Q. Huang, X. Lv, J. Pu, W. Zhu, S. Lu, D. Jin, L. Liu, Z. Shi, and J. Yang. 2022. The threat of potentially pathogenic bacteria in the feces of bats. Microbiology Spectrum, e01802-22. https://doi.org/10.1128/spectrum.01802-22 [xujianguo@icdc.cn]

Jang, S. S., J. Y. Noh, M. C. Kim, H. A. Lim, M. S. Song, and H. K. Kim. 2022. α2, 3-linked sialic acids are the potential attachment receptor for Shaan virus infection in MARC-145 cells. Microbiology Spectrum, 10(4): e01256-22 [khk1329@chungbuk.ac.kr]

Kamau, J., K. Ergunay, P. W. Webala, S. A. Justi, B. P. Bourke, M. W. Kamau, J. Hassell, M. N. Chege, D. K. Mwaura, C. Simiyu, and S. Kibiwot. 2022. A novel coronavirus and a broad range of viruses in Kenyan cave bats. Viruses, 14(12): 2820. https://doi.org/10.3390/v14122820 [ekoray@hacettepe.edu.tr]

Karagulov, A. I., T. U. Argimbayeva, Z. D. Omarova, A. B. Tulendibayev, D. L. Zh, M. Svotina, A. M. Melisbek, N. A. Aubakir, S. M. Barmak, K. T. Sultankulova, and D. A. Alibekova. 2022. The prevalence of viral pathogens among bats in Kazakhstan. Viruses, 14(12): 2743. [98.constantine.98@gmail.com]

Kirejczyk, S. G. M., B. R. Amman, A. J. Schuh, T. K. Sealy, C. G. Albariño, J. Zhang, C. C. Brown, and J. S. Towner. 2022. Histopathologic and immunohistochemical evaluation of induced lesions, tissue tropism and host responses following experimental infection of Egyptian rousette bats (*Rousettus aegyptiacus*) with the zoonotic paramyxovirus, sosuga virus. Viruses, 14(6): 1278. https://doi.org/10.3390/v14061278 [jit8@cdc.gov]

Lebarbenchon, C., S. M. Goodman, A. O. G. Hoarau, G. Le Minter, A. dos Santos, M. C. Schoeman, C. Leculier, H. Raoul, E. S. Gudo, and P. Mavingui. 2022. Bombali ebolavirus in Mops condylurus bats [sic] (Molossidae), Mozambique. Emerging Infectious Diseases, 12: 2583–2585. DOI: 10.3201/eid2812.220853 [no author email address provided]

Meza, D. K., N. Mollentze, A. Broos, C. Tello, W. Valderrama, S. Recuenco6, J. E. Carrera, C. Shiva, N. Falcon, M. Viana, and D. G. Streicker. 2022. Ecological determinants of rabies virus dynamics in vampire bats and spillover to livestock. Proceedings of the Royal Society B., Biological Sciences, 289: 20220860. http://doi.org/10.1098/rspb.2022.0860 [d.villa-meza.1@research.gla.ac.uk]

Montecino-Latorre D, T. Goldstein, T. R. Kelly, D. J. Wolking, A. Kindunda, G. Kongo, S. O. Bel-Nono, R. R. Kazwala, R. D. Suu-Ire, C. M. Barker, C. K. Johnson, and J. A. K. Mazet. 2022. Seasonal shedding of coronavirus by straw-colored fruit bats at urban roosts in Africa. PLoS ONE, 17(9): e0274490. https://doi.org/10.1371/journal.pone.0274490 [dmontecino@wcs.org]

Moraga-Fernández, A., M. Sánchez-Sánchez, J. Queirós, A. M. Lopes, J. Vicente, X. Pardavila, J. Sereno-Cadierno, P. C. Alves, J. de la Fuente, and I. G. Fernández de Mera. 2022. A study of viral pathogens in bat species in the Iberian Peninsula: Identification of new coronavirus genetic variants. International Journal of Veterinary Science and Medicine, 10(1): 100–110. https://doi.org/10.1080/23144599.2022.2139985 [mariaisabel.garcia@uclm.es]

Morcatty, T.Q., P. E. Pereyra, A. Ardiansyah, M. A. Imron, K. Hedger, M. Campera, K. Nekaris, and V. Nijman. 2022. Risk of viral infectious diseases from live bats, primates, rodents and carnivores for sale in Indonesian wildlife markets. Viruses, 14(12): 2756. https://doi.org/10.3390/v14122756 [tqueiroz-morcatty@brookes.ac.uk]

Motta, G. H., L. P. Guimarães, E. R. Fernandes, F. Guedes, L. R.M. de Sá, S. dos Ramos Silva, O. G. Ribeiro, and I. S. S. Katz. 2022. Rabies virus isolated from insectivorous bats induces different inflammatory responses in experimental model. Journal of Neuroimmunology, 373: 577974. https://doi.org/10.1016/j.jneuroim.2022.577974 [ianasuly@gmail.com]

Mougari, S., C. Gonzalez, O. Reynard, and B. Horvat. 2022. Fruit bats as natural reservoir of highly pathogenic henipaviruses: Balance between antiviral defense and viral tolerance. Current Opinion in Virology, 54: 101228. https://doi.org/10.1016/j.coviro.2022.101228 [branka.horvat@inserm.fr]

Orellana-Vásquez, H. and L. Barragán-Tabares. 2022. Consecuencias de la pandemia por COVID-19 en una población de murciélagos, dentro de una comunidad indígena de los Andes ecuatorianos. ACI Avances en Ciencias e Ingenierías, 14(2): 1–7. https://doi.org/10.18272/aci.v14i2.2307 [hernanorellanavasquez@gmail.com]

Pace, C., M. Haulena, M. Strobel, G. McGregor, and S. Raverty. 2022. A review of neoplasms in a population of Jamaican fruit bats (*Artibeus jamaicensis*) under human care. Journal of Zoo and Wildlife Medicine, 53(3): 583–592. [c.noelpace@gmail.com]

Schuh, A. J., B. R. Amman, J. C. Guito, J. C. Graziano, T. K. Sealy, S. G. M. Kirejczyk, and J. S. Towner. 2022. Natural reservoir *Rousettus aegyptiacus* bat host model of orthonairovirus infection identifies potential zoonotic spillover mechanisms. Scientific Reports, 12(1): 1–13. [wuc2@cdc.gov]

Straka, T. M., and C. C. Voigt. 2022. Threat perception, emotions and social trust of global bat experts before and during the COVID-19 pandemic. Sustainability, 14(18): 11242. https://doi.org/10.3390/su141811242 [tanja.straka@tu-berlin.de]

Subedi, D., D. Chandran, S. Subedi, and K. P. Acharya. 2022. Ecological and socioeconomic factors in the occurrence of rabies: A forgotten scenario. Infectious Disease Reports, 14(6): 979–986. https://doi.org/10.3390/idr14060097 [subedideepu26@gmail.com]

Van Brussel, K., J. E. Mahar, A. Susana Ortiz-Baez, M. Carrai, D. Spielman, W. S. J. Boardman, M. L. Baker, J. A. Beatty, J. L. Geoghegan, V. R. Barrs, and E. C. Holmes. 2022. Faecal virome of the Australian grey-headed flying fox from urban/suburban environments contains novel

coronaviruses, retroviruses and sapoviruses. Virology, 576: 42–51. https://doi.org/10.1016/j.virol.2022.09.002 [edward.holmes@sydney.edu.au]

Violet-Lozano, L., V. Haach, C. M. Barboza, J. dos Santos, B. F. Gomes, T. de C. P. de Souza, P. Carnieli Junior, C. W. Arns, H. B. de C. R. Batista, P. M. Roehe, and A. C. Franco. 2022. No molecular evidence for influenza A virus and coronavirus in bats belonging to the families *Phyllostomidae, Vespertilionidae*, and *Molossidae* [sic] in the state of São Paulo, Brazil. Brazilian Journal of Microbiology. https://doi.org/10.1007/s42770-022-00878-z [linaviolet14@gmail.com]

Wang, Z., G. Huang, M. Huang, Q. Dai, Y. Hu, J. Zhou, and F. Wei. 2022. Global patterns of phylogenetic diversity and transmission of bat coronavirus. Science China Life Sciences, https://doi.org/10.1007/s11427-022-2221-5 [weifw@ioz.ac.cn]

Weiss S., L. E. Sudi, A. Düx, C. D. Mangu, N. E. Ntinginya, G. M. Shirima, S. Köndgen, G. Schubert, P. T. Witkowski, J.-J. Muyembe, S. Ahuka, B. Klempa, F. H. Leendertz, and D. H. Krüger. 2022. Kiwira virus, a newfound hantavirus discovered in free-tailed bats (Molossidae) in East and Central Africa. Viruses, 14(11): 2368. https://doi.org/10.3390/v14112368 [boris.klempa@savba.sk]

DISTRIBUTION/FAUNAL STUDIES

Arianom, I. M., E. Erianto, and H. Ardian. 2022. Keanekaragaman Jenis Kelelawar (Chiroptera) Di Hutan Tembawang Dusun Penyalimau Empaong Desa Penyalimau Kabupaten Sanggau Provinsi Kalimantan Barat. (Editor's note: article is written almost entirely in Indonesian, with an Abstract in English. Rough translation of title: The diversity of bat species (Chiroptera) in the Tembawang Forest, Penyalimau Empaong hamlet, Penyalimau village, Sanggau District, West Kalimantan province.) Jurnal Lingkungan Hutan Tropis, 1(1): 170–176. https://jurnal.untan.ac.id/index.php/jlht/index [imadearianom.bopeas.200897@gmail.com]

Bhattarai, P. K., B. Sharma, S. Ghimire, S. Sharma, and B. Bhattarai. 2022. A note on bat faunal assessment in Karuna bat cave, Baglung, Nepal. Mammalia, 86(6): 585–590. https://doi.org/10.1515/mammalia-2022-0029 [prabhatkiran79@gmail.com]

Bruno, M., and F. Falcão. 2022. *Pteronotus rubiginosus* (Wagner, 1843): first record of the bat family Mormoopidae in the southeastern region of Brazil. Check List, 18(5): 1017–1022. https://doi.org/10.15560/18.5.1017 [michaelbrunobio@hotmail.com]

Cardoso, F. H. de S., A. C. da S. Lima, A. C., C. L. da S. Costa, S. B. Mendes, A. P. M. Olímpio, E. da C. Fraga, and M. C. Barros. 2022. First record of *Eumops glaucinus* (Wager, 1843) (Chiroptera, Molossidae) to the Brazilian state of Maranhão. Papéis Avulsos De Zoologia, 62: e202262064. https://doi.org/10.11606/1807-0205/2022.62.064 [mbdene@yahoo.com.br]

Daly, G., and G. Hoye. 2022. Survey of bats on the south coast and ranges of the Shoalhaven region in New South Wales. Australian Zoologist, doi: https://doi.org/10.7882/AZ.2022.042 [gaiaresearch@shoalhaven.net.au]

Faiz-ur-Rahman, T. R., A. J. Zulkamal, I. U. Mohammad Salim, M. S. Haider Ali, and F. A. Raqeeb Ullah. 2022. Zaib-Ur-Rahman and Iftikhar Ahmad. Record of *Pipistrellus tenuis* (Temminck, 1831) from some selected areas in Khyber Pakhtunkhwa, Pakistan. Pure and Applied Biology, 12(1): 501–507. [Faizkhan046@gmail.com]

García Morales, R., M. E. Jacome-Flores, S. Hernández-Rodríguez, and E. Pérez-Netzahual. 2022. Nuevos registros de *Vampyrodes major* (Chiroptera: Phyllostomidae) para Tabasco, México. Mammalogy Notes, 8(2): 336. https://doi.org/10.47603/mano.v8n2.336 [r.garciamorales83@gmail.com]

Guevara, N., M. López, and Y. Juárez. 2022. Ampliación en la distribución de *Pteronotus mesoamericanus* (Smith, 1972) en la República de Panamá. (=Extension in the distribution of *Pteronotus mesoamericanus* (Smith, 1972) in the Republic of Panama.) Revista Mexicana De Mastozoología (Nueva Época), 12(1): 73–77. https://doi.org/10.22201/ie.20074484e.2022.12.1.346 [nelson2295@hotmail.com]

Hasan, N. H., U. S. Daud, A. Amat, Y. C. Lok, M. F. Mohd Johar, J. Gompoyo, and Y. T. F. Tuh. 2022. New distribution record of the rare bat *Hypsugo* cf. *vordermanni* (Chiroptera, Vespertilionidae) from the Crocker Range Park, Sabah, Malaysian Borneo. Biodiversity Data Journal, 10: e87860. https://doi.org/10.3897/BDJ.10.e87860 [hhaliza@ums.edu.my]

Khandal, D. 2022. A chiropteran conundrum: The story of the three lost bats of Rajasthan. Rajasthan Biodiversity, https://rajasthanbiodiversity.org/a-chiropteran-conundrum-the-story-of-the-three-lost-bats-of-rajasthan/ [no author e-mail address provided]

Lewis, M. A., E. A. Ferrall, J. S. Johnson, K. M. Morris, N. W. Sharp, J. M. Stober, K. E. Torrey, and A. J. Edelman. 2022. Extralimital occurrences of southeastern myotis in Alabama and Georgia. Southeastern Naturalist, 21(3): 211–219. [No author email address provided. Contact Lewis at Biology Program, University of West Georgia, Carrollton, GA 30118]

Montgomery, C. B., and A. S. Hogue. 2022. The first confirmed occurrence of *Myotis septentrionalis* (northern long-eared bat) on the Delmarva peninsula. Northeastern Naturalist, 29(2): N35–N39. [Montgomery: Salisbury University, Henson School of Science and Technology, Salisbury, MD 21801]

Nistreanu, V., V. Caldari, A. Larion, and N. Dibolscaia. 2022. Bat fauna (Mammalia: Chiroptera) from Saharna limestone mines, Republic of Moldova. Buletinul Academiei de Ştiinţe a Moldovei. Ştiinţele vieţii, 2(346): 64–71. [vicnistreanu@gmail.com]

Pacheco-Figueroa, C. J., J. de D. Valdez-Leal, F. A. Cervantes, R. del C. Luna-Ruíz, E. E. Mata-Zayas, and J. C. Saenz. 2022. Documentation of a road-killed spectral bat (*Vampyrum spectrum*) and first report of the species in Tabasco, México. Therya Notes, 3: 98–103. https://doi.org/10.12933/therya_notes-22-78 [juan.valdez@ujat.mx]

Palacios-Mosquera L, V. D. Palacios-Mayoral, Y. del C. Copete-Mosquera A. M. Jimenez-Ortega, H. Mantilla-Meluk, and P. M. Velazco. 2022. Range extension and distribution update

of *Hsunycteris cadenai* (Chiroptera: Phyllostomidae). Revista de la Academia Colombiana de Ciencias Exactas, Físicas y Naturales, 46(180): 690–696. doi: https://doi.org/10.18257/raccefyn.1631 [lepamo8@gmail.com]

Prakarsa, T. B. P., R. A. Putri, Y. F. Rahmawati, and A. D. Dalee. 2022. Diversity of the cave-dwelling bat (Chiroptera) in the Ngobaran coastal area, Karst of Gunung Sewu. Jurnal Biodjati, 7(2): DOI: https://doi.org/10.15575/biodjati.v7i2.20163 [no author email provided. Contact Prakarsa at Biology Study Program, Faculty of Mathematics and Natural Science, Universitas Negeri Yogyakarta. Jl. Colombo No 1. Yogykarta 55281, Indonesia]

Rodríguez-Moreno, A., E. Y. Martínez-Hernández, and J. A. Fernández. 2022. A Brazilian free-tailed bat *Tadarida brasiliensis* (I. Geoffroy, 1824) (Chiroptera, Molossidae), colony in Santa Eulalia, Chihuahua, Mexico, with records of other bat species. Check List, 18(6): 1369–1375. https://doi.org/10.15560/18.6.1369 [afernandezf@uach.mx]

Saikia, U., and A. B. Meetei. 2022. Diversity, distribution, and abundance status of small mammalian fauna (Chiroptera: Rodentia: Eulipotyphla) of Manipur, India. Journal of Threatened Taxa, 14(9): 21751–21768. https://doi.org/10.11609/jott.8050.14.9.21751-21768 [uttamzsi@gmail.com]

Salvi, R., and S. Parmar. 2022. Micro chiropteran bats: Diversity and roosting sites in Girwa Tehsil of Udaipur District of Rajasthan (India). International Journal of Fauna and Biological Studies, 9(4): 39–43. https://doi.org/10.22271/23940522.2022.v9.i4a.921 [no author email provided. Contact Salvi at Department of Zoology, Shree Bhogilal Pandya Govt. College, Dungarpur, Rajasthan, India]

Shpak, A., L. Godlevska, A. Larchanka, M. Savchenko, P. Vorobei, U. Molchan, and A. Mikhailau. 2022. Data on the summer bat fauna of Belarus in 2017–2020. Theriologia Ukrainica, 23: 20–30. http://doi.org/10.15407/TU2305 [shpak.dvergr@gmail.com]

Singh, S., V. Elangovan, and P. K. Misra. 2022. Diversity and distribution of chiropteran fauna in Bundelkhand region of Uttar Pradesh. International Journal of Entomology Research, 7(8): 17–29. [no author email address provided. Contact Misra at Department of Zoology, School of Life Sciences, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, India]

Son, N. T., A. P. Yuzefovich, and S. V. Kruskop. 2022. First documented bat records on the Hon Tre Island, Nha Trang Bay, Vietnam. Russian Journal of Theriology, 21(2): 115–122. doi:10.15298/rusjtheriol.21.2.02 [yuzefovich2015elf@gmail.com]

Ul Hasan, M. A., and T. Kingston. 2022. Bats of Bangladesh—A systematic review of the diversity and distribution with recommendations for future research Diversity, 14(12): 1042. https://doi.org/10.3390/d14121042 [md-ashraf.ul-hasan@ttu.edu]

ECHOLOCATION

Brinkløv, S. M. M., L. Jakobsen, and L. A Miller. 2022. Echolocation in bats, odontocetes, birds, and insectivores. Pp. 419–457 *in* C. Erbe and J. A. Thomas (eds) Exploring Animal

Behavior Through Sound: Volume 1. Springer, Cham., https://doi.org/10.1007/978-3-030-97540-1_12 [Lee@biology.sdu.dk] ISBN: 978-3-030-97538-8 (hardcover print)

Carmichael, S. 2022. Could a moth's stealth technology make our world a little quieter? Microscopy Today, 30(6): 8–9. doi:10.1017/S1551929522001249 [carmichael.stephen@mayo.edu]

Chornelia, A., and A. C. Hughes. 2022. Phenotypic traits evolution and morphological traits associated with echolocation calls in cryptic horseshoe bats (Rhinolophidae). Journal of Systematics and Evolution. https://doi.org/10.1111/jse.12924 [ach_conservation2@hotmail.com]

Fernández, Y., N. J. Dowdy, and W. E. Conner. 2022. High duty cycle moth sounds jam bat echolocation: bats counter with compensatory changes in buzz duration. Journal of Experimental Biology, 225(18): jeb244187. doi: https://doi.org/10.1242/jeb.244187 [yohami.fdelgado@gmail.com]

Jespersen, C., D. Docherty, J. Hallam, C. Albertsen, and L. Jakobsen. 2022. Drone exploration of bat echolocation: A UAV-borne multimicrophone array to study bat echolocation. Ecology and Evolution, 12: e9577. https://doi.org/10.1002/ece3.9577 [lasse@biology.sdu.dk]

Knight, K. 2022. Fast-fire moths are better jammers, but bats can outsmart them. Journal of Experimental Biology, 225(18): jeb244954. doi: https://doi.org/10.1242/jeb.244954 [kathryn.knight@biologists.com]

Luo, J., M. Lu, J. Luo, and C. F. Moss. 2022. Echo feedback mediates noise-induced vocal modifications in flying bats. Journal of Comparative Physiology A, pp. 1–12. https://doi.org/10.1007/s00359-022-01585-8 [jluo@ccnu.edu.cn]

Pulver, C. A., E. Celiker, C. Woodrow, I. Geipel, C. D. Soulsbury, D. A. Cullen, S. M. Rogers, D. Veitch, and F. Montealegre-Z. 2022. Ear pinnae in a neotropical [sic] katydid (Orthoptera: Tettigoniidae) function as ultrasound guides for bat detection. eLife, 11: e77628. https://doi.org/10.7554/eLife.77628 [ECeliker@lincoln.ac.uk]

Salles, A., M. J. Wohlgemuth, and C. F. Moss. 2022. Neural coding of 3D spatial location, orientation, and action selection in echolocating bats. Trends in Neurosciences, https://doi.org/10.1016/j.tins.2022.09.008 [salles@uic.edu]

Schoeppler, D., K. Kost, H.-U. Schnitzler, and A. Denzinger. 2022. Transmitter and receiver of the low frequency horseshoe bat *Rhinolophus paradoxolophus* are functionally matched for fluttering target detection. Journal of Comparative Physiology A, https://doi.org/10.1007/s00359-022-01571-0 [diana.schoeppler@uni-tuebingen.de]

Tan, X., Y. Li, K. Sun, L. Jin, and J. Feng. 2022. Mutual mother-pup acoustic identification in Asian particolored bats. Ecology and Evolution, 12: e9554. https://doi.org/10.1002/ece3.9554 [jinlr915@nenu.edu.cn]

Teshima, Y., T. Tsuchiya, and S. Hiryu. 2022. Why use the finite difference time domain method for studying echolocation bats?. The Journal of the Acoustical Society of America, 152(4): A250–A250. https://doi.org/10.1121/10.0016173 [yuteshima18@gmail.com]

Webster, C., A. Tuninetti, J. Granger, S. S. I. A. U. Grafe, and R. Müller. 2022. Field study of bats in Brunei Darussalam. The Journal of the Acoustical Society of America, 152: A69–A69. https://doi.org/10.1121/10.0015570 [cfjwebster17@tamu.edu]

Ye, H., and J. Luo. 2022. Perceptual hearing sensitivity during vocal production. iScience, 25(11): 105435. https://doi.org/10.1016/j.isci.2022.105435 [jluo@ccnu.edu.cn]

ECOLOGY

Abdel-Hamid, F., and A. R. Alqahtani. 2022. Morphological characters and feeding habits of insectivorous Kuhl's pipistrelle bat *Pipistrellus kuhlii* Cretzschmar, 1830, in different riverine habitats. Saudi Journal of Biological Sciences, 29(12): 103490. https://doi.org/10.1016/j.sjbs.2022.103490 [no author e-mail provided. Contact Abdel-Hamid at Departments of Zoology, Faculty of Science, Al-Azhar University in Cairo, Egypt]

Andersen, B. R., and K. Geluso. 2022. Roosts of northern long-eared myotis (*Myotis septentrionalis*) at the western edge of the Great Plains. Western North American Naturalist, 82(3): https://scholarsarchive.byu.edu/wnan/vol82/iss3/13 [no author e-mail provided]

Armstrong, A. J., F. M. Walker, C. J. Sobek, C. J. Sanville, S. L. Martin, and J. M. Szewczak. 2022. Bat use of hollows in California's old-growth redwood forests: From DNA to ecology. Animals, 12(21): 2950. https://doi.org/10.3390/ani12212950 [aja40@humboldt.edu]

Balzer, E. W., T. S. McBurney, and H. G. Broders. 2022. Little brown Myotis roosts are spatially associated with foraging resources on Prince Edward Island. Wildlife Society Bulletin, p. e1405. https://doi.org/10.1002/wsb.1405 [hugh.broders@uwaterloo.ca]

Brighton, C. H., L. N. Kloepper, C. D. Harding, L. Larkman, K. McGowan, L. Zusi, and G. K. Taylor. 2022. Raptors avoid the confusion effect by targeting fixed points in dense aerial prey aggregations. Nature Communications, 13(4778). https://doi.org/10.1038/s41467-022-32354-5 [caroline.brighton@biology.ox.ac.uk]

Burrell, G. E., and S. M. Bergeson. 2022. Roosting behavior of northern long-eared bats (*Myotis septentrionalis*) in an urban-adjacent forest fragment. Forests, 13(12): 1972. https://doi.org/10.3390/f13121972 [galen.burrell@gmail.com]

Buxton, M. N., A. C. Gaskett, J. M. Lord, and D. E. Pattemore. 2022. A global review demonstrating the importance of nocturnal pollinators for crop plants. Journal of Applied Ecology, pp. 1–12. https://doi.org/10.1111/1365-2664.14284 [max.buxton@plantandfood.co.nz]

Carvalho, W. D., L. M. Rosalino, B. da Silva Xavier, I. J. de Castro, R. Hilário, T. M. Marques, J. J. de Toledo, M. V. Vieira, J. M. Palmeirim, and K. Mustin. 2022. The relative importance of

forest cover and patch-level drivers for phyllostomid bat communities in the Amazonian Savannas. Landscape Ecology, pp.1–14. https://doi.org/10.1007/s10980-022-01565-y [wilruoca@hotmail.com]

Colorado-Durán, W. B., E. K. Espinosa-Francisco, F. Sierra-Vázquez, and A. A. Castro-Luna. 2022. Dispersal of *Hoffmannia excelsa* (Rubiaceae) by the Toltec fruit-eating bat (*Artibeus toltecus*) in central Veracruz, México. Therya Notes, 3: 6–9. https://doi.org/10.12933/therya_notes-22-60 [castrolun@gmail.com]

De Oliveira, M. B., M. L. Brandão, J. L. P. Cordeiro, L. F. B. de Oliveira, and A. L. Peracchi. 2022. Trophic structure and foraging strategies in a bat community in northern Pantanal, Brazil. Mammalia, https://doi.org/10.1515/mammalia-2021-0196 [oliveira01marcione@gmail.com]

Ditchfield, A. D., J. P. Maires Hoppe, G. M. Andrade, A. S. Tahara, F. de M. Martins, M. Scabello, M. Oprea, R. Z. Coutinho, V. T. Pimenta, and T. B. Vieira. 2022. Change in the composition of cave-dwelling bats after a 53-year interval at the Gruta do Limoeiro (Espírito Santo, Brazil). Mammalia, https://doi.org/10.1515/mammalia-2021-0094 [vieiratb@ufpa.br]

Ferreira, M. M., B. da S. Xavier, P. E. D. Bobrowiec, I. J. de Castro, R. Hilário, A. C. da Cunha, L. L. Oliveira, J. J. de Toledo, and W. D. Carvalho. 20232. Bat diversity is driven by elevation and distance to the nearest watercourse in a *terra firme* forest in the northeastern Brazilian Amazon. Journal of Tropical Ecology, 39: E1. doi:10.1017/S0266467422000438 [uthiramartins@gmail.com]

Foti, M., M. T. Spena, V. Fisichella, A. Mascetti, M. Colnaghi, M. Grasso, C. Piraino, F. Sciurba, and R. Grasso. 2022. Cultivable bacteria associated with the microbiota of troglophile bats. Animals, 12(19): 2684. https://doi.org/10.3390/ani12192684 [malinvet@unime.it]

Geluso, K. 2022. Immediate effects of a wildfire on bats in a ponderosa pine (*Pinus ponderosa*) forest. Western North American Naturalist, 82(3): 577–582. https://doi.org/10.3398/064.082.0312 [gelusok1@unk.edu]

Gorman, K. M., E. L. Barr, T. Nocera, and W. M. Ford. 2022. Characteristics of day-roosts used by northern long-eared bats (*Myotis septentrionalis*) in coastal New York. Northeastern Naturalist, 29(2): 153–170. [Gorman: Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, 149 Cheatham Hall, 310 West Campus Drive, Blacksburg, VA 24061]

Gutierrez-Sanabria, D. R., and D. J. Lizcano. 2022. Dinámica poblacional y fidelidad de refugio de *Carollia brevicauda* (Quiroptera: Phyllostomidae) en un refugio artificial, en Los Andes nororientales de Colombia. Mammalogy Notes, 8(1): 203, pp. 1–13. https://doi.org/10.47603/mano.v8n1.203 [diecolo24@gmail.com]

Handayani, T. 2022. Seed dispersal of Annonaceae in the Bogor Botanical Gardens, Indonesia. Prosiding Seminar Nasional Masyarakat Biodiversitas Indonesia, 8(2): 136–141. DOI: https://doi.org/10.13057/psnmbi/m080205 [irtri@yahoo.co.id]

Hernández-Ruz, E. J., W. Gonçalves, F. O. do Nascimento Pereira, I. F. de França,, G. B. de Souza Junior, C. G. Santos, and S. Farias. 2022. Predation on *Rhamphocelus carbo* (Pallas, 1764) (Aves: Thraupidae) by the neotropical [sic] carnivorous bat *Vampyrum spectrum* (Linnaeus, 1758) (Mammalia: Phyllostomidae) in a forest management area of eastern Amazon, Brazil). Boletim Do Museu Paraense Emílio Goeldi - Ciências Naturais, 17(2): 557–561. https://doi.org/10.46357/bcnaturais.v17i2.576 [emilhjh@ufpa.br]

Liévano-Latorre, L. F., I. G. Varassin, and T. B. Zanata. 2022. Evolutionary history and precipitation seasonality shape niche overlap in Neotropical bat–plant pollination networks. Biotropica, https://doi.org/10.1111/btp.13181 [luisafer.lievano@gmail.com]

Lorenzo, C., C. Lorenzo-Monterrubio, J. E. Bolaños, and G. Tapia-Ramírez. 2022. Use of abandoned buildings by mammals in tropical forest sites with no forest control. Therya Notes, 3: 18–23. https://doi.org/10.12933/therya_notes-22-63 [gloria.tapia@estudianteposgrado.ecosur.mx]

Malan, G., E. Harris, T. Harris, and A. Monadjem. 2022. A bat hawk *Macheiramphus alcinus* pair preyed primarily on bats and birds that forage in clutter-edge and open-air habitat groups. African Zoology 57(3): 165–169. [No author email address provided]

McSweeny, T. and D. M. Brooks. 2022. Some observations of severe weather events on a large urban population of free-tailed bats (*Tadarida brasiliensis*). The Southwestern Naturalist, 66(4): 333–338. https://doi.org/10.1894/0038-4909-66.4.333 [tim_macsweeny@yahoo.com]. (Editor's note: the paper belongs to Vol. 66, which was supposed to be published in December of 2021, but it appeared in December of 2022.)

Medina-Bello, K. I., E. Vázquez-Rueda, and J. Ayala-Berdón. 2022. Ecological interaction between *Artibeus jamaicensis* and *Microdesmia arborea* in a deciduous forest of central México. Therya Notes, 3: 115–118. https://doi.org/10.12933/therya_notes-22-81 [jorgeayalaberdon@gmail.com]

Oelbaum, P. J., T. S. M. Teixeira, E. L. Clare, and H. G. Broders. 2022. Variation in diet of frugivorous bats in fragments of Brazil's Atlantic Forest associated with vegetation density. Journal of Mammalogy, 103(5): 1058–1071. https://doi.org/10.1093/jmammal/gyac024 [hugh.broders@uwaterloo.ca]

Ortega-García, S., and R. A. Saldaña-Vázquez. 2022. Synthesis of knowledge of the plant diet of nectar-feeding bats of México. Therya, 13(3): 335–343. [sortega@cieco.unam.mx]

Page, R. A., and D. K. N. Dechmann. 2022. Roost making in bats. Current Biology, 32(22): R1252–R1259. https://doi.org/10.1016/j.cub.2022.10.040 [PageR@si.edu]

Pellón, J. J., E. F. Medina-Espinoza, B. K. Lim, F. Corneja, and R. A. Medellín. 2022. Eat what you can, when you can: relatively high arthropod consumption by frugivorous bats in Amazonian Peru. Mammalian Biology, https://doi.org/10.1007/s42991-022-00327-2 [juanpe2104@gmail.com]

Ridgley, F. N., K. M. Bohn, I. Salazar, S. Thompson, and M. Gamba-Rios. 2022. Use and distribution of roosts by Florida bonneted bats in Miami Dade County, Florida, USA: Addition to Webb et al. 2021. [Frank.Ridgley@miamidade.gov]

Segura-Trujillo, C. A., S. T. Álvarez-Castañeda, S. Castañeda-Rico, and J. E. Maldonado. 2022. Taxonomic versus ecological prey traits among arthropodophagous bats: implications for surveying trophic partitioning patterns. Journal of Mammalogy, 103(5): 1071–1083. https://doi.org/10.1093/jmammal/gyac027 [sticul@cibnor.mx]

Sélem-Salas, C. I., C. M. Alamilla, D. A. C. Carrillo, and J. A. P. Alayola. 2022. Diversidad morfológica y alimentaria en murciélagos neotropicales. (= Morphological and food diversity in Neotropical bats.) Bioagrociencias, 15(2): 137–146. [ssalas@correo.uady.mx]

Sengupta, A. 2022. Animal-mediated seed dispersal in India: Implications for conservation of India's biodiversity. Biotropica, 54: 1320–1330. https://doi.org/10.1111/btp.12982 [asmita.sengupta@gmail.com]

Sil-Berra, L. M., C. Sánchez-Hernández, M. de L. Romero-Almaraz, and V. H. Reynoso. 2022. Bat species diversity and abundance of trophic guilds after a major hurricane along an anthropic disturbance gradient. Diversity, 14(10): 818. https://doi.org/10.3390/d14100818 [cornelio@unam.mx]

Silva, A. C. F. V., A. A. M. de Barros, D. N. S. Machado, E. C. Lourenço, H. G. Bergallo, E. F. Guimarães, L. C. Moura, and L. de Moraes Costa. 2022. Novos registros para a dieta de *Carollia perspicillata* (Linnaeus, 1758) (Chiroptera, Phyllostomidae) e para a flora da Ilha Grande, estado do Rio de Janeiro, Brasil. Notas Sobre Mamíferos Sudamericanos, 4: https://doi.org/10.31687/SaremNMS22.11.3 [no author email address provided]

Swartz, E., S. M. Weier, M. E. Pretorius, and M. Keith. 2022. Natural vegetation edges promote bat activity in macadamia orchards in northeastern South Africa. African Journal of Wildlife Research, 52(1): https://doi.org/10.3957/056.052.015 [sinaweier.univen@gmail.com]

Torquetti, C. G., T. P. de Carvalho, R. M. P. de Freitas, M. B. Freitas, A. T. B. Guimarães, and B. Soto-Blanco. 2023. Influence of landscape ecology and physiological implications in bats from different trophic guilds. Science of The Total Environment, 857(3): 159631. https://doi.org/10.1016/j.scitotenv.2022.159631 [benito@ufmg.br]

Vasconcelos, S. D., E. Barbier, and T. M. Barbosa. 2022. Life post-death: Colonization of a bat carcass by *Microcerella halli* (Engel, 1931) (Diptera: Sarcophagidae) in a Neotropical cave. Papéis Avulsos De Zoologia, 62: e202262065. https://doi.org/10.11606/1807-0205/2022.62.065 [tacianomoura7@gmail.com]

Vilches-Piñones, K.I., C. Matus-Olivares, G. Catalán, and F. Lisón. 2022. Effect of forest areas configuration on the community of insectivorous bats in agroforestry landscapes. Austral Ecology, pp. 1–13. https://doi.org/10.1111/aec.13268 [flison@udec.cl]

Wray, A. K., and M. Z. Peery. 2022. Comparing little brown and big brown bat isotopic niches over the past century in an agriculturally dominated landscape. Journal of Mammalogy, 103(5): 1045–1057. https://doi.org/10.1093/jmammal/gyac018 [awray1@uwyo.edu]

EVOLUTION

Fitzpatrick, L. L. J., V. Nijman, R. Ligabue-Braun, and K. A.-I. Nekaris. 2022. The fast and the furriest: investigating the rate of selection on mammalian toxins. Toxins, 14(12): 842. https://doi.org/10.3390/toxins14120842 [19148055@brookes.ac.uk]

FLIGHT

Rahman, A., and D. Tafti. 2022. Role of wing inertia in maneuvering bat flights. Bioinspiration & Biomimetics, DOI 10.1088/1748-3190/ac9fb1. [dtafti@exchange.vt.edu]

GENOMICS

Chua1P. Y. S., C. Carøe, A. Crampton-Platt, C. S. Reyes-Avila, G. Jones, D. G. Streicker, and K. Bohmann. 2022. A two-step metagenomics approach for the identification and mitochondrial DNA contig assembly of vertebrate prey from the blood meals of common vampire bats (*Desmodus rotundus*). Metabarcoding and Metagenomics, 6: 75–87. DOI 10.3897/mbmg.6.78756 [physiliachua@gmail.com]

Li, J., K. Sun, W. Dai, H. Leng, and J. Feng. 2022. Divergence in interspecific and intersubspecific gene expression between two closely related horseshoe bats (*Rhinolophus*). Journal of Mammalogy, gyac103, https://doi.org/10.1093/jmammal/gyac103 [sunkp129@nenu.edu.cn]

Li, J., K. Sun, W. Dai, H. Leng, A. Li, and J. Feng. 2022. Extensive adaptive variation in gene expression within and between closely related horseshoe bats (Chiroptera, *Rhinolophus*) revealed by three organs. Animals, 12(23): 3432. https://doi.org/10.3390/ani12233432 [fengj@nenu.edu.cn]

Nawae, W., C. Sonthirod, T. Yoocha, P. Waiyamitra, P. Soisook, S. Tangphatsornruang, and W. Pootakham. 2022. Genome assembly of the Pendlebury's roundleaf bat, *Hipposideros pendleburyi*, revealed the expansion of *Tc1/Mariner* DNA transposons in Rhinolophoidea. DNA Research, 29(5): dsac026. https://doi.org/10.1093/dnares/dsac026 [wirulda@alumni.stanford.edu]

Paulat, N. S., E. McGuire, K. Subramanian, A. B. Osmanski, D. D. Moreno-Santillán, D. A. Ray, and J. Xing. 2022. Transposable elements in bats show differential accumulation patterns determined by class and functionality. Life, 12(8): 1190. https://doi.org/10.3390/life12081190 [jinchuan.xing@rutgers.edu]

HIBERNATION

Currie, S. E., G. Körtner, and F. Geiser. 2022. Pronounced differences in heart rate and metabolism distinguish daily torpor and short-term hibernation in two bat species. Scientific

Reports, 12(1): 21721, pp. 1–10. https://doi.org/10.1038/s41598-022-25590-8 [shannon.e.currie@gmail.com]

Fjelldal, M. A., C. Stawski, R. Sørås, and J. Wright. 2022. Determining the different phases of torpor from skin- or body temperature data in heterotherms. Journal of Thermal Biology, 111: 103396. https://doi.org/10.1016/j.jtherbio.2022.103396 [mari.a.fjelldal@ntnu.no]

Jansen, E. A., E. Korsten, M. J. Schillemans, M. Boonman, and H. G. .J. A. Limpens. 2022. A method for actively surveying mass hibernation sites of the common pipistrelle (*Pipistrellus pipistrellus*) in the urban environment. Lutra, 65(1): 201–219. [herman.limpens@Zoogdier vereniging.nl]

Măntoiu, D. Ş., I. C. Mirea, I. C. Şandric, A. G. Cîşlariu, I. Gherghel, S. Constantin, and O. T. Moldovan. 2022. Bat dynamics modelling as a tool for conservation management in subterranean environments. PLoS ONE, 17(10): e0275984. https://doi.org/10.1371/journal.pone.0275984 [stephen.mantoiu@gmail.com]

Verhees, J. J. F., J. C. Buys, P. H. van Hoof, H. W. G. Heijligers. and W. F. de Boer. 2022. Long-term trends of bats hibernating in small artificial hibernacula in northern Limburg and population dynamics explained by climatic conditions. Lutra, 65(1): 119–133. [jjf.verhees@hotmail.com]

Wright, P. G. R., T. Kitching, R. Hanniffy, M. B. Palacios, K. McAney, and H. Schofield. 2022. Effect of roost management on populations trends of *Rhinolophus hipposideros* and *Rhinolophus ferrumequinum* in Britain and Ireland. Conservation Evidence Journal, 19: 21–26. [patrickwright@vwt.org.uk]

HISTORY OF CHIROPTEROLOGY

Griffiths, T. A. 2022. '*Shout hurrah!*' New thoughts on the origin and meaning of the bat species name *Ia io*, created in 1902 by Oldfield Thomas FRS. Notes and Records—The Royal Society Journal of the History of Science, 76(3): 337–350. http://doi.org/10.1098/rsnr.2022.0006 [thomas.alan.griffiths@gmail.com]

IMMUNOLOGY

Moreno-Santillán, D. D., C. Machain-Williams, G. Hernández-Montes, and J. Ortega. 2022. Transcriptomic analysis elucidates evolution of the major histocompatibility complex class I in neotropical [sic] bats. Journal of Mammalogy, 103(5): 1084–1093. https://doi.org/10.1093/jmammal/gyac052 [artibeus2@aol.com]

Otálora-Ardila, A., J. J. Flores-Martínez, C. Rosales, A. Salame-Méndez, and L. G. H. Montalvo. 2022. Physiological and ecological correlates of the cellular and humoral innate immune responses in an insular desert bat: the fish-eating myotis (*Myotis vivesi*). Diversity, 14(10): 781. https://doi.org/10.3390/d14100781 [gherrera@ib.unam.mx]

Seltmann, A., S. A. Troxell, J. Schad, M. Fritze, L. D. Bailey, C. C. Voigt, and G. Á Czirják. 2022. Differences in acute phase response to bacterial, fungal and viral antigens in greater mouse-eared bats (*Myotis myotis*). Scientific Reports, 12(1): 1–13. https://doi.org/10.1038/s41598-022-18240-6 [czirjak@izw-berlin.de]

Toshkova, N., V. Zhelyazkova, S. Justesen, and J. D. Dimitrov. 2023. Conservative pattern of interaction of bat and human IgG antibodies with FcRn. Developmental & Comparative Immunology, 139: 104579. https://doi.org/10.1016/j.dci.2022.104579 [niyatoshkova@gmail.com]

KARYOTYPES

Muanglen, N., P. Piyatrakulchai, N. Donbundit, A. Tanomtong, and S. Ditcharoen. 2022. Chromosomal description and molecular cytogenetic markers of Nepalese whiskered myotis, *Myotis muricola* (Chiroptera: Vespertilionidae) from Thailand. Science, Technology, and Engineering Journal (STEJ), 8(2): 99–110. [sukhonthip_d@rmutt.ac.th]

Rajičić, M., I. Budinski, M. Miljević, B. Bajić, M. Paunović, M. Vujošević, and J. Blagojević. 2022. The new highest number of B chromosomes (Bs) in Leisler's bat *Nyctalus leisleri* (Kuhl, 1817). Comparative Cytogenetics 16(3): 173–184. https://doi.org/10.3897/compcytogen.v16.i3.89911 [marija.rajicic@ibiss.bg.ac.rs]

MACHINES ON AN INDUSTRIAL SHOP FLOOR CAN MANEUVER USING A BAT-INSPIRED ECHOLOCATION SYSTEM; HUMANS CAN DO THE SAME

Akbarzadeh, S., X. Gu, Z. Wu and B. Lo. 2022. A novel active human echolocation device. 2022 IEEE-EMBS International Conference on Wearable and Implantable Body Sensor Networks (BSN), pp. 1–4. doi: 10.1109/BSN56160.2022.9928448 [No author email address provided]

Estrada Jimenez, L. A., S. N. Hojjati and J. Barata. 2022. Self-organization of a highly flexible shop floor – From muti-agent based interactions to an echolocation-inspired automation system. 2022 IEEE International Conference on Systems, Man, and Cybernetics (SMC), pp. 1109–1114. doi: 10.1109/SMC53654.2022.9945187 [No author email address provided]

NATURAL HISTORY

Ospina-Garcés, S. M., L. León-Paniagua, P. A. Aguilar-Rodríguez, and G. M. C. MacSwiney. 2022. Natural history of the fishing bat *Noctilio leporinus* (Chiroptera: Noctilionidae) in the Gulf of Mexico. Mammalia, https://doi.org/10.1515/mammalia-2022-0098 [cmacswiney@uv.mx]

PALEONTOLOGY

Lopatin, A. V. 2022. Early Pleistocene horseshoe bat *Rhinolophus macrorhinus cimmerius* subsp. nov. (Rhinolophidae, Chiroptera) from the Taurida Cave in Crimea. Doklady Biological Sciences, 506: 119–127. https://doi.org/10.1134/S0012496622050076 [alopat@paleo.ru]

PARASITOLOGY

Alcantara, D. M. C., G. Graciolli, M. Antunes Junior, R. Toma, and S. S. Nihei. 2022. Biogeographical events, not cospeciation, might be the main drivers in the historical association between *Noctiliostrebla* species (Streblidae) and their bulldog bat hosts. Biological Journal of the Linnean Society, 137(4): 583–602. https://doi.org/10.1093/biolinnean/blac097 [danielmxm@gmail.com]

Bassini-Silva, R., F. C. Jacinavicius, C. Welbourn, R. Ochoa, and D. M. Barros-Battesti. 2022. *Whartonia pachywhartoni* Vercammen-Grandjean, 1966 (Acari: Trombidiformes: Leeuwenhoekiidae): lost types in the USNM. Zoosymposia, 22: 153–153. [no author email provided]

Bezerra, R. H. S., and A. Bocchiglieri. 2022. Ectoparasitic flies of bats (Mammalia: Chiroptera) in urban green areas of northeastern Brazil. Parasitology Research, https://doi.org/10.1007/s00436-022-07703-4 [rayhellem@hotmail.com]

Costa, T. F., D. J. B. Coutinho, A. K. S. M. Simas, G. V. Santos, R. M. S. Nogueira, F. B. Costa, M. C. Barros, E. da C. Fraga, and A. P. da Costa. 2022. *Litomosoides brasiliensis* (Nematoda: Onchocercidae) infecting chiropterans in the Legal Amazon region, Brazil. Brazilian Journal of Veterinary Parasitology, 31(4): e011722.c https://doi.org/10.1590/S1984-29612022059 [andrea.costa@professor.uema.br]

Da Silva, A. dos S., E. Barbier, W. R. Telino Júnior, L. A. M. da Silva, and J. B. de Oliveira. 2022. Parasitism on bats by bat flies in remnants of a humid forest enclave area in Northeastern Brazil. Veterinary Parasitology: Regional Studies and Reports, 100826. https://doi.org/10.1016/j.vprsr.2022.100826 [jaqueline.boliveira@ufrpe.br]

Dornelas Júnior, L. F., F. A. C. Pessoa, F. de C. Jacinavicius, R Bassini-Silva, M. B. Labruna, and L. M. A. Camargo. 2022. Levantamento bibliográfico: biodiversidade de ectoparasitos de morcegos. Revista Científica da Faculdade de Educação e Meio Ambiente, 13(edespccs). https://revista.faema.edu.br/index.php/Revista-FAEMA/article/view/1161 [leormando@hotmail.com]

Dundarova, H., M. Orlova, N. Anisimov, S. Baskakova, G. Shakula, F. Shakula, S. Shakula, and K. Amirekul, 2022. A new species of *Spinturnix* (Acari: Spinturnicidae) from the Turkestani long-eared bat *Otonycteris leucophaea* (Chiroptera: Vespertilionidae) in Kazakhstan. Zootaxa, 5222(5): 443–456. DOI: 10.11646/zootaxa.5222.5.3 [no author email address provided]

Hayer, S., B. P. Sturm, S. Büsse, T. H. Büscher, and S. N. Gorb. 2022. Louse flies holding on mammals' hair: Comparative functional morphology of specialized attachment devices of ectoparasites (Diptera: Hippoboscoidea). Journal of Morphology, pp. 1–16. https://doi.org/10.1002/jmor.21523 [sarah.hayer@gmx.de]

Hekimoglu, O., M. Elverici, and T. Yorulmaz. 2022. A survey of hard ticks associated with cave dwelling mammals in Turkey. Ticks and Tick-borne Diseases, 13(6): 102008. Doi: 10.1016/j.ttbdis.2022.102008 [mert.elverici@erzincan.edu.tr]

Kamani, J., J. González-Miguel, E. G. Msheliza, and T. L. Goldberg. 2022. Straw-colored fruit bats (*Eidolon helvum*) and their bat flies (*Cyclopodia greefi*) in Nigeria host viruses with multifarious modes of transmission. Vector-Borne and Zoonotic Diseases, pp. 545–552. http://doi.org/10.1089/vbz.2022.0025 [tony.goldberg@wisc.edu]

Lobato-Bailón, L., A. López-Morales, R. Quintela, M. P. Ribas, R. Molina-López, E. Obon, S. Napp, L. Pailler-García, J. Espunyes, and Ó. Cabezón. 2022. Lack of detection of *Toxoplasma gondii* in *Pipistrellus* spp. Bats from densely cat-populated areas of NE Spain. Pathogens, 11(12): 1451. https://doi.org/10.3390/pathogens11121451 [l.lobatobailon@gmail.com]

Mancilla-Agrono, L. Y., L. F. Banguero-Micolta, P. A. Ossa-López, H. E. Ramírez-Chaves, G. J. Castaño-Villa, and F. A. Rivera-Páez. 2022. Is *Borrelia burgdorferi* sensu stricto in South America? First molecular evidence of its presence in Colombia. Tropical Medicine and Infectious Disease, 7(12): 428. [fredy.rivera@ucaldas.edu.co]

Mello, R. M., R. S. Laurindo, L. C. Silva, M. V. Pyles, and L. F. O. Bernardi. 2022. Configuration and composition of human-dominated tropical landscapes affect the prevalence and average intensity of mite and fly infestation in Phyllostomidae bats. Parasitology Research, https://doi.org/10.1007/s00436-022-07704-3 [rodrigomellojf@gmail.com]

Moguel-Chin, W., D. I. Hernández-Mena, M. Torres-Castro, R. C. Barrientos-Medina, S. F. Hernández-Betancourt, M. C. MacSwiney, L. García-Prieto, V. M. Vidal-Martínez, C. I. Selem-Salas, and J. A. Panti-May. 2022. Survey on helminths of bats in the Yucatan Peninsula: Infection levels, molecular information, and host-parasite networks. Parasitology, pp. 1–42. doi:10.1017/S0031182022001627 [alonso.panti@correo.uady.mx]

Morales-Malacara, J. B., and G. López-Ortega. 2022. A new species of the genus *Periglischrus* (Acari: Spinturnicidae) on *Leptonycteris nivalis* (Chiroptera: Phyllostomidae) from Mexico, including a key to species of the *vargasi* species group. Journal of Medical Entomology, tjac151. https://doi.org/10.1093/jme/tjac151 [morales.malacara@gmail.com]

Orlova, M. V., A. I. Larchanka, I. G. Dolgova, and V. V. Dziamianchyk. 2022. Unusual findings of fleas (Siphonaptera: Ctenophthalmidae, Ceratophyllidae) on bats (Chiroptera: Vespertilionidae) in Belarus: case report. Ecologica Montenegrina, 57: 37–43. [masha_orlova@mail.com]

Ossa-López, P. A., L. Y. Mancilla-Agrono, L. F. B. Micolta, H. E. Ramírez-Chaves, J. D. C. Agudelo, S. Muñoz-Leal, M. B. Labruna, V. Lloyd, and F. A. Rivera-Páez. 2022. Morphological and molecular confirmation of *Ornithodoros Hasei* [sic] (Schulze, 1935) (Acari: Argasidae) in Colombia. SSRN, pp.1–14. https://ssrn.com/abstract=4240833 [fredy.rivera@ucaldas.edu.co]

Pena, S. A., A. B. Alencastre-Santos, J. B. da Silva, L. L. Correia, G. L. Urbieta, G. Graciolli, L. Palheta, and T. B. Vieia. 2022. Bats (Mammalia, Chiroptera) and bat flies (Diptera, Streblidae) from the Cazumbá-Iracema and Chico Mendes Reserve, Western Brazilian Amazon. Parasitology Research, https://doi.org/10.1007/s00436-022-07741-y [sialpena@gmail.com]

Pilatasig, A. L. 2022. Primer reporte del parasitismo de *Ixodes luciae* Sénevet, 1940 (Acari: Ixodidae) sobre dos especies de murciélagos *Sturnira giannae* y *Glossophaga soricina* (Chiroptera: Phyllostomidae). Revista Argentina de Parasitología, 11(2): 7–10. [No author email address provided]

Ratzlaff, F. R., F. D. Fernandes, V. Osmari, D. Silva, J. S. de P. Vasconcellos, P. Braunig, F. S. F. Vogel, S. de Á Botton, H. F. dos Santos, J. F. Cargnelutti, E. T. Caldart, A. Campos, J. A. de M. Filho, J. F. Soares, R. Fagundes-Moreira, A. A. Witt, S. M. Pacheco, and L. A. Sangioni. 2022. Prevalence and molecular detection of *Leishmania* spp. in bats from Rio Grande do Sul state, Brazil. Parasitology Research, 121: 3193–3202. https://doi.org/10.1007/s00436-022-07639-9 [fagner.fernandes@acad.ufsm.br]

Stekolnikov, A. A., J. Quetglas, C. Ibáñez, and S. Sánchez-Navarro. 2022. Contribution to the fauna of chiggers (Acariformes: Trombiculidae) parasitizing bats in Spain. Acarologia, 62(4): 1201–1209. https://doi.org/10.24349/qojp-y0ow [No author email address provided]

Szentiványi, T., S. Hornok, Á. B. Kovács, N. Takács, M. Gyuranecz, W. Markotter, P. Christe, and O. Glaizot. 2022. Polyctenidae (Hemiptera: Cimicoidea) species in the Afrotropical region: Distribution, host specificity, and first insights to their molecular phylogeny. Ecology and Evolution, 12: e9357. https://doi.org/10.1002/ece3.9357 [tamaraszentivanyi@gmail.com]

Toshkova, N., B. Zlatkov, A. Fakirova, V. Zhelyazkova, and N. Simov. 2022. First record of *Psorergatoides* Fain, 1959 (Acari, Cheyletoidea, Psorergatidae) for the Balkan Peninsula with description of the cutaneous lesions on the wing membrane of its hosts *Myotis myotis* (Borkhausen, 1797) and *Myotis blythii* (Tomes, 1857) (Chiroptera, Vespertilionidae). Biodiversity Data Journal, 10: e89514. https://doi.org/10.3897/BDJ.10.e89514 [nia.toshkova@iber.bas.bg]

Vlaschenko, A., C. Răileanu, O. Tauchmann, D. Muzyka, and V. Bohodist, S. Filatov, O. Rodenko, I. Tovstukha, and C. Silaghi. 2022. First data on bacteria associated with bat ectoparasites collected in Kharkiv oblast, Northeastern Ukraine. Parasites & Vectors, 15(443). https://doi.org/10.1186/s13071-022-05582-3 [anton.vlaschenko@gmail.com]

PHYSIOLOGY

Barratt, A. E., L. Gonsalves, and C. Turbill. 2022. Winter torpor and activity patterns of a fishing bat (*Myotis macropus*) in a mild climate. Journal of Mammalogy, gyac061. https://doi.org/10.1093/jmammal/gyac061 [c.turbill@westernsydney.edu.au]

Ilyina, T. N., and I. V. Baishnikova. 2022. Retinol and α-tocopherol content in the liver and skeletal muscle of bats (Chiroptera) during hibernation and summer activity. Journal of Evolutionary Biochemistry and Physiology, 58(6): 1697–1707. https://doi.org/10.1134/S0022093022060035 [iravbai@mail.ru]

Leung, M. C.-Y., D. G. Reid, and W. D. Halliday. 2022. Sun hats for bat boxes: mitigating the risk of overheating at northern latitudes. Northwestern Naturalist, 103(3): 226–235. https://doi.org/10.1898/NWN22-03 [No author e-mail address provided]

Marsden, G. E., M. C. Schoeman, and D. Vosloo. 2022. Rewarming rates of seven insectivorous bat species along an altitudinal gradient in South Africa. Journal of Thermal Biology, 110: 103341. https://doi.org/10.1016/j.jtherbio.2022.103341 [gmarsden94@gmail.com]

Medina-Bello, K. I., R. Vázquez-Fuerte, and J. Ayala-Berdon. 2022. The big brown bat (*Eptesicus fuscus*) reduces its body mass during winter in a tropical montane ecosystem of central Mexico. Mammalia, https://doi.org/10.1515/mammalia-2022-0031 [jorgeayalaberdon@gmail.com]

REPRODUCTION

Andrianiaina, A., S. Andry, A. Gentles, S. Guth, J.-M. Héraud, H. C. Ranaivoson, N. A. F. Ravelomanantsoa, T. Treuer, and C. E. Brook. 2022. Reproduction, seasonal morphology, and juvenile growth in three Malagasy fruit bats. Journal of Mammalogy, 2022;, gyac072. https://doi.org/10.1093/jmammal/gyac072 [cbrook@uchicago.edu]

Farias, T. D. O., A. F. A. Figueiredo, N. T. Wnuk, S.A. Talamoni, and G. M. J. Costa. 2022. Testis and brown adipose tissue xenografts from yellowish myotis (*Myotis levis*). Reproduction and Fertility, 3(4): 287–300. DOI: https://doi.org/10.1530/RAF-22-0056 [gmjc@ufmg.br]

Pimentel, P. B., C. S. Santigo, J. F. Ferraz, E. Morielle-Versute, S. R. Taboga, C. C. Souza, and M. R. Beguelini. 2022. Morphophysiology of the male reproductive accessory glands of the bat *Pteronotus gymnonotus* (Mormoopidae: Chiroptera). Tissue and Cell, 101991. https://doi.org/10.1016/j.tice.2022.101991 [polly.pb06@gmail.com]

Rensel, L., K. E. Hodges, and C. L. Lausen. 2022. Maternity colony social structure of myotis in British Columbia, Canada. Behavioral Ecology and Sociobiology, 76(159): https://doi.org/10.1007/s00265-022-03265-8 [leah.rensel@umconnect.umt.edu]

Ribas, M. R., S. C. Batista, J. M. F. Kramer, and J. M. R. Aranha. 2022. Reproduction of *Artibeus lituratus* and *Sturnira lilium* (Chiroptera: Phyllosrtomidae) in a semideciduous seasonal forest fragment in southern Brazil. Acta Biológica Paranaense, 51: e86448. [mateusribas07@gmail.com]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Alcantara, D. M. C., G. Graciolli, M. Antunes Junior, R. Toma, and S. S. Nihei. 2022. Biogeographical events, not cospeciation, might be the main drivers in the historical association between *Noctiliostrebla* species (Streblidae) and their bulldog bat hosts. Biological Journal of the Linnean Society, 137(4): 583–602. https://doi.org/10.1093/biolinnean/blac097 [danielmxm@gmail.com]. (Editor's note: though this article fits well under PARASITOLOGY, it is my judgement that bat systematists will also find it very interesting.)

Camacho, M. A., D. Cadar, B. Horváth, A. Merino-Viteri, and J. Murienne. 2022. Revised phylogeny from complete mitochondrial genomes of phyllostomid bats resolves subfamilial

classification. Zoological Journal of the Linnean Society, 196(4): 1591–1607. https://doi.org/10.1093/zoolinnean/zlac055 [macamachom@puce.edu.ec]

Da Silva, N. K. N., C. Y. Nagamachi, L. R. R. Rodrigues, P. C. M. O'Brien, F. Yang, M. A. Ferguson-Smith, and J. C. Pieczarka. 2022. Chromosome painting and phylogenetic analysis suggest that the genus *Lophostoma* (Chiroptera, Phyllostomidae) is paraphyletic. Scientific Reports, 12: 19514. https://doi.org/10.1038/s41598-022-21391-1 [julio@ufpa.br]

Esquivel, D. A., M. J. R. Pereira, J. D. Stuhler, D. M. Rossoni, P. M. Velazco, and F. M. Bianchi. 2022. Multiples lines of evidence unveil cryptic diversity in the *Lophostoma brasiliense* (Chiroptera: Phyllostomidae) complex. Systematics and Biodiversity, 20(1): DOI: 10.1080/14772000.2022.2110172 [diegodaem@gmail.com]

Jorge, F. R., S. Muñoz-Leal, G. M. B. de Oliveira, M. C. A. Serpa, M. M. L. Magalhães, L. M. B. de Oliveira, F. B. P. Moura, B. M. Teixeira, and M. B. Labruna. 2022. Novel *Borrelia* genotypes from Brazil indicate a new group of *Borrelia* spp. associated with South American bats. Journal of Medical Entomology, tjac160. https://doi.org/10.1093/jme/tjac160 [labruna@usp.br]

Lopatin, A. V. 2022. Early Pleistocene horseshoe bat *Rhinolophus macrorhinus cimmerius subsp. nov*. (Rhinolophidae, Chiroptera) from the Taurida Cave in Crimea. Doklady Biological Sciences, 506: 119–127. https://doi.org/10.1134/S0012496622050076 [alopat@paleo.ru]

Novaes, R. L. M., V. C. Cláudio, M. M. Díaz, D. E. Wilson, M. Weksler, and R. Moratelli. 2022. Argentinean *Myotis* (Chiroptera, Vespertilionidae), including the description of a new species from the Yungas. Vertebrate Zoology, 72: 1187–1216. https://doi.org/10.3897/vz.72.e90958 [robertoleonan@gmail.com]

Novaes, R. L. M., A. Rodríguez-San Pedro, M. M. Saldarriaga-Córdoba, O. Aguilera-Acuña, D. E. Wilson, and R. Moratelli. 2022. Systematic review of *Myotis* (Chiroptera, Vespertilionidae) from Chile based on molecular, morphological, and bioacoustic data. Zootaxa, 5188(5): 430–452. [robertoleonan@gmail.com]

Smith, P., and P. Teta. 2022. Confused identities: the case of the chauve–souris septième or chauve–souris brun–blanchâtre of Azara (1801). Therya Notes, 3: 104–109. https://doi.org/10.12933/therya_notes-22-79 [faunaparaguay@gmail.com]

Tavares, V. da C., A. L. Gardner, M. M. Mcdonough, J. E. Maldonado, E. E. Gutiérrez, P. M. Velazco, and G. S. T. Garbino. 2022. Historical DNA of rare yellow-eared bats *Vampyressa* Thomas, 1900 (Chiroptera, Phyllostomidae) clarifies phylogeny and species boundaries within the genus. Systematics and Biodiversity, 20(1): DOI: 10.1080/14772000.2022.2117247 [val.c.tavares@gmail.com]

Taylor, P. J., E. Strydom, L. Richards, W. Markotter, D. C. Toussaint, T. Kearney, F. P. D. (W.) Cotterill, A. Howard, S. M. Weier, M. Keith, G. Neef, M. L. Mamba, S. Magagula, and A. Monadjem. 2022. Integrative taxonomic analysis of new collections from the central Angolan

highlands resolves the taxonomy of African pipistrelloid bats on a continental scale. Zoological Journal of the Linnean Society, 196(4): 1570–1590. https://doi.org/10.1093/zoolinnean/zlac071 [taylorpj@ufs.ac.za]

Tidière, M., E. Portanier, S. Jacquet, S. M. Goodman, G. Monnier, G. Beuneux, J.-F. Desmet, C. Kaerle, G. Queney, M. Barataud, and D. Pontier. 2022. Species delineation and genetic structure of two *Chaerephon* species (*C. pusillus* and *C. leucogaster*) on Madagascar and the Comoro archipelago. Ecology and Evolution, 12: e9566. https://doi.org/10.1002/ece3.9566 [mtidiere@gmail.com]

Yuzefovich, A. P., I. V. Artyushin, A. E. Skopin, N. T. Son, and S. V. Kruskop. 2022. Taxonomic diversity of the *Hipposideros larvatus* species complex (Chiroptera: Hipposideridae) in mainland Asia. Zootaxa, 5200(1): 73–95. [no author e-mail address provided]

TECHNIQUES FOR STUDYING BATS

Bergmann, A., L. S. Burchardt, B. Wimmer, K. Kugelschafter, F. Gloza-Rausch, and M. Knörnschild. 2022. The soundscape of swarming: Proof of concept for a noninvasive acoustic species identification of swarming *Myotis* bats. Ecology and Evolution, 12: e9439. https://doi.org/10.1002/ece3.9439 [anja.bergmann@mfn.berlin]

Carr, A., A. Weatherall, M. R. Zeale, A. Rachwald, and G. Jones. 2023. A method for rapid assessment of bat richness using woodland structure characteristics. Forest Ecology and Management, 529: 120680. https://doi.org/10.1016/j.foreco.2022.120680 [a.carr@ibles.waw.pl]

Cole, H. J., D. G. Gomes, and J. R. Barber. 2022. EcoCountHelper: an R package and analytical pipeline for the analysis of ecological count data using GLMMs, and a case study of bats in Grand Teton National Park. PeerJ, 10: e14509. https://doi.org/10.7717/peerj.14509 [hunterjcole25@gmail.com]

Howard, A., A. Monadjem, D. MacFadyen, and C. T. Chimimba. 2022. Testing the efficacy of bat monitoring methods for identification and species surveys in KwaZulu-Natal province, South Africa. African Zoology, DOI: 10.1080/15627020.2022.2138722 [alex.asterhof@gmail.com]

Jansen, E. A., E. Korsten, M. J. Schillemans, M. Boonman, and H. G. Limpens. 2022. Een methode voor actief onderzoek naar massawinterverblijfplaatsen van de dwergvleermuis (*Pipistrellus pipistrellus*) in stedelijke omgeving. (Editor's note: entirely in Dutch. =A method for active investigation of mass wintering sites of the pipistrellus (*Pipistrellus pipistrellus*) in urban environments.) Lutra, 65(1): 213–233. http://www.zoogdiervereniging.nl [herman.limpens@zoogdiervereniging.nl]

Lo Cascio, A., S. Kasel, and G. Ford. 2022. A new method employing species-specific thresholding identifies acoustically overlapping bats. Ecosphere, 13(11): e4278. https://doi.org/10.1002/ecs2.4278 [amlocascio@student.unimelb.edu.au]

Oswald, J. N., A. M. Van Cise, A. Dassow, T. Elliott, M. T. Johnson, A. Ravignani, and J. Podos. 2022. A collection of best practices for the collection and analysis of bioacoustic data. Applied Sciences, 12*:* 12046. https://doi.org/10.3390/app122312046 [jno@st-andrews.ac.uk]

Thomas, R. J., and S. P. Davison. 2022. Seasonal swarming behavior of *Myotis* bats revealed by integrated monitoring, involving passive acoustic monitoring with automated analysis, trapping, and video monitoring. Ecology and Evolution, 12: e9344. https://doi.org/10.1002/ece3.9344 [linda@batswales.co.uk]

Voigt, C. C., C. Scherer, and V. Runkel. 2022. Modeling the power of acoustic monitoring to predict bat fatalities at wind turbines. Conservation Science and Practice, e12841. https://doi.org/10.1111/csp2.12841 [voigt@izw-berlin.de]

Webala, P. W., S. Musila, R. Syingi, and Z. A. Okwany. 2022. Bats in Kenyan pit latrines: Non-invasive sampling by photography. African Journal of Ecology, pp. 1–4. https://doi.org/10.1111/aje.12998 [paul.webala@gmail.com]

WHITE-NOSE SYNDROME

Aimberg, E., M. Becker, J. Ramsey, and K. Smucker. 2022. Montana's 2022 annual white-nose syndrome surveillance report. Montana Fish, Wildlife, and Parks, Pp. 1–26. [https://fwp.mt.gov/binaries/content/assets/fwp/conservation/wildlife-reports/bats/wns-surveillance-annual-report-2022-10_10_22.pdf]

Avilla, L. R., B. Hines, and C. L. Elliott. 2022. A survey of bats at Lilley Cornett Woods Appalachian Ecological Research Station, Letcher County, Kentucky, before the arrival of white-nosed syndrome. Journal of the Kentucky Academy of Science, 83(1-2): 1–9. https://doi.org/10.3101/kyac-83-01-02 [charles.elliott@eku.edu]

Eiamcharoen, P., A. Gelli, B. A. Byrne, and M. K. Keel. 2022. Characterization of *Pseudogymnoascus destructans* conidial adherence to extracellular matrix: Association with fungal secreted proteases and identification of candidate extracellular matrix binding proteins. Microbial Pathogenesis, 174: 105895. https://doi.org/10.1016/j.micpath.2022.105895 [peiamcharoen@ucdavis.edu]

Forney, R., G. Rios-Sotelo, A. Linfauer, C. K. R. Willis, and J. Voyles. 2022. Temperature shifts associated with bat arousals during hibernation inhibit the growth of *Pseudogymnoascus destructans*. Royal Society Open Science, 9211986211986. http://doi.org/10.1098/rsos.211986 [jvoyles@unr.edu]

Gabriel, K. T., A. G. McDonald, K. E. Lutsch, P. E. Pattavina, K. M. Morris, E. A. Ferrall, S. A. Crow Jr, and C. T. Cornelison. 2022. Development of a multi-year white-nose syndrome mitigation strategy using antifungal volatile organic compounds. Plos one, 17(12): e0278603. [No author email address provided]

Gómez-Rodríguez, R. A., V. Sánchez-Cordero, D. Boyer, J. E. Schondube, Á. Rodríguez-Moreno, and G. Gutiérrez-Granados. 2022. Risk of infection of white-nose syndrome in North

American vespertilionid bats in Mexico. Ecological Informatics, 72: 101869. https://doi.org/10.1016/j.ecoinf.2022.101869 [gabriel.gutierrez@zaragoza.unam.mx]

Hammesfahr, A., C. C. Rega-Brodsky, K. Womack-Bulliner, and J. Whitney. 2022. Roost characteristics of a tricolored bat *Perimyotis subflavus* in the Missouri Ozarks. Transactions of the Kansas Academy of Science, 125(3-4): 159–164. [no author e-mail provided]

Kim, Y.-S., M.-S. Yang, C.-G. Jeong, C.-U. Chung, and J.-K. Oem. 2022. First isolation of *Pseudogymnoascus destructans*, the fungal causative agent of white-nose syndrome, in Korean bats (*Myotis petax*). Journal of Fungi, 8(10): 1072. https://doi.org/10.3390/jof8101072 [jku0623@jbnu.ac.kr]

Pannkuk, E. L., N. A. Y. Dorville, S. Bansal, S. Bansal, Y. A. Dzal, Q. E. Fletcher, K. J. Norquay, A. J. Fornace Jr, and C. K. Willis. 2022. White-nose syndrome disrupts the splenic lipidome of little brown bats (*Myotis lucifugus*) at early disease stages. Journal of Proteome Research, https://doi.org/10.1021/acs.jproteome.2c00600 [elp44@georgetown.edu]

Patrick, J. K., A. S. Winter, D. C. Woodhams, and D. E. Northup. 2022. The mycobiome of bats in the American southwest is structured by geography, bat species, and behavior. Research Square; DOI: 10.21203/rs.3.rs-2092895/v1 [patrick.kearns@umb.edu]. (Editor's Note: the first author's name is spelled differently in two different bibliographic versions of this published report—it may not be accurately reported herein.)

Shapiro, H. G., A. S. Willcox, E. V. Willcox, and M. L. Verant. 2022. US National Park visitor perceptions and behavioral intentions towards actions to prevent white-nose syndrome. PloS one, 17(11): e0278024. [No author email address provided]

Smith, L. M., J. A. Gore, T. J. Doonan, and C. J. Campbell. 2022. Tricolored bats at a southern range edge exhibit partial migration northward in autumn. Movement Ecology, 10(56): 1–13. https://doi.org/10.1186/s40462-022-00358-x [Lisa.Smith@myfwc.com]

Wiens, A. M., and W. E. Thogmartin. 2022. Gaussian process forecasts *Pseudogymnoascus destructans* will cover coterminous United States by 2030. Ecology and Evolution, 12(11): e9547. https://doi.org/10.1002/ece3.9547 [awiens@usgs.gov]

Farewell From the Editor

Greetings to old friends, colleagues, and interested bat researchers from around the world. I hope this finds you doing well and that your holidays were all you hoped they would be. I apologize for the lateness in the printing and mailing of the 2023 Winter issue but I experienced circumstances beyond my control.

As most of you know, after nearly 20 years of being the Publisher and Managing Editor of *Bat Research News*, this is the last year I am able to continue doing this, making this the final issue of the journal/newsletter. It may or may not continue under the direction of a professional group of bat researchers to whom I have offered ownership. As of printing of this final issue of the journal, I have not received a definite "yay or nay."

Rest assured that if someone does take over *Bat Research News*, I will pass on your renewal information to the new owners. I will continue to run the website for another year and hope to find a permanent place for all 63 volumes of *Bat Research News* within that time as well.

My sincerest thanks to Al Kurta, the Editor for Feature Articles, and to Tom Griffiths, Editor for Recent Literature. Al has been the Editor for Feature Articles and many other things since before I started as managing editor. Without Al's help and guidance over the years, *BRN* would not have been possible. Tom has been an Editor of *BRN* since the early 1980's (see the Recent Literature section), and reprised his role as Editor for Recent Literature in 2015 after his tenure as a college administrator ended. Since that time, Tom—who is also my husband—has spent countless hours putting together the Recent Literature section of *BRN* again. Neither Al nor Tom has gotten anything out of their efforts except my deepest gratitude for their many hours of work and dedication. I also thank all the previous editors of and contributors to *BRN* for their work, without which 63 years of *BRN* would not have been possible.

Finally, my sincerest thanks to all of you for your years of support. It has been a wonderful experience working with (and for) you over the years, and I hope you have enjoyed most of those years too. Thank you for your years of dedication to bats, and I wish you the very best in whatever you do, whatever your plans may be, or wherever you may travel! Keep up the good work!

Best wishes,

ANNOUNCEMENTS

Bat Research News Website

Most likely the *BRN* website will be available for at least another year but if you need anything from back issues, please contact me, Margaret Griffiths (margaret.griffiths01@gmail.com). I hope to find a repository for the 63 volumes of *BRN* during that time. Thank you!

Back Issues of *Bat Research News*

Many back issues are available on the *Bat Research News* website. To download back issues, click on the "Past Volumes" link found on the home page, and then on the volume you would like to download. I am working on adding more past issues to the site so stay tuned. If you or someone you know need back issues not available on the *BRN* site, please contact the Managing Editor, Margaret Griffiths (margaret.griffiths01@gmail.com).

FUTURE MEETINGS and EVENTS

ALL Professional Meetings and Events

Please check the respective website of all professional societies as to whether professional meetings will be face-to-face, virtual, or hybrid.

2023

The 2023 Northeast Bat Working Group Meeting will be held January 18–20, 2023, at the Hilton Burlington Lake Champlain Hotel, in Burlington, Vermont. For registration information, please see the NEBWG website: https://www.nebwg.org/register.

The Annual NASBR meeting will be held 11–14 October 2023, at the Fort Garry Hotel, in Winnipeg, Manitoba, Canada. Check the NASBR website for updates — https://www.nasbr.org/.

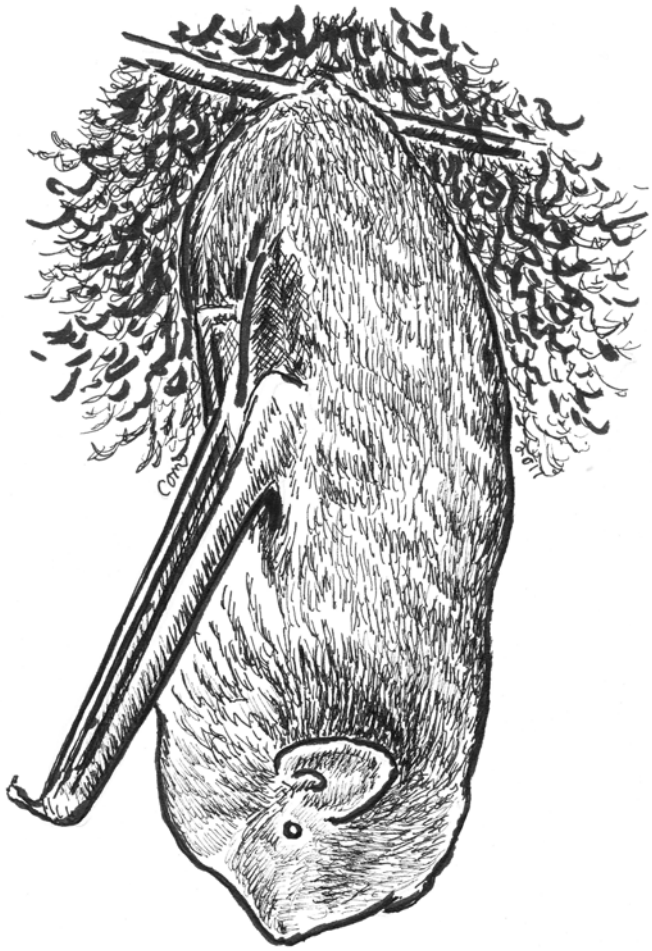
2024

The Annual NASBR meeting will be held in October 2024, in Mexico City, Mexico. Dates TBD. Check the NASBR website for updates — https://www.nasbr.org/.

2025

The Annual NASBR meeting will be held in Edmonton, Alberta, Canada in 2025. Dates TBD. Check the NASBR website for updates — https://www.nasbr.org/.

BAT RESEARCH NEWS



VOLUME 63: NO. 5 **WINTER 2022**

Abstracts of Papers Presented at the

19th International Bat Research Conference (IBRC) and
50th Annual Symposium of the North American Society for Bat Research
Austin, Texas, USA
August 7th – 12th, 2022

The following abstracts are from papers presented at the 19th International Bat Research Conference (IBRC) and 50th Annual Symposium of the North American Society for Bat Research (NASBR). Meeting abstracts were submitted by Emma Wilcox, Program Director for NASBR. Abstracts are arranged in alphabetical order by first author and, except for minor formatting changes, are published as received. E-mail contact information for authors is not available.

Assessing Species Richness, Abundance, and Activity Patterns of Bats in New Jersey
Amani Abdelsalam[1], Camilo A. Calderón-Acevedo[2,3] and J. Angel Soto-Centeno[2,4]
1 Department of Biological Sciences, Rutgers University, Newark, USA; 2 Department of Earth and Environmental Science, Rutgers University, Newark, USA; 3 Department of Environmental and Forest Biology, The State University of New York College of Environmental Science and Forestry, Syracuse, USA; 4 Department of Mammalogy, American Museum of Natural History, New York, USA

Two of the greatest threats facing bats in North America are anthropogenic disturbance and white-nose syndrome (WNS). New Jersey (NJ) is one of the most urbanized states in the United States and is located near the epicenter of the WNS outbreak. Although NJ supports nine species of bats, five of them are currently listed as Threatened, Vulnerable, or Endangered by the International Union for Conservation of Nature Red List. To properly address the threats facing bats, it is crucial to first understand basic aspects of their biology, such as habitat use and patterns of activity. Here, we investigated the species richness, abundance, and activity patterns of NJ bats by placing ultrasonic detectors at two rural and two urban sites throughout the state. The detectors passively recorded echolocation calls from sunset to sunrise for six nights per month from June to November 2021. We expected activity to peak during July−August across all sites, but this was only observed in the rural sites. The greatest peak in activity at both urban sites occurred in September–October. Results from Welch's ANOVA and Games-Howell post-hoc tests revealed significant differences in activity patterns across some urban and rural sites, but not others. We found that species richness was highest at one of the rural sites, but not both. Relative abundance was only significantly lower at one of the urban sites; the other urban site had the second highest abundance of bats. Our study may provide insight into which habitats must be maintained to promote bat biodiversity.

State of the Bats: North American Expert Elicitation Species Assessment
Amanda M. Adams, Michael Whitby and Winifred F. Frick
Bat Conservation International, Austin, USA

The North American Bat Conservation Alliance (NABCA) State of the Bats report will characterize the current conservation status of North American bats and provide a baseline assessment for future efforts to assess the status and trends of bats via the North American Bat Monitoring Program (NABat). We created an online assessment portal for assessing all species across their range within each country, Canada, Mexico, and the United States, to conduct a four-point expert elicitation based on NatureServe criteria for range extent, population size, population trend, and impact of threats. We had 15 experts assess 17 species in Canada, 42 experts for 89 species in Mexico, and 47 experts for 45 species in the U.S. The assessment identified range sizes that should be reassessed based on the current estimates in the Global Biodiversity Information Facility (GBIF). The experts also identified the major threats facing each species and the expected impact of these threats over the next 15 years. Our ultimate goals are to provide a public-facing report of these results to promote bat conservation continentally and make this assessment interface transferable for use in future efforts.

The Importance of Water Availability to Bats: Climate Warming and Increasing Global Aridity
Rick A. Adams[1] and Mark A. Hayes[2]
1 School of Biological Sciences, University of Northern Colorado, Greeley, USA; 2 U.S. Fish and Wildlife Service, Sacramento, USA

Environmental chance due to climate warming is accelerating in most of the world's arid regions, pushing already xeric ecosystems towards drier conditions and expanding desert landscapes. These changes will alter community structures and species interactions globally. Because many arid regions, especially semi-arid zones, are relatively high in bat species richness, reactions of bat populations to increasing and intensifying droughts will affect food web dynamics and ecosystems services on nearly every continent. Although there is evidence that some species have preadaptations for surviving decreasing available water resources in arid regions, many species may succumb to the pace of climate warming and landscape xerification. As drought and aridity increase, may drinking sources will inevitably be lost, increasing competition for progressively limited resources, thereby affecting bats during the reproductive season when they are most vulnerable. Herein, we review how climate warming and increasing drought are currently altering bat population dynamics and model future viability of some species and populations. Documented declines in some bat populations, reductions in species richness, and changes in distributional ranges are already occurring in hardest hit areas and some models have been developed to predict future outcomes for bats living on the leading edge of climate disruption.

Role of Micro-RNAs in the Pathogenesis of White-Nose Syndrome in *Myotis lucifugus*
Anouska Agarwal[1], Craig K.R. Willis[1] and Anuraag Shrivastav[1,2]
1 Department of Biology, University of Winnipeg, Winnipeg, CAN; 2 Research Institute of Oncology and Hematology, CancerCare Manitoba, Winnipeg, CAN

White-nose syndrome (WNS), caused by the fungus *Pseudogymnoascus destructans* (Pd), causes bats to arouse from torpor too frequently during hibernation leading to rapid depletion of winter fat reserves. Metabolic pathways like the insulin signaling pathway, affect metabolism during the critical pre-hibernation phase when bats accumulate fat, as well as during hibernation when bats must fuel the transition from torpor to arousal. We are testing the hypothesis that microRNAs (miRNAs) associated with fat metabolism and other metabolic pathways influence WNS pathogenesis and bat survival. miRNAs are small non-coding regions of single-stranded RNA that affect various metabolic pathways by regulating

gene expression. A previous study identified 43 candidate miRNAs specific to WNS-positive bats that were not found in any WNS-negative bats. These 43 miRNAs could be of significance to WNS pathogenesis. We used bioinformatics tools, miRNA target pathway verification and gene target prediction to identify 4 of these 43 miRNAs that could affect WNS survival because they influence insulin signaling, fat metabolism and immune function. We will next capture and tag bats from WNS-affected sites in Manitoba, Canada and collect samples to assess the expression of miRNAs and their potential effects on target genes and bat survival. For example, bats with overexpression of miRNAs that inhibit insulin pathway genes during fall could have poor body condition and low overwinter survival. Our project will help improve understanding of WNS pathogenesis and has the potential to help identify populations or colonies that are at particular risk from the disease using miRNAs as biomarkers.

Where are the Bats?

Ludmilla M.S. Aguiar
Department of Zoology, Universidade de Brasilia, Brasília, BRA

Field surveys are necessary to overcome Wallacean shortfalls. The task is even more important when human pressure on tropical—megadiverse—ecosystems is considered. However, due to financial constraints, spatial and temporal prioritization is required. Here, we used the concept of environmental complementarity to identify non-surveyed regions for bats that are environmentally different from other already surveyed regions. We highlighted regions in Brazil where field inventories could be conducted to locate new occurrences or even new bat species. We based our analysis on environmental characterization aiming to identify dissimilar regions to those already sampled for bats in Brazil. We used 21 environmental variables to characterize 1,531 unique localities where bats occur. Then, we applied the parameters of a generalized linear model (GLM) to extrapolate the expected values of the environmental variables for the entire country. We compared the predicted values of localities with newly described bat species occurrence against the values for other bat species. We found that sites from which recently discovered species were described are environmentally distinct from the sites where previously described species occur. Therefore, new occurrences and even new species could be found in regions that are environmentally dissimilar from those already surveyed. By crossing the model with a human footprint map, we defined temporal priorities for field inventories. Regions such as the Northern Cerrado and Western Caatinga should be surveyed first. Similar approaches could be undertaken for other biological groups or regions, allowing the identification of spatial congruence and the development of a comprehensive national program for biological field inventories. Newly described species occurred in environments dissimilar to those previously identified, showing that environmental complementarity analysis is a valid approach to define priority regions for new bat inventories.

A Population in Perpetual Motion: Highly Dynamic Roosting Behaviour and Genetic Structure in a Tropical Bat

Samantha Aguillon[1], Gildas Le Minter[1], Camille Lebarbenchon[1], Axel O. G. Hoarau[1], Céline Toty1, Léa Joffrin[1], Riana V. Ramanantsalama[1], Stéphane Augros[2], Clara Castex[1], Avril Duchet[1], Pablo Tortosa[1], Patrick Mavingui[1] and Muriel Dietrich[1]
1 UMR PIMIT (Processus Infectieux en Milieu Insulaire Tropical), Université de La Réunion / INSERM / CNRS / IRD, Sainte-Clotilde, REU ; 2 Cabinet ECO-MED Océan Indien, Saint-Denis, REU

Although island endemic bats are particularly threatened, little information is known on their biology. Here, we studied the phenology, roosting behavior and genetic structure of the Reunion free-tailed bat (*Mormopterus francoismoutoui*). This tropical bat is endemic to Reunion Island (Indian Ocean) and roosts in caves, cliff crevices, as well as in human structures (buildings, bridges). We set up a fine-scale monitoring of 19 roosts over 27 months and collected extensive data from 6721 individuals. We analyzed roost size and composition, sexual and age-associated segregation of individuals, as well as the reproductive phenology and body condition of individuals. Using both mitochondrial and microsatellite markers, we also studied genetic diversity and population demographic history to assess potential sexual differences in dispersal strategies. We revealed highly dynamic roosting behavior, with marked seasonal sex-ratio variation, associated with distinct patterns of sexual aggregation among roosts. Interestingly, our data also suggested a long interruption of the reproductive cycle in this tropical bat. We showed a high genetic diversity within the population and a strong genetic structure, but surprisingly not associated with geography. Altogether, our results suggest a complex social organization in this bat, shaped by both important sex-specific seasonal and spatial movements, with probable multiple historical colonization events of the island. Such information is crucial for the delineation and the success of sustainable conservation projects. The Reunion free-tailed bat is a known reservoir of viruses, thus our results may also serve at understanding how host biology shapes infection dynamics in bats.

The Role of Sexual Segregation and Reproduction in Viral and Bacterial Shedding in Bats

Samantha Aguillon, Magali Turpin, Avril Duchet, Gildas Le Minter, Camille Lebarbenchon, Axel O. G. Hoarau, Céline Toty, Léa Joffrin, Clara Castex, Riana V. Ramanantsalama, Patrick Mavingui, Pablo Tortosa and *Muriel Dietrich
Processus Infectieux en Milieu Insulaire Tropical, Université de la Réunion, Sainte-Clotilde, REU

Infection dynamics in bats are likely influenced by the unique ecology of this diverse group of mammals. However, fine-scale spatio-temporal sampling of bats is challenging and our understanding of transmission remains limited. We investigated Paramyxovirus and *Leptospira* bacteria shedding in the free-tailed bat *Mormopterus francoismoutoui*, based on an extensive 2-years longitudinal sampling across 19 colonies in Reunion Island. The PCR screening of 5,417 individual urine samples revealed similar patterns of infection dynamics between Paramyxovirus and *Leptospira*, with synchronized and recurrent epidemic waves. Infection prevalence was not associated with the colony size, nor with the presence of juveniles, which remain uninfected during the first months of their lives. Higher prevalence within colonies was clearly correlated to periods of sexual segregation and reproduction. Indeed, pregnancy in females and mating in males were the drivers of infection in adults, although this was not correlated to a lower body condition in reproductively active individuals. Among infected individuals, pregnant females are those presenting more coinfections. Our results highlight the major role of reproduction in infection dynamics and suggest some tradeoffs between reproduction and infection, both in female and male bats. We also illustrate a probable protection of juveniles by maternal antibodies, and suggest a major role of juveniles in the dispersal of infections through scattering between colonies after weaning. Presented data show how investigating endemic species within relatively small islands provides an ideal context for setting up spatiotemporal sampling design and is thus crucial to explore how the heterogeneity of bat populations influences infection patterns.

The Role of Heat Stressed Indian Flying Foxes in Propagation of Antimicrobial Resistance in the Environment

Touseef Ahmed[1], Aitezaz Ahsan[2], Sajida Noureen[3], Muhammad Farooq Tahir[4], Hamid Irshad[2], Armaghan Shahzad[2], Abdul Ali[2], Arshad Javid[5], Mamoona Arshad[5] and Tigga Kingston[1]

1 Department of Biological Sciences, Texas Tech University, Texas, USA; 2 Animal Health Research Laboratories, National Agricultural Research Center, Islamabad, PAK: 3 University of Haripur, Khyber Pakhtunkhwa, PAK; 4 Health Security Partners, Washington DC, USA; 5 University of Veterinary and Animal Sciences Lahore, PAK

Extreme heat is an underlying, less known driver of Antimicrobial Resistance (AMR) propagation in the environment that can operate in at least two ways. First, extreme heat can induce cellular structural changes in bacteria similar to those resulting from antibiotic stress, conferring antibiotic resistance. Second, extreme heat events can induce behavioral changes in taxa involved in AMR propagation in the environment. Extreme heat has created conservation challenges for *Pteropus* species, and may also propagate AMR in both stated ways, first by advancing thermoregulatory behaviors of Indian flying foxes (*Pteropus medius*), which results in frequent contact with water, containing antimicrobial residues. Second, it may induce structural changes in the gut microbiota of flying foxes that confer resistance. We recorded temperature at roost level and monitored thermoregulatory behaviors using video scan-sampling technique to establish the intensity of heat stress experienced by *P. medius* in central and northern regions of Pakistan. We isolated *Escherichia coli* from the fecal samples and established the relationship between heat stress and resistance-related genetic mutation. We further tested resistant isolates for extended-spectrum β-lactamases (ESBL) producing *E.coli* as an indicator of AMR acquired from the environment (wastewater). To date, we have isolated *E.coli* from 52% of (120/230) fecal samples. Isolated *E.coli* showed resistance toward rifampicin (90%) and important β-Lactam antibiotics such as Cephradine (30%), Oxytetracycline (32.5%) and Ampicillin (25%). Knowledge about the internal and external drivers of heat driven AMR propagation from fruit bats will provide a foundation for environmental antimicrobial stewardship, a One Health priority.

Altitudinal Variation of Bats (Mammalia, Chiroptera) on The North-Eastern Aspect of Mount Manengouba, Western Cameroon

Djame-Gomeh Aicha[1], Manga Mongombe Aaron[2], Takuo Jean Michel[3], *Bakwo Fils Eric Moise[2] and Bilong Bilong Charles Felix[1]
1 Department of Animal Biology; Faculty of Sciences; University of Yaoundé, CMR; 2 Departement of Biological Sciences; Faculty of Sciences; University of Maroua, CMR; 3 Environnement Recherche et Développement, CMR

Bat elevational distribution can help ecologists understand how climatic conditions limit species ranges and, as a result, can be used as a proxy to predict how species will respond to climate change. This study was aimed at determining the diversity and altitudinal distribution of bats on the north-eastern aspect of Mount Manengouba. From August to December 2019, we conducted field surveys using standard mist-nets in three elevational ranges: Range I (500−1000 m), Range II (1001−1500 m), and Range III (1501−2000 m). During 30 sampling nights, we recorded 194 bats belonging to five families, 11 genera, and 14 species. Of the 14 species recorded, seven were frugivorous bats and seven were insectivorous bats. Species richness peaked at 1,240 m and 1,900 m, and there was an increase in the species richness with altitude. The altitudinal Range III recorded the highest number of species (10) followed by Range II (06), and Range I (05). The only species recorded in all three elevational ranges were *Eidolon helvum* and *Myonycteris torquata*. Analysis of similarity revealed that the three altitudinal ranges were similar in terms of bat species composition ($R = 0.29$, $p > 0.001$). Also, there was no significant difference in bat species abundance between the altitudinal bands. Altitude and species richness were also weakly correlated and not significant. The result suggests that Mount Manengouba follows a bimodal pattern of bat species richness. The importance of the Cameroon Highlands in the conservation of many bat species is further underscored in this study.

The Evolution of Body Size in Flying Foxes and Related Bats

Francisca C. Almeida[1,2], Norberto P. Giannini[3], Damián Fernández[1], Kristofer Helgen[4] and Nancy B. Simmons[5]
1 Departamento de Ecología, Genética y Evolución, Universidad de Buenos Aires, ARG; 2 Instituto de Ecología, Genética y Evolución de Buenos Aires, CONICET, ARG; 3 Unidad Ejecutora Miguel Lillo, CONICET, Tucumán, ARG; 4 Australian Museum Research Institute, Sydney, AUS; 5 American Museum of Natural History, New York

Flying foxes (*Pteropus* and allies; Pteropodidae: Pteropodinae) comprise c. 75 paleotropical phytophagous species ranging from 0.02 to 1.5 kg. A previous analysis of body size evolution in bats suggested a trend towards increasing size in Pteropodidae, which, together with lineage-specific apomorphic variation, culminated in the largest bat species in Pteropodinae. The latter inhabit islands of the Pacific and Indian Oceans, with only a few species found in continental SE Asia and Australia. It has been observed that when two or more *Pteropus* species co-occur in an island, they tend to differ in body size. Such pattern could be the result of selection through character displacement, or species sorting. To study the role of selection in the evolution of pteropodine body size, we compiled molecular data and built a taxonomically comprehensive phylogeny of the subfamily. Then we carefully reviewed geographic distributions to determine species sympatry, and applied phylogenetic comparative methods to fit different models of continuous-character evolution to condyle-basal length change as proxy of body size across pteropodine species, and separately in *Pteropus*. We confirm that sympatric species tend to have non- or little-overlapping sizes; wider overlap was observed in islands with >2 species, chiefly due to the presence of widespread species. The selected model, Ornstein-Uhlenbeck with different size optima dependent upon the sympatry/allopatry status, suggests that body-size evolution responded to selective pressures, which is consistent with predominant character displacement, although species sorting cannot be ruled out completely.

Sensory Individuality in Echolocating Bats

Eran Amichai[1] and Hannah ter Hofstede[1]
1 Ecology, Evolution, Environment and Society Graduate Program, Department of Biological Sciences, Dartmouth College, Hanover, USA

Behavioral differences between individuals of the same species are as important as differences between species. If individual behaviors are stable over time, they can be identified as 'behavioral reaction norms' (BRN), providing the phenotypic substrate for natural selection. However, specific mechanisms leading to BRNs are not well known. Since behavioral reactions depend on sensory input, sensory individuality may provide a basis for some BRNs. Big brown bats are generalist aerial hunters that forage in a variety of habitats (e.g., over-water, vegetation-edge, open-air). Bats adapt their echolocation behavior to suit the environment by using long calls at long intervals in open spaces and short calls at short intervals in cluttered spaces. We hypothesize that individual bats are predisposed to use short or long calls and intervals and that this predisposition is stable over time, constituting a sensory BRN. We predict that an individual's sensory BRN will be a good predictor of its preferred environment: that 'short' individuals will tend to spend more time in cluttered environments than 'long' individuals. We measured echolocation call parameters of bats performing a standardized task and then quantified environment preference by measuring time spent flying in either a cluttered (containing trees) or open part of a large flight chamber. Preliminary analysis suggests that bats exhibit sensory BRNs that correlate with environment time allocation, supporting the proposed hypothesis. Sensory BRNs may be a mechanism to reduce intra-specific competition and illustrate how variation in a trait can be adaptive in itself, not merely by providing fodder for selection.

Winter Growth Patterns of *Pseudogymnoascus destructans*, the Causative Agent of White-Nose Syndrome, in the Southeastern United States

Jessica R. Anderson[1], Makayla Ferrari[2], Jordyn R. Upton[2], Andrew J. Edelman[1], Susan C. Loeb[3], Thomas McElroy[4] and Christopher T. Cornelison[2]
1 Department of Natural Resources, University of West Georgia, Carrollton, USA; 2 Department of Molecular and Cellular Biology, Kennesaw State University, Kennesaw, USA; 3 US Forest Service, Southern Research Station, Clemson, USA; 4 Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, USA

Since introduction to North America in 2006, white-nose syndrome (WNS) has caused significant population declines of up to 90% in 3 native bat species, and has the potential to cause diagnostic symptoms in 6 additional species. *Pseudogymnoascus destructans* (*Pd*), the causative agent of WNS, is a psychrophilic fungus that can persist within environmental reservoirs throughout the year. With the increasing risk of *Pd* spread, more focus has been placed on anthropogenic structures as winter hibernacula for bats. During the winter, bats have lowered body temperature and down-regulation of the immune system, increasing their susceptibility to *Pd*. Our objective was to quantify changes in *Pd* burden on tri-colored bats (*Perimyotis subflavus*) throughout the winter season at both traditional (caves, mines, and tunnels) and nontraditional (bridges and culverts) bat hibernacula. Through the 2021 winter season, we sampled 2 caves, 1 mine, 2 tunnels, 2 bridges, and 7 culverts throughout Alabama, Florida, Georgia, and South Carolina. After DNA extraction, *Pd* burdens were quantified via qPCR. Initial sampling results suggest that fungal loads increase with the progression of the winter season at sites positive for Pd. The number of *Pd* positive bats sampled is highest during the late hibernation period (March) in comparison to earlier sampling periods. These results can be used to guide management strategies that monitor bat populations.

A Conceptual Framework to Integrate Cold-survival Strategies, with a Focus on Bats

Giorgia G. Auteri
University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, USA

Freezing temperatures are inherently challenging for life, which is water based. How species cope with these conditions fundamentally shapes ecological and evolutionary processes. Despite this, there is no comprehensive conceptual framework for cold-survival strategies—seasonal migration, cold resistance and torpor. Here, I propose a framework with four components for conceptualizing and quantifying cold-survival strategies. Cold-survival strategies are (i) collectively encompassed by the proposed framework, and that this full breadth of strategies should be considered in focal species or systems (comprehensive consideration). These strategies also (ii) exist on a spectrum, such that species can exhibit partial use of strategies, (iii) are non-exclusive, such that some species use multiple strategies concurrently (combined use) and (iv) should collectively vary inversely and proportionally with one another when controlling for the external environment (e.g. when considering species that occur in sympatry in their summer range), such that use of one strategy reduces, collectively, the use of others (proportional use). This framework is relevant to understanding fundamental patterns and processes in evolution, ecology, physiology and conservation biology. Bats, which have long been recognized as a group that exhibits trade-offs between migration and hibernation, may be a particularly accessible group in which to explore these relationships.

Landscape Features Associated with Bat Fatalities at Wind Energy Facilities in North America

Erin F. Baerwald
Department of Ecosystem Science and Management, University of Northern British Columbia, Prince George, CAN

Currently, fatalities at wind energy facilities are one of the greatest known sources of mortality for migratory bats in North America. Between 840,000 and 1.7 million bats were killed by wind turbines in the U.S. and Canada from 2000–2011 but fatalities across North America increase by several hundred thousand annually. Of these fatalities, ~72% are of three species of migratory tree-roosting bats. Recent analyses suggest that fatalities at wind energy facilities are negatively affecting populations of hoary bat and these three species are being considered for listing in Canada. To reduce the impacts of wind energy on bat populations, developers and operators can locate projects in "low fatality risk" areas, but this is challenging because habitat use by migratory tree-roosting species of bat is not well-understood. Intuitively, high-risk areas are within spaces that provide high quality habitat for bats and/or concentrate migrating bats (e.g., riparian corridors), but these spaces are not well-defined. However, modelling based on fatality data of migratory tree-roosting bats from >50 wind energy facilities in Ontario, Canada suggest that fatality risk is correlated with habitat features such as distance to forest and proportion of water, cropland, and urban areas. The data also suggest that fatality rates are correlated more with habitat surrounding a facility (i.e., within a 25 km radius) than within a facility (i.e., within a 1 km or 5 km radius). Landscape features associated with increased fatality rates vary among species however, highlighting the need for species-specific management plans.

Does Wildfire Smoke Affect Summer Foraging Behavior in Endangered Little Brown Bats?

Ershiya Bagheri, Sophia Brown and Craig K.R. Willis
Department of Biology and Centre for Forest Interdisciplinary Research, University of Winnipeg, Winnipeg, CAN

Climate change threatens biodiversity and understanding how animals respond to shifts in environmental variables is important for determining impacts on ecosystems. Most studies focus on direct effects of climate change (e.g., climate envelope analyses) but indirect effects may also cause population impacts. In Canada, three bat species are endangered by white-nose syndrome but they face other threats which could slow population recoveries. We tested the hypothesis that wildfire smoke (a potential indirect effect of climate change), affects access to food and water for little brown bats (*Myotis lucifugus*). We predicted that bats would forage less, and have smaller home ranges, on nights with low air quality from wildfire smoke. During the lactation period in July 2021, I captured bats from maternity colonies near Kenora, Ontario, Canada. I attached radiotransmitters to 15 bats and used telemetry to follow individuals for 21 nights, from July 10th to 31st. Forest fires within ~10 km of the study site caused dramatic variation in air quality on different nights during the study. After controlling for other environmental variables (e.g., wind, temperature), we found that wildfire smoke dramatically reduced foraging time and home range size with many bats remaining in their roosts on nights with especially poor air quality. Our results highlight a potential indirect effect of climate change on bats. Bats may be particularly susceptible to this effect if smoke attenuates or dampens echolocation calls but other wildlife species could also be affected.

Dialogue of the Deaf? Vocalization and Flight Behavior in Hearing-impaired Bats

A. Leonie Baier1, Eva S. Mardus[1,2,3], Thejasvi Beleyur[1], Ella Z. Lattenkamp[2] and Holger R. Goerlitz[1]

1 Acoustic and Functional Ecology Group, Max Planck Institute for Ornithology, Seewiesen, DEU; 2 Division of Neurobiology, Department Biology II, Ludwig Maximilians University Munich, Munich, DEU; 3 Graduate School of Systemic Neurosciences, Ludwig Maximilians University Munich, Munich, DEU

Bats not only orient and forage with their ears, but they also communicate with each other using a rich repertoire of complex calls and songs. Unlike most mammals, in which the vocal repertoire is innate, bats have been considered vocal learners. Vocal learning refers to an animal's ability to acquire new vocalizations through imitation using auditory feedback. Deafening experiments are therefore critical to verify vocal learning, but they can also illuminate other aspects of behavior. Here we compared echolocation and flight of two groups of *Phyllostomus discolor*: three normal-hearing bats and three bats that had been acoustically deafened at birth. Pups of both groups had thrived and grown into adults that are socially integrated in the colony and keen flyers in dim-light conditions. However, we hypothesized that (i) in darkness and unknown surroundings, hearing-impaired bats would not fly and (ii) in darkness and known surroundings, hearing-impaired bats could not navigate unknown obstacles. We recorded behavior via 3D thermal imaging and four multi-channel microphone arrays. We found that (i) all deafened bats voluntarily took flight off a starting platform in the center of the dark flight room, and that (ii) deafened bats could fly without colliding with the obstacles. However, the duration of their flights was shortened compared to the normal-hearing control bats. During flight, deafened bats vocalized at higher amplitudes and with broader frequency spectra than the controls. Our results provide fascinating insights into innate vs. learned behavior and how the lack of hearing affects acoustic specialists like bats.

Detailed Annotations Boost Classification Performance in Automated Bat Acoustic Identification

Santiago Martínez Balvanera[1], Everardo Gustavo Robredo Ezquivelzeta[2], Veronica Zamora-Gutierrez[3], Maria Cristina MacSwiney González[4], Oisin Mac Aodha[5] and Kate E. Jones[1]

1 Centre for Biodiversity and Environment Research, University College London, London, GBR; 2 Comisión Nacional para el Uso y Conocimiento de la Biodiversidad, Mexico City, MEX; 3 Centro Interdisciplinario de Investigación para el Desarrollo Integral Regional, Instituto Politécnico Nacional, Durango, MEX; 4 Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, MEX; 5 School of Informatics, University of Edinburgh, Edinburgh, GBR

The manual curation of reference bat call recordings is a key process in the development of automated bat call identification (ID) systems. Experts annotate each recording to identify the species of the recorded calls, and these annotations are then used to train detection and classification deep learning (DL) models. Multiple annotation protocols have been used with differing levels of detail on the exact spectro-temporal location of the bat calls. While the most common approach is to indicate the species at a file level, some studies have also recorded the onset time of each call or used a bounding box to locate each call within the spectrogram. However, it is unclear what type of annotation protocol is more efficient for the development of ID systems. Using a dataset of Mexican bat calls with highly detailed annotations we explore the implications of different annotation protocols by comparing the classification performance of DL models trained to exploit the localization information of the annotations. We find that classification performance increases significantly when using detailed annotations, from 5−10% accuracy increase. This performance boost is greater when the number of recordings per species in the training dataset is low, from 5−20 recordings, while at 25 recordings per species the performance difference diminishes. These results suggest that when the number of recordings per species is a limitation, special attention should be made to providing detailed annotations to enhance the performance of classifiers.

Gut Microbial Community in Different Species of European Bats

Hana Bandouchova[1], Petr Linhart[1,2], Katerina Zukalova[1], Sarka Bednarikova[1], Heliana Dundarova3, Vendula Kalocsanyiova[1], Monika Nemcova[1], Vladimir Piacek[1], Jana Sedlackova[1], Lucie Veitova[1], Jan Zukal[1,4] and Jiri Pikula[1]

1 Department of Ecology and Zoo Animals, Game, Fish and Bee Diseases, University of Veterinary Sciences Brno, Brno, CZE; 2 Department of Animal Protection and Welfare and Veterinary Public Health, University of Veterinary Sciences Brno, Brno, CZE; 3 Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, BGR; 4 Institute of Vertebrate Biology, Academy of Sciences Czech Republic, Brno, CZE

The influence of microbiota on physiological functions in the organism, including the immune response to pathogens, is currently an important topic in human and veterinary medicine. Previously, microbiome analysis was based on the identification of culturable microorganisms. At present, with the development of sequencing technologies, new possibilities for the analysis of the microbial community are opening. Here, we analyzed microbiome in insectivorous bats based on rectal swab sampling. Feces are commonly used to analyze the composition of the microbial community, but it is not always possible to collect feces from a bat, so we decided to test the use of a rectal swab. The sample was treated with DNA/RNA Shield immediately after collection. After DNA isolation and amplification of the entire 16S rRNA region, we used MinION, a third-generation sequencer. The subsequent analysis was performed using bioinformatic tools (nanopolish, fastp, Kraken2 and the Krona pie chart). The Silva 16S rRNA database was used for identification of individual reads. The amount of DNA was monitored continuously by fluorometry. In most rectal swabs, sufficient amount of bacterial DNA was obtained to analyze the composition of the microbial community. The analysis of the microbiome in several bat species revealed the largest proportion of proteobacteria, namely the class Gammaproteobacteria and the order Enterobacterales. Firmicutes was the second most abundant phylum. Bacilli class or the genus *Mycoplasma* were relatively highly abundant in the majority of samples. A relatively large variability in gut microbiota was found between individual bats even within the same bat species.

Correlations Between Physical and Environmental Drivers, High Bat Abundance, and Species Richness in Brazilian Caves

Jennifer S. Barros[1],[2] and Enrico Bernard[2]

1 Programa de Pós-graduação em Biologia Animal, Universidade Federal de Pernambuco, Recife, BRA; 2 Laboratório de Ciência Aplicada a Conservação da Biodiversidade, Universidade Federal de Pernambuco, Recife, BRA

Bats select their roosts in a species-specific way. This selection is likely related to the different physiological and adaptive needs of each species. Unlike species whose individuals roost solitarily, roost selection is more critical for species forming exceptionally large colonies due to their additional requirements for population maintenance. Using captures, bioacoustics, and automated censuses, we evaluated how physical and environmental variables (cave size, ceiling characteristics, environmental stability, temperature, and humidity) influence the formation of exceptionally large bat colonies, bat species richness and composition in caves in northeastern Brazil. *Pteronotus* (Mormoopidae) colonies were positively related to cave size, stability, and ceiling characteristics. The presence of those colonies strongly influenced temperature variation inside caves. Bat species richness was also positively correlated to cave size, stability, and temperature. Species other than *Pteronotus* showed a preference

for different climatic and ceiling characteristics. Our results indicate an indirect influence of the large colonies of *Pteronotus* on the richness and occupation of other species inside caves. On the other hand, caves favor species coexistence, as they offer a greater range of microenvironments, reducing niche overlap in their interior. *P. gymnonotus* and *P. personatus* are both key and umbrella species for cave ecosystems, stressing the need for specific conservation strategies for these species and their roosts in Brazil.

Factors Affecting Searcher Efficiency and Scavenger Removal of Bat Carcasses in Brazilian Wind Farms

Marília A. S. Barros[1,2], Luciana Iannuzzi[3], Isabelle L. H. Silva[4], Aída Otálora-Ardila[2] and Enrico Bernard[2]

1 Programa de Pós-Graduação em Biologia Animal, Universidade Federal de Pernambuco, Recife, BRA; 2 Laboratório de Ciência Aplicada à Conservação da Biodiversidade, Departamento de Zoologia, Universidade Federal de Pernambuco, Recife, BRA; 3 Laboratório de Taxonomia e Ecologia de Insetos, Departamento de Zoologia, Universidade Federal de Pernambuco, Recife, BRA; 4 Programa de Pós-Graduação em Biologia Vegetal, Universidade Federal de Pernambuco, Recife, BRA

Bat fatalities at wind farms have been reported worldwide, and environmental impact assessments depend essentially on searches for carcasses around wind turbines to quantify these impacts. However, part of the carcasses may go undetected by search teams or be removed by scavengers during search intervals, so these biases must be evaluated and taken into account in fatality estimation. We investigated the influence of different factors on searcher efficiency and scavenger removal in a dry forest area in northeastern Brazil, one of the regions with the highest density of wind turbines in the Neotropics. We conducted searcher efficiency and scavenger removal trials around 34 wind turbines from January 2017 to January 2018. Searcher efficiency was influenced by cover type, season and carcass size, ranging between 12% for small bats in shrub vegetation during the rainy season and 96% for large bats in absent/sparse vegetation during the dry season. Carcass type and season affected scavenger removal; carcass persistence time was shorter for chicks (1.2 days) than for bats and mice (2.1 days), and the probability of a carcass persisting for a whole day was higher in the rainy season, while the probability of carcass persistence for seven, 14 and 28 days was higher in the dry season. Scavenger community was composed of canids, birds of prey and insects, with systematic removal of carcasses by the crab-eating fox throughout the year and by dung beetles in the rainy season. Based on our findings, impact assessments of wind farms on bats should conduct searcher efficiency trials in all seasons and cover types around wind turbines, using bat carcasses/models of different sizes. Scavenger removal trials should also cover all seasons, and can use mouse carcasses (but not chick carcasses) as surrogates for bats.

Habitat Fragmentation and Infection Dynamics in Neotropical Bat Communities

Daniel J. Becker[1], Lauren R. Lock[1], Kristin E. Dyer[1], Germán Botto Nuñez[2], Kelly A. Speer[3], Dmitriy V. Volokhov[4], M. Brock Fenton[5] and Nancy B. Simmons[6]

1 Department of Biology, University of Oklahoma, Norman, USA; 2 Departamento de Métodos Cuantitativos, Universidad de La República, Montevideo, URY; 3 National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA; 4 Center for Biologics Evaluation and Research, U.S. Food and Drug Administration, Silver Spring, USA; 5 Department of Biology, University of Western Ontario, London, CAN; 6 Department of Mammalogy, American Museum of Natural History, New York, USA

Habitat fragmentation can alter the composition of host communities, rates of movement among habitat patches, and transmission processes within populations. For highly mobile and diverse Neotropical bat species, consequences of fragmentation may be highly dependent on host evolutionary history, dietary habits, and pathogen transmission mode. Here, we discuss the results of long-term field studies of bat immunity and infection with common and genetically diverse bacterial pathogens (i.e., hemoplasmas, *Bartonella* spp.) and DNA viruses (i.e., herpesviruses) in Belize and Uruguay. Focusing first on a seven-year mark–recapture study of common vampire bats (*Desmodus rotundus*) in Belize, we show that the dietary niche of intact reserve bats has converged on that of bats in remnant forest among an agricultural matrix, with knock-on effects for homogenizing temporal patterns of infection prevalence. In subsets of repeatedly sampled individuals, more pronounced dietary shifts towards livestock prey coincided with gains in bacterial infection, possibly indicating resource-driven tolerance or greater bat–bat or bat–livestock contact. In Belize, occasional inter-roost movement of vampire bats homogenized the diversity of herpesviruses, whereas we observed strong geographic structure in the diversity of vampire bat herpesviruses in Uruguay. At the scale of entire bat communities, habitat fragmentation in Belize was associated with marked reductions in the diversity and sharing of hemoplasma genotypes between host species, likely a result of fragmented habitats harboring a nested subset of bat diversity. We lastly discuss in-progress work assessing consistency of fragmentation differences in cellular immunity and infection prevalence of these pathogens across bat species.

Bats Reduce Insect Density and Defoliation in Temperate Forests: An Exclusion Experiment

Elizabeth A. Beilke[1,2] and Joy M. O'Keefe[1,2]

1 Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign, Urbana, USA; 2 Center for Bat Research, Outreach, and Conservation, Indiana State University, Terre Haute, USA

Insectivorous bats are voracious predators capable of suppressing prey populations in agricultural ecosystems, yet the question of how bats impact forests is largely unexplored. We used a field experiment to test the hypothesis that insectivorous bats reduce defoliation through their top-down suppression of forest-defoliating insects. We performed this experiment between late May and mid-August of 2018–2020 in the central hardwoods region of the United States. We excluded bats but not birds from 20 large, sub-canopy forest plots, each paired with an experimental control plot. We monitored the change in leaf area and insect density for 9–10 random oak or hickory seedlings per plot (196 treatment and 200 control seedlings in total). On average, seedling defoliation was five times greater where bats were excluded. Additionally, bats' impact on oaks was three times greater than for hickory seedlings, which may be related to the greater occurrence of oak vs. hickory-defoliators in bat diets. By the end of the study, insect density was three times greater on seedlings in bat-excluded versus control plots. We show that insectivorous bats drive top-down species cascades influencing the structure and composition of forests and may thus play an integral role in forest ecosystems.

The Sweet Physiology of Bats

Andrea Bernal-Rivera[1], Jasmin Camacho[1], Jerrica Jamison[2], Natalia Sandoval Herrera[3], Nicolas Rohner[1] and Kenneth Welch Jr.[4]

1 Stowers Institute for Medical Research, Kansas City, USA, 2 Department of Cell and Systems Biology, University of Toronto Scarborough, Toronto, CAN, 3 Department of Ecology and Evolution, University of Toronto Scarborough, Toronto, CAN, 4 Department of Biological Sciences, University of Toronto Scarborough, Toronto, CAN

High sugar diets have long been associated with negative health consequences in mammals, like diabetes. Animals that consume high volumes of sugar have adaptations to negate the consequences of their diet. In bats, both frugivorous and nectarivorous bats consume far more sugar than their insectivorous counterparts. However, despite their similarly high sugar content, fruits and nectar differ in nutrient density. These differences may impact sugar metabolism in such a way that the bats that specialize on either diet would have drastically different ways of coping with the sugar they eat. We performed in vivo metabolomics and respirometry to survey the sugar assimilation of bats across dietary guilds. When bats were given an oral dose of stable isotope glucose based on body weight, glucose appeared in the blood at different rates depending on the bats' dietary specialization. Fruit and nectar bats showed high and fast assimilation curves. Insectivorous and carnivorous bats showed low and slow assimilation curves. Furthermore, nectar and fruit bats showed blood glucose levels above 750 mg/dL, the highest values ever reported for any mammal. While nectar and fruit bats showed similar assimilation curves, we find, along with respirometry data, that nectar bats metabolized recently ingested sugar substantially more slowly than fruit bats. These results show that bats from different diets have different physiological mechanisms to deal with the sugar present in their diets, which are seen in the distinct speed and level of their glucose assimilation and metabolism.

Response of Bats to Severe Bark Beetle Outbreaks and Ensuing Successional Changes
Amanda J. Bevan and Rick A. Adams
School of Biological Sciences, University of Northern Colorado, Greeley, USA

Climate change has increased the frequency and severity of disturbance events globally, including widespread bark beetle outbreaks in North America and Europe. Forests recovering from intense outbreaks undergo a series of successional changes including competitive release of forest-floor vegetation. Although bats are known to be impacted by altered habitat structure, how bats are affected by beetle kill and ensuing changes in food web structure remains elusive. Colorado's Front Range bats are segregated into foraging guilds including forest, open, edge, and generalist species. I measured overstory and understory vegetative changes, surveyed nocturnal insects using Malaise traps and sweep nets, and deployed Wildlife Acoustics SM2BAT detectors within severely affected forests (>50% mortality) in various successional stages to quantify how disturbance and recovery alters bat assemblage composition and activity (calls/night) in 2020. Results from a Non-metric Multidimensional Scaling ordination indicated there is some cohesion of species-specific responses to forest succession consistent with foraging guilds. Activity levels of open habitat and two forest-foraging species are positively correlated with beetle-affected forests containing high volumes of decayed coarse woody debris and greater cover of forbs. These results suggest that my data on insect abundance and diversity may reveal bottom-up processes influencing bat responses to changes in food web structures at these sites. This study will contribute to our understanding of the impacts of climate change on bats in high elevation ecosystems as these habitats are expected to become increasingly important refuges from climate warming at lower elevations.

Helping Bat Conservation Take Flight: What Messaging is Most Effective at Making People Care about Bats?
E. Blythe Beynon1, Daniel K. Riskin[2] and Shelby H. Riskin[1]
1 Department of Ecology and Evolutionary Biology, University of Toronto St. George Campus, Toronto, CAN; 2 Department of Biology, University of Toronto Mississauga, CAN

Online videos are often used to generate support for conservation, but it's unknown what messaging is most effective. To compare the effectiveness of different messages, we created a series of four videos to improve awareness and encourage conservation action on behalf of bats. Each video contained the same 90 s introduction explaining bats' unwarranted reputation, and the same 30 s conclusion encouraging participants to support bat conservation. Three of the videos also included a message about either (a) the charisma of bats, (b) the threats faced by bats, or (c) the critical roles bats play in ecosystems. Because many outreach campaigns rely on flagship species, we predicted that for bats, messages highlighting their charisma would be more effective than other strategies. Using an online platform, we showed 401 members of the public one of the videos and surveyed their knowledge and attitudes on bats, and views on the environment before and after watching the video. We paid participants USD$1.50 and offered them an additional USD$2.00 to keep or donate in any proportion to Bat Conservation International. Contrary to our prediction, explaining the important role bats play in ecosystems was most effective at improving attitudes towards bats ($p = 0.0351$). However, donation amounts and knowledge gains did not differ among the four treatments. Instead, participants' initial environmental values were the best predictors of behavior, suggesting that for conservation, short-term messaging may be less effective than long-term efforts aimed at shifting environmental values.

Fruit Bats of Sindh Pakistan: Historical Impacting Factors and Implications for Modern Conservation Efforts
Brenda L. Bhatti
Current Independent Research, Jaffrey, NH, USA

In 2000, a baseline study in and near Karachi in the province of Sindh, Pakistan, was undertaken to determine location, presence, and impacts to any of the four species of fruit bats historically reported for the area: *Cynopertus sphinx*, *Pteropus giganteus*, *Rousettus aegyptiacus*, and *Rousettus leschenaulti*. The underlying hypothesis was that there would be no apparent change from historically reported ranges within Sindh. An extensive literature search was completed at the Lubee Foundation (Gainesville, Florida) to identify species' distribution, as well as potential tree species and suitable habitat types in urban, outlier, and agricultural areas. A field investigation was conducted in March 2000, during which twenty sites were visited, and a variety of methods were employed to search for potential roost and forage sites. Eleven individuals, identified as *Rousettus leschenaulti* based on the length of the second phalanx of the third digit, were captured in Karachi, Malir, and Thatta. Many factors were identified through direct observations, along with scientist and citizen inquiries, that may impact the fruit bats in this region, including roost competition and harassment by house crows (*Corvus splendens*) and black kites (*Milvus migrans*), light pollution, and eradication as crop pests in agricultural areas. Other direct and notable impacts were considered that included religious beliefs, medicinal uses, displacement due to purposeful or inadvertent habitat destruction, direct killing due to fear or misperceptions, and direct killing as perceived nuisances or dangers to humans. The conclusion, based on the limited dataset, was that these four species were not evidently present within the extent of historically reported ranges within the Karachi, Malir, and Thatta areas of Sindh in March 2000. Subsequent review of accounts for Sindh and Pakistan in the past twenty years compares and contrasts the impacting factors, evolving human attitudes, and opportunities for modern conservation efforts.

UAV-based Line Transect Surveys to Measure Bat Occupancy, Abundance, and Species Composition at Wind Energy Facilities
Larisa J. Bishop-Boros, Michael B. Gerringer,, Kimberly K. Bay and Leigh Ann H. Starcevich
Western EcoSystems Technology, Inc., Cheyenne, USA

The population size of most bat species is unknown, which presents a major conservation and management challenge because population trends and impacts of fatalities at operational wind energy facilities are difficult to determine. Passive acoustic detection methods are commonly used to measure bat activity and species occupancy but cannot be used to calculate bat density or abundance because the number of individuals cannot be determined from acoustic detections. In 2020, we used an Unmanned Aerial Vehicle (UAV) equipped with an onboard thermal camera and modified SM4BAT detector to simultaneously record bat calls and thermal videos. In 2021, we collected UAV data along 0.5 or 1-km transects at two Midwestern wind sites and one mitigation site during the fall migratory season, considered the riskiest period for bats at wind facilities. We deployed a grid of 1617 passive detectors per site to compare and validate UAV data. Big brown bat, eastern red bat, hoary bat, and silver-haired bat were the most commonly identified species and the most common fatalities at study sites. Machine learning algorithms detected bat thermal traces, and statistical methods were used to model bat abundance and calculate trends in species occupancy and abundance. Over seven visits at one wind site, bat density per UAV transect declined per km^2, and a decreasing trend in passive acoustic activity simultaneously corroborated the UAV trend. Unlike vehicular sampling, our approach surveys airspace in the rotor-swept zone of wind turbines, increases spatial coverage, and can detect non-echolocating bats.

Taking Flight Biology Beyond the Lab: Ecology and Diversity Inform Biomechanics

David B Boerma[1,2], Andrea D Rummel[3] and Sharon M Swartz[4,5]
1 Department of Biomedical Sciences, Cornell University, Ithaca, USA; 2 Department of Mammalogy, American Museum of Natural History, New York, USA; 3 Department of Ecology and Evolutionary Biology, Princeton University, Princeton, USA; 4 Department of Ecology, Evolution, and Organismal Biology, Brown University, Providence, USA; 5 School of Engineering, Brown University, Providence, USA

Field-based biomechanics has the potential to produce fundamental insights into organismal evolution and diversity for two primary reasons: 1) natural selection acts upon organismal performance, and variation in performance often arises from variation in biomechanics; and 2) biomechanics is inherently integrative, situated at the intersection of traits that interact to drive diversification, such as animal form, function, and ecology. However, bat flight biomechanics research has historically taken place in laboratories, often with captive-bred animals, where essential tools such as wind tunnels and high-speed videography are easily accessible. Lab-based work establishes fundamental form-function relationships and mechanical strategies for bat flight, but are often constrained to few species and are unable to measure animals directly in the environments where natural selection acts. Field-based biomechanics research bridges this gap, allowing access to greater species diversity and ecological context for drawing concrete conclusions about flight performance in natural environments and its significance for bat evolution. Here, we highlight our efforts to push bat flight research out of the lab and into the field by focusing on three broad areas of active investigation: 1) roosting ecology and the evolution of bat landing maneuvers; 2) proximal-to-distal variation in intramuscular temperature in bat wings and its effect on the physiology and mechanics of flight; and 3) linking biomechanics and ecology in predatory pursuit by insect-eating bats.

Prevalence, Distribution and Diversity of Bartonella in Small Mammal and Bat Communities Across Land Covers, Cambodia

Sophie A. Borthwick[1], Alan T. Hitch[2], Erica S. Neves[1], Dolyce H.W. Low[1], Lena Chng[1], Gavin J.D. Smith[1,3,4,5] and Ian H. Mendenhall[1]
1 Program in Emerging Infectious Disease, Duke-NUS Medical School, SGP; 2 Department of Wildlife, Fish and Conservation Biology, University of California, Davis, USA; 3 Centre for Outbreak Preparedness, Duke-NUS Medical School, SGP; 4 SingHealth Duke-NUS Global Health Institute, SingHealth Duke-NUS Academic Medical Centre, SGP; 5 Duke Global Health Institute, Duke University, Durham, USA; 6 Forestry Administration, Phnom Penh, KHM; 7 General Directorate of Animal Health and Production, Phnom Penh, KHM

Bartonella species are Gram-negative, facultative intracellular bacteria that represent the only genus in the family Bartonellaceae. Small mammals and bats are natural reservoirs of many *Bartonella* species. We investigated *Bartonella* presence, distribution and diversity in small mammals and bats across 227 probabilistic locations in 23 provinces and 22 opportunistic locations in Cambodia from 2016 to 2020. A total of 3,515 small mammal and bat blood and lung spleen kidney (LSK) samples were screened with pan-bartonella PCR primers targeting the beta subunit of bacterial RNA polymerase (rpoB) gene. *Bartonella* DNA was detected in 13.8% of small mammals and bats collected during this project including 26 small mammal species and 62 bat species. Highest prevalence was detected in *Rattus tanezumi* (42%) and *Rhinolophus acuminatus* (39%). Phylogenetic analyses of 204 rpoB gene sequences showing *Bartonella* genotypes circulating in bat and small mammal populations across Cambodia.

Aging Bat Carcasses at Wind Energy Facilities Using Mouse Surrogates

Nicholas W. Boulanger[1], Brittany B. McGill[1], Brandi Danielle Stevenson[1], Donald I Solick[1,2] and Michael D. Whitby[1]
1 Bat Conservation International, Austin, USA; 2 Vesper Bat Detection Services, Fort Collins, USA

The expansion of wind energy has helped reduce global reliance on fossil fuels, but has also negatively impacted migratory bat populations. Properly aging bat carcasses during wind facility monitoring projects is critical to evaluating the effectiveness of fatality minimization strategies. However, current techniques for determining the time of death for bat carcasses lack empirical justification. In this study, 38 mice were sacrificed and placed under turbines as surrogates for natural bat fatalities at a wind energy facility in Iowa. The carcasses were checked periodically for several key decomposition characteristics: desiccation or loss of eyes, distinct odor, removability of dorsal fur, and presence of infestation. We built generalized linear mixed models to assess the predictive value of these characteristics. Models that included four factors outperformed ones that included only two or three. The most predictive factor was the status of the eyes, while the presence of infestation was the least predictive. Artificially created wounds and time of the migration period did not significantly affect the decay rate. Applying this information to bats, we developed a decision tree for accurately aging carcasses within three days of death in the field based on readily observable decomposition characteristics. The results from this study may be broadly applicable across bat species and climates in the eastern United States.

Manipulating Hibernacula to Manage Bats has Potential, but also has Potential Pitfalls

Justin G. Boyles[1], Virgil Brack, Jr.[2] and Liam P. McGuire[3]
1 Cooperative Wildlife Research Laboratory and School of Biological Sciences, Southern Illinois University, Carbondale, USA; 2 Environmental Solutions & Innovations, Inc., Cincinnati, USA; 3 Department of Biology, University of Waterloo, Waterloo, CAN

Manipulation of microclimates in subterranean sites has gained renewed interest as a management strategy for hibernating bats facing white-nose syndrome (WNS). WNS creates an energy imbalance for hibernating bats and ultimately leads to starvation. Many researchers and management agencies therefore suggest that modifying hibernacula to meet conditions historically thought to minimize energy expenditure during hibernation

is a viable intervention. We agree that modifying hibernacula has great potential as a management strategy. However, this strategy, as currently implemented, carries high risk because the cavernicolous bat system has all the hallmarks of a system prone to falling into an ecological trap. We present an individual-based energetic model that demonstrates risk of creating an ecological trap likely increases as conditions approach those often targeted in hibernaculum manipulations. When realistic levels of variation in ambient conditions are considered, target microclimates are risky for hibernating bats, and sites with "ideal" midwinter ambient temperatures can lead to energy expenditure as high, or higher, than sites historically considered warmer than ideal. With that in mind, we suggest the goal should not be to achieve any specific midwinter temperature in a site, but instead to target manipulations that create a variety of conditions to guard against the risks posed by naturally variable conditions. More generally, we argue that we should place a premium on a cautious and conservative approach to manipulating subterranean sites for management of hibernating bats because we are short on scientific understanding and capable of imposing significant injury to the system if we are wrong.

Range Expansion of the Gray Myotis in Indiana

Darwin C. Brack[1], Virgil Brack, Jr.[1] and Bradford Westrich[2]
1 Environmental Solutions & Innovations, Inc., Cincinnati, USA; 2 Division of Fish & Wildlife, Indiana Department of Natural Resources, Bloomington, USA

Species often exist across a broad landscape where they are irregularly distributed; range maps and descriptions often fail to capture precise range boundaries or elements of seasonality, abundance, or reproduction and ranges expand or contract across time. The range of the gray myotis (*Myotis grisescens*) is typically described as cave regions of the southeastern United States, Missouri to Alabama, while caves farther north are not used. Thus, although this bat is common in parts of Kentucky, it has historically been absent from Indiana. However, during recent years the gray myotis has become increasingly common in the state. Populations of gray myotis were documented in three karst areas across southern Indiana, all separated by >50 km. Populations were documented (capture, observation and/or acoustic) simultaneously during all seasons. After 3 years of surveys and year-round monitoring, summer populations appear to be increasing at two locations (at least), with reproduction confirmed at one location and likely at another. Winter populations have increased 1,750% since 2017, when only 368 gray myotis were located. In total, five caves and 1 mine are confirmed to be used by gray myotis during at least one season. Interestingly, strong spring and autumn activity was documented at three caves and 1 mine, two of which are the furthest north of any gray myotis population in Indiana and range-wide. These data indicate that a range expansion is in progress and help inform conservation and management decisions, including potential conflicts with other protected species.

Lures, Planes, and Break-away Collars: Strategies to Locate Roosts of Elusive High-flying Bats

Elizabeth C. Braun de Torrez[1,2], Jonas P. Borkholder[1], Dillan J. Hoyt[1], Jeffery A. Gore[1] and Holly K. Ober[2,3]
1 Florida Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, Gainesville, USA; 2 Wildlife Ecology and Conservation, University of Florida, Gainesville, USA 3 Department of Forest Ecosystems and Society, Oregon State University, Corvallis, USA

Rare, high-flying and long-distance foraging bats are extremely challenging to capture and track. Endangered Florida bonneted bats (*Eumops floridanus*, Molossidae) traverse extensive areas at high altitudes and may be roost limited. At the time of listing, virtually nothing was known about their natural roosting habitat and no reliable methods were in place to locate new roosts. Between 2015 and 2022, we used various passive and active strategies (acoustic surveys, emergence observations, peeper cameras, passive integrated transponders [PIT] tags, acoustic lures, aerial radiotelemetry) to locate and characterize roosting habitat of E. floridanus across their range. Because molossids often quickly remove glue-on radiotransmitters, we developed an alternative break-away collar to effectively track bats to roosts. We found these collars typically remained attached for the transmitter's lifespan but dropped off over time as intended, with few negative effects to bats. We located 31 natural roosts predominantly in cavity trees within forested wetlands and pine flatwoods, some occupied for several years. Roost trees were larger and further from surrounding vegetation than randomly selected non-roost trees. Fewer than 2% of total trees measured had cavities, suggesting that suitable cavities are very limited on the landscape. Further, documented roost losses and abandonment following hurricanes, wildfires, decay, and management activities indicate that E. floridanus faces ongoing threats to its roosting habitat and long-term recovery. Using strategies tailored to its biology, we were able to exponentially increase our understanding of roost selection for this rare species. Such methods may be more broadly applicable to other bat species.

A Dual Isotope (δ2H, 87Sr/86Sr) Approach to Studying the Movements of Myotis lucifugus in Newfoundland, Canada

Caralie T. Brewer[1], Vaughan Grimes[2,3], Jessica Humber[4], Fred Longstaffe[5] and Erin E. Fraser[1]
1 School of Science and the Environment, Memorial University, Corner Brook, CAN; 2 Department of Archaeology, Memorial University, St. John's, CAN; 3 Department of Earth Sciences, Memorial University, St. John's, CAN; 4 Department of Fisheries, Forestry, and Agriculture, Government of Newfoundland and Labrador, Corner Brook, CAN; 5 Department of Earth Sciences, University of Western Ontario, London, CAN

Analyses of biochemical markers are frequently used to study animal migration and dispersal but are limited in their precision and commonly most effective at large geographical scales. Further, such studies are often limited to investigating animal origin during the formation of a single tissue. These shortcomings can be addressed by using multiple isotopic systems and comparing the biochemical compositions of multiple tissues to make inferences about various life stages. Thus, we investigated seasonal movements of *Myotis lucifugus* in Newfoundland, Canada, using stable hydrogen (δ2H) and strontium (87Sr/86Sr) isotope analyses of fur, and lifetime movements using comparisons between strontium isotope analyses of fur, teeth, and bones. Employing publicly available databases, we developed isoscapes of δ2Hprecipitation and bioavailable 87Sr/86Sr for the region. To infer the relationship between δ2Hprecipitation and that in bat fur, we established a local transfer function using 23 pre-deceased individuals found within their period of summer residency. Strontium isotope analysis of fur from these individuals reflected the underlying bedrock signature, with high variation among individuals found in distinct regions of insular Newfoundland (Western $\bar{x}$ = 0.7117; Central $\bar{x}$ = 0.7138; Eastern $\bar{x}$ = 0.7099). Strontium isotope analyses of fur, teeth, and bone tissues from a subset of these individuals showed similar land-use patterns in early life (reflected in bones, teeth; n = 10, $\bar{x}|T\text{-}B|$ = 0.0002) and a combination of regional movements (n = 3) and natal philopatry (n = 7) in late life (reflected in fur). These techniques show promise for future investigations of migratory bat species by identifying movements with finer resolution than historically achieved using intrinsic markers.

Adaptive Radiations of Miniopterus? Comparing the Eco-morphology of Sister Clades

Stefania Briones[1,2], Roberta Mason-Gamer[1], Terrence C. Demos[2] and Bruce D. Patterson[2]
1 Department of Biological Sciences, University of Illinois, Chicago, USA; 2 Field Museum of Natural History, Chicago, USA

The long-fingered bats (Miniopteridae, all in the genus Miniopterus) include ~40 currently recognized species, with 15 of these occurring in the Afrotropics and 12 on Madagascar. Their wing morphology and flight capabilities appear to be unique among vespertilionoid bats, allowing them to forage both in open spaces as well as in clutter-edge areas. The Afrotropics are home to several other bat families of clutter-edge specialists absent from Madagascar, including Rhinolophidae, smaller Hipposideridae and Nycteridae. Has this assemblage-level context affected the morphological radiations of the two groups of *Miniopterus*? A new UCE-based phylogeny clearly resolves the Afrotopical *Miniopteru*s exclusive of *M. inflatus* as the sister group of the Malagasy taxa—both have the same ages. By quantifying flight-related wing measurements and examining the size and density of the morphospaces occupied by the two sister assemblages, we test whether the Malagasy *Miniopterus* constitute an adaptive radiation in the absence of other bat competitors.

Tracking Down Fruit – the Sensory Ecology of Frugivorous Bats

Alyson F Brokaw[1,2], Rachel A Page[3] and Michael Smotherman[2]
1 Department of Biological Sciences, Lehigh University, Bethlehem, USA; 2 Department of Biology, Texas A&M University, College Station, USA; 3 Smithsonian Tropical Research Institute, Gamboa, PAN

Animals rely on a variety of sensory cues to detect, discriminate, and localize critical resources, including food and mates. While much attention has focused on the acoustic cues bats use to navigate their world, the role of olfaction in the lives of bats remains underexplored. Olfactory detection and localization strategies have been described in terrestrial animals, but bats face the unique added challenges of flight and echolocation. Therefore, bats may display unique strategies to accomplish olfactory localization tasks. By integrating morphological analysis and field experiments, we sought to quantify the olfactory search behaviors and strategies used by Neotropical fruit-eating bats during foraging. We first developed a set of behavioral assays to quantify the olfactory search behaviors of fruit-eating bats at the Lamanai Field Research Center in northern Belize. By pairing these assays with automated video tracking software, we found evidence that bats can exploit odor concentration gradients to locate odor sources while crawling. We later extended these assays to characterize the olfactory search behaviors of bats in flight at the Smithsonian Tropical Research Institute in Gamboa, Panama. Though bats can follow odor gradients when crawling, they appear unlikely to use odor plume structure to locate food resources in flight. Instead, bats used serial sampling and route-following strategies that integrate olfaction and echolocation to quickly and efficiently find and evaluate a rewarded odor. This work highlights the value of collaboration, patience, and challenging assumptions in the study of animal behavior, especially in bats.

How Genetics has Changed the Distribution and Natural History of Some North American Bats: Eastern Red Bats Breeding in California

Patricia E. Brown and William E. Rainey
Brown-Berry Biological Consulting, Bishop, USA

When I started studying bats in 1968, there was one North American red bat (*Lasiurus borealis*). In 1988, Barker et al. split the species, describing western red bats (*L. blossevillii/frantzii*) as occurring west of the Continental Divide based primarily on genetic data. No specimens from CA, AZ, NV, or Utah were in this analysis. From 2014–2021, we recorded echolocation signals of western red bats on three California Channel Islands (Santa Cruz, Santa Catalina, and San Nicolas) as well as some sequences that were lower in frequency than those typical of western red bats and higher than those of western yellow bats (*Dasypterus xanthinus*). On Santa Cruz Island, we captured two juvenile male red bats in July 2017 and another in 2018. A wing punch from the 2018 capture was analyzed for 16S mtDNA and identified as an eastern red bat. Subsequent analyses of mainland California red bat preserved tissue samples by D. Fraser (CDFW Wildlife Genetics Research Lab) identified four additional eastern red bats collected between 1997 and 2016: a female (Los Angeles County); male and pregnant female (Santa Barbara County); female (San Diego County). Geluso and Valdez (2019) expanded the eastern red bat range to eastern Arizona and Utah. Are the two species sympatric over all or part of their range in the west? Graduate student Zeinab (Rose) Haidar is currently examining museum and public health specimens and tissue from red bat captures to determine if the pelage, morphometrics and DNA support any geographic hypothesis. Since both eastern and western red bats occur and breed in California, a new common name is needed for *Lasiurus borealis*.

Public Perceptions of Bats and Their Management at a Recreation Site in the Southeastern United States

Rebecca L. Brown[1], Shari L. Rodriguez[1], William C. Bridges[2], Patrick J. Rosopa[3] and Susan C. Loeb[4]
1 Department of Forestry & Environmental Science, Clemson University, Clemson, USA; 2 School of Mathematical and Statistical Sciences, Clemson University, Clemson, USA; 3 Department of Psychology, Clemson University, Clemson, USA; 4 U.S. Forest Service, Southern Research Station, Clemson, USA

High bat mortality from white-nose syndrome (WNS) has increased the need to manage hibernation sites, including caves, tunnels, and mines that are managed as recreation sites. Conservation of recovering bat populations may require restricting public access to sites, making it essential to understand public perceptions, what factors predict attitudes towards bats, and what factors lead to support for bat management. We used Stumphouse Tunnel, a recreation site and *Perimyotis subflavus* bat hibernaculum in northwestern South Carolina as a case study to assess public knowledge of and attitudes towards bats and measured their support for management options at the site. We conducted surveys at the tunnel, by mail, and by email. Despite site educational signage, 60% of respondents had not heard of WNS. A positive attitude towards bats was related to positive experiences with bats, caring and biophilia-related beliefs about wildlife, and knowledge about bats ($R^2 = 0.48$). Support for bat management at Stumphouse Tunnel was associated with a higher perceived level of responsibility of wildlife agencies and organizations to conserve bats, attitudes towards restricting access at recreation sites, caring and biophilia-related beliefs about wildlife, and attitudes towards bats ($R^2 = 0.42$). Respondents familiar with WNS were more likely to strongly support tunnel closure during hibernation ($\chi^2 = 15.4$, df = 6, $p = 0.017$). Outreach providing positive bat experiences is expected to lead to more positive attitudes towards bats. Increased education about WNS and other threats bats face internationally may increase support for management that restricts access to recreation sites.

Use of Forested Habitat Near a Hibernaculum by Little Brown Bats During Fall Swarm

Sophia R. Brown and Craig K. R. Willis
Department of Biology and Centre for Forest Interdisciplinary Research, University of Winnipeg, Winnipeg, CAN

Identifying and protecting critical habitat is fundamental to endangered species conservation. Little brown bats (*Myotis lucifugus*) are listed as endangered by the IUCN and in Canada because of population declines from white-nose syndrome (WNS). Canada has defined hibernacula as critical habitat and numerous hibernacula therefore benefit from protection. Although not yet classified as critical habitat, data also exist on

maternity roosts of little brown bats. However, little is known about fall habitat requirements when bats swarm at entrances of hibernacula, mate, and fatten for hibernation. Understanding whether bats roost and feed close to swarm sites, and identifying these habitats, could enable management actions that help bats accumulate larger fat reserves and survive the winter with WNS. To determine fall habitat use, we radio-tagged 40 little brown bats near a known hibernaculum and swarming site in Manitoba, Canada in September 2021 and tracked them to roosts and foraging locations for up to 30 days. Most bats (n = 21) were never detected again and, presumably left the study area. Those that remained roosted exclusively in natural structures (n = 12 roosts, 6 bats), including snags, live trees, and caves despite the presence of suitable man-made structures in the study area. Foraging home range size varied widely (62 m^2–23.6 km^2, n = 8 bats), with the furthest foraging location fix being 15 km away from the hibernaculum. My results suggest that large forested areas around hibernacula may require protection to help bat populations recover.

Variation in Bat Community Structure Across an Urban-Agricultural Landscape
Galen E. Burrell and Scott M. Bergeson
Department of Biology, Purdue University Fort Wayne, Fort Wayne, USA

In the past 20 years, bat species in the Midwestern United States have experienced population declines, partly because human development is reducing the occurrence of uninterrupted natural areas. As this trend continues, it is important to identify habitat features that support diverse bat communities in and around developing areas. In the summers of 2020–2021, we investigated differences in bat activity and community composition along an urban-rural gradient created by Fort Wayne, Indiana and the surrounding agricultural land. We deployed passive acoustic detectors at 22 field sites – 11 in urban areas and 11 in rural. We sampled each site 4 to 7 consecutive nights, twice throughout the summer. In urban areas, we sampled 217 nights and collected 22,463 bat calls across both summers (1,070 ± 225 calls/site). In rural areas, we sampled 220 nights and collected 36,745 bat calls (1,750 ± 288 calls/site). Based on preliminary analysis using Bat Call Identification software, we detected 9 total species across our study sites. The highest proportion of calls were attributed to big brown bats (*Eptesicus fuscus*) in both urban (46.5% ± 4.8%) and rural areas (48.6% ± 3.8%). However, calls from *Myotis* species were detected more often in rural (4.4% ± 2.0%) than in urban areas (1.5% ± 0.5%). Further analysis with PRESENCE software will elucidate relationships between bat occupancy and environmental variables associated with individual sites at multiple scales. This will provide insight into the plot- and landscape-level factors that promote active, diverse bat communities in the Midwestern United States.

Roosting and Foraging Ecology of Female Tri-colored Bats in Tennessee, USA
Ashleigh B. Cable and Emma V. Willcox
Department of Forestry, Wildlife, and Fisheries, University of Tennessee, Knoxville, USA

The tri-colored bat (*Perimyotis subflavus*) has been negatively affected by white-nose syndrome across the eastern portion of its range. Populations have declined both in winter hibernacula and on the summer landscape. The United States Fish and Wildlife Service has announced a formal species status review to determine if federal listing is warranted. Despite once being a common bat, studies that have assessed the summer roosting needs of the species are limited. Moreover, there are no published studies determining its foraging affinities. We conducted 63 mist-net surveys from May–August from 2019–2021 in Tennessee, USA to target female tri-colored bats. We examined 17 roost trees used by 6 female tri-colored bats. Additionally, we collected foraging data for 6 females using biangulation. The best roost models indicated that they select trees with more canopy volume in areas with higher tree species richness in the 0.1 ha surrounding plot. Bats used an average of 2.1 roosts ± 0.6 SE during the tracking period. Overall foraging areas (95% kernel) were 2580.2 ha ± 1605.3 SE and the mean maximum foraging distance was 4.3 km ± 1.7 SE. Bats foraged in areas with more water, more development (i.e., paved rural roads in this case), more forest, and less open areas than available on the landscape. Managing forests for tree species richness and retaining live trees with large canopy volume during the maternity season might benefit female tri-colored bats. This might especially be important near water bodies, as female tri-colored bats used those areas for foraging.

Niche Tracking of Dry Conditions in the Spotted Bat (*Euderma maculatum*)
Camilo A. Calderón-Acevedo*1,2* Xitlaly Franquez[3] and J. Angel Soto-Centeno[1,4]
1 Department of Earth and Environmental Science, Rutgers University, Newark, USA; 2 Department of Environmental and Forest Biology, The State University of New York College of Environmental Science and Forestry, Syracuse, USA, 3 Keck Science Department, Pitzer College, Claremont, USA; 4 Department of Mammalogy, American Museum of Natural History, New York, USA

The Spotted Bat (*Euderma maculatum*) ranges from British Columbia in Canada to central Mexico, crossing the United States over the Rocky Mountains. Despite being easily detected given its audible echolocation calls, little is known about the biology of this species, or the types of habitats it occupies across its distribution. We explored the present-day potential distribution of *E. maculatum* using ecological niche modeling (ENM), to evaluate the available suitable habitat for this species and document the ecoregions where it is likely to be found. Furthermore, we used model projections to the past and the future to quantify if there have been significant changes in available suitable habitat for *E. maculatum* across time. Our predictive ENMs revealed a broad area of suitable habitat for *E. maculatum* extending its potential distribution from 27 ecoregions suggested by its observation records to 87 ecoregions spanning dry areas and deserts. From the Last Glacial Maximum to the present, the projected distribution showed a northeastward shift with higher suitability in Mexico in the past than in the present. Future climate change scenarios show that its potential distribution will shift further northward into British Columbia, but with a small magnitude of change between the best- and worst-case greenhouse gas emission scenarios. Our modeling framework provides novel information to help conservation biologists refine biological inventories of one of the least known North American bat species.

Implementing a Long-Term Bat Monitoring Plan in National Parks Within the Mojave Desert Region
Allen W. Calvert and Kimber N. Godfrey
US National Park Service, Mojave Desert Inventory and Monitoring Network, Boulder City, USA

The Mojave Desert Inventory and Monitoring Network (MOJN) conducts long-term research of natural resources within nine National Park units that span the Mojave and Great Basin deserts of Nevada, Arizona, and California. Due to the decline of bat populations across the country; primarily from White-Nose Syndrome (WNS) and wind energy development, a need for tracking populations across the network was identified. In 2017, a bat monitoring protocol was developed to collect baseline population data before the arrival of WNS in the region. Winter and summer acoustic data are collected following a modified version of the North American Bat Monitoring Program (NABat). A combination of priority and non-priority sampling cells were selected. A total of 32 NABat monitoring cells have been established across six park units. A total of 20 species

have been detected across all parks. Long term analysis will look to detect trends in species composition over time at each park. Capture surveys are conducted in the same six park units during spring to swab bats for the presence of the fungus that causes WNS. Lastly, large scale capture and acoustic efforts, known as bat blitzes, are conducted in one of the six park units on a yearly rotation in collaboration with several state and federal agencies. Collaboration between park and MOJN staff have been integral in implementing long-term monitoring in the network.

High-resolution Seasonally-explicit Distribution Models Reveal Bat Migration at the Macroecological Scale

C. J. Campbell1, Michael W. Belitz[1,2], Robert P. Guralnick[2], Robert J. Fletcher[3] and Hannah B. Vander Zanden[1]
1 Department of Biology, University of Florida, Gainesville USA; 2 Florida Museum of Natural History, University of Florida, Gainesville USA; 3 Department of Wildlife Ecology and Conservation, University of Florida, Gainesville USA

Animal migration is a complex behavior that can partially determine a species' ability to respond to anthropogenic impacts, habitat loss, and shifting climate conditions. However, migratory strategy and linkages are poorly understood for many bat species. To overcome these challenges, we leverage a novel methodological toolkit to characterize population-level migratory strategies from presence-only occurrence data. This toolkit is designed to compensate for data biases and gaps often inherent to data collected in unstructured or variable methods. This approach can be applied to all species for which even limited information exists and is not restricted to relatively well-studied species. We then developed seasonally-explicit distribution models for each of the 149 species of North American bats for which sufficient occurrence data exist. Models were subject to multiple rounds of expert validation. For each species, we quantified migratory distance, range size change, and degree of seasonality in joint models representing year-round distributions. Our approach builds on current knowledge of bat migration by quantitatively describing species-level seasonal distributions and identifying regions of seasonal occurrence and turnover. We hope that this framework will produce useful qualifications of bat migratory traits, which we plan to incorporate into future models to predict which individual- and species-level morphological and life-history characteristics are key predictors of migratory strategy. Additionally, we anticipate that this project will produce several useful data products that will be helpful in assessing current distributions and shifts, areas of highest migratory activity and expansion, and risks to migratory bats associated with human activity.

High Velocity Range-Shifts and Limited Refugia Predicted for Bat Communities in Drought-Risk Areas of the Northern Hemisphere

Mattia Piccioli Cappelli[1,7], Rachel V. Blakey[2], *Daniel A. R. Taylor[3], Jon Flanders[3], Trish Badeen[3], Sally R. Butts[4,5], Winifred F. Frick[3,6] and Hugo Rebello[7]
1 Department of Theoretical and Applied Sciences, University of Insubria, Varese, ITA; 2 La Kretz Center for California Conservation Science, Institute of the Environment and Sustainability, University of California, Los Angeles, USA; 3 Bat Conservation International, Austin, USA; 4 U.S. Department of the Interior Bureau of Land Management, Washington D.C., USA; 5 U.S. Department of Agriculture Forest Service, Region 6, Portland, USA; 6 Ecology and Evolutionary Biology, University of California, Santa Cruz, USA; 7 CIBIO/InBIO, School of Agriculture, University of Lisbon, Lisbon, PTA

Bat species occupying semi-arid regions face an uncertain future due to increases in drought frequency and severity. In this study we modelled the potential effect of climate change on bat communities within two high-drought risk regions of the world, assessed the magnitude and direction of the predicted shifts in climatic suitability, and identified climate change refugia and species at greatest risk. We compared climate suitability models for 43 species using three global climate models and emissions scenarios for current and future climates within the two regions, the Western Palearctic and Western North America. Our models predicted an overall reduction in bat richness. Areas projected to support high species richness in the current climate coincided with greatest predicted species loss. For species with the potential to extend their range, high velocity range shifts would be required to adapt to these changes, particularly in the Western Palearctic, which had additional barriers to movement. Predicted refugia were limited and occurred in similar areas across continents. Climate suitability was predicted to contract for around half of study species, with nine identified as species at risk due to low overlap between current and future modelled ranges. The best-case scenario for future bat diversity in these regions is likely to be reduced species richness, with many species facing rapid range expansion over challenging landscapes to access climatically suitable areas. Conservation of bats in these regions will likely depend on protection of identified refugia and networks of water sources, as well as global measures to protect biodiversity.

Bat Roosts in Culvert Structures and Implications for Conservation

Jill M. Carpenter
LSA Associates, Irvine, USA

Culverts are often mentioned along with bridges in the context of anthropogenic structures that provide bat roosting habitat; however, the paucity of available information about culvert roosts threatens the conservation of bats roosting in these structures in some regions. Data collected throughout southern California in the United States over a 14-year period show that at least eleven bat species, including species considered to have high conservation concern, roost in culvert structures. These structures include concrete box culverts, concrete arch culverts, concrete pipe culverts, and corrugated metal pipe culverts. Occupied culverts are found in a variety of habitats, including heavily urbanized landscapes, and bats have been observed day roosting (including maternity roosting), night roosting, and even mating within culvert structures. Roost features used by bats in culverts vary widely and can include overlap joints, expansion joints, manhole access shafts, drainage pipes, open concrete surfaces, and bird nests. Misconceptions about what constitutes suitable roosting habitat for bats in culverts can result in these structures being overlooked during the environmental review process, and consequently impacts to bats roosting in culverts are often not adequately minimized or mitigated. Bats roosting in these structures are also vulnerable to disturbance from human entry, vandalism, and increases in artificial light at night (ALAN) in areas adjacent to the roost. Because roosting habitat is a limited and declining resource for bats, overlooking culverts or less-commonly encountered features in culverts as roosts can have profound conservation and management implications.

Building an Effective Time Machine from Genomic Data

Bryan Carstens
Ohio State University, Columbus, USA

Genomic data represent an unparalleled source of information regarding the history of species. Evolutionary biologists have developed a variety of analytical tools for extracting information from genomic data, but the two strategies with the most active development – inferring the phylogenetic relationships among clades and adaption within populations – obscure the seminal question of the field. In the coming decade, genomic

data will allow us to move past existing dichotomies (e.g., clades or populations, selection or demography) and develop a richer view of the formation of species. The number of described bat species is steadily increasing, along with the recognition that there are likely many additional hidden species. While a variety of tools are available for delimiting species using genomic data, inferences about historical demography and speciation are far more likely to be correct when environmental, ecological, behavioral, and morphological trait data are incorporated. Given that theoretical and conceptual advances in several disciplines (e.g., landscape genetics, species delimitation, phylogeography) enable researchers to make increasingly detailed inferences about the historical processes that act in the broad space between a single population and clearly distinct species, investigations should move past mere species delimitation and infer the processes that contribute to the formation of bat species. Doing so in a manner that also considers the environment and the phenotype will elucidate how adaptations contribute to the ongoing diversification within Chiroptera.

Social Complexity in Bats: Networks, Relationships, and Strategies

Gerald G. Carter[1,2]
1 Department of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus, USA; 2 Smithsonian Tropical Research Institute, Panama City, PAN

Recent advances in automated data collection and social networks analysis have generated exciting new insights into the social structures of many animals, including some bats. These insights include identifying, for instance, how roost switching leads to emergent communities, how kinship predicts associations, and how social network structure impacts pathogen transmission. In this talk, I will discuss four open questions: (1) What are the main challenges for interpreting analyses of bat social networks? (2) To what extent are social networks shaped by the bats' social preferences versus sampling biases and the constraints of habitat? (3) To what extent do bats direct their time and energy towards maintaining specific social ties? (4) What is the evidence that individuals attempt to manage the quantity and quality of those social ties? In other words, are there 'social networking strategies' in bats? I will draw largely from studies on vampire bats, but also from other bat species. Finally, I will highlight the potential for gaining general insights from applying standardized methods across bat populations and species.

Monkeying Around with Bat Scapulae

Richard T. Carter[1] and Rick A. Adams[2]
1 East Tennessee State University, Johnson City, USA; 2 University of Northern Colorado, Greeley, USA

The evolutionary origin of flight in mammals remains unknown and identifying even if the ancestor to bats was arboreal or terrestrial remains elusive. With little fossil evidence we are forced to look to contemporary bats for genetic and morphological signals of past evolutionary events. We use morphometrics of the scapula identified by primatologists and paleontologists in differentiating arboreal versus terrestrial primates to test the question of ancestry for bats. Because adaptations for arboreality are distinctively specialized, if bats came from such an ancestor, morphological evidence should be present in contemporary forms. Arboreal scapula in suspensory taxa share the following characteristics: narrow and elongated scapula, cranially oriented glenohumeral joints, openness of glenohumeral fossa, longer and more oblique scapular spines, and wider infraspinous fossa near the scapular neck. We measured these as well as other morphometrics on Old (Pteropodidae) and New World (Phyllostomidae) fruit bats to assess if they possess arboreal traits of the scapula. Both families of fruit bats would likely have experienced similar selective pressures over time. Individuals from each family spanning a range of overlapping body sizes were considered. Geometric morphometric analysis of the scapulae found significant separation along the PC1 axis between families. There were also significant differences between the families in many of the arboreal characters measured, with pteropodids showing significantly more arboreal specializations (derivations) in scapular morphology, whereas phyllostomids possessing character states lacking specializations. Our data indicate that pteropodids are significantly more adapted to climbing and suspensory locomotion than are phyllostomids.

DeAMPlifying the Immune Response: Antimicrobial Peptides Evolution in Chiroptera

Francisco X. Castellanos[1], Diana Moreno-Santillán[2], Angelique P. Corthals[3], Katie R. Martin[4], Marianne S. Moore[5], Marisa C. W. Lim[6], Tanya M. Lama[7], Nicole S. Paulat[1], Nicolette Sipperly[7], Liliana M. Davalos[7] and David A. Ray[1]
1 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 2 Department of Integrative Biology, University of California, Berkeley, USA; 3 Department of Sciences, John Jay College of Criminal Justice, New York, USA; 4 Department of Biology, University of Central Florida, Orlando, USA; 5 Science and Mathematics, Arizona State University, Tempe, USA; 6 10X Genomics, Pleasanton, USA; 7 Department of Ecology and Evolution, Stony Brook University, New York, USA

High viral tolerance coupled with an extraordinary immune response makes bats a good model to study host-pathogen evolution. Although many immune-related gene gains and losses have been previously documented in bat genomes, important gene families such as antimicrobial peptides (AMPs) that trigger innate immunity upon invasion by extraneous agents remain understudied. We analyzed gene family evolution in Chiroptera to determine how AMPs are phylogenetically distributed in bats and assess the performance of bioinformatics pipelines designed to annotate genome assemblies. A bat-specific AMPs dataset was constructed with a homology search on 20 high-quality bat genome assemblies, using amino acid AMPs sequences curated from ENSEMBL and NCBI with Orthofisher and Ampir. The resulting dataset was subsequently included in an exhaustive downstream analysis to predict gene position using MAKER2 and Amplify. Several AMP families were recovered, including the major antimicrobial peptides: defensins. While α-defensins appear to have been lost in 9 out of 20 species, β-defensins were more diverse and found in multiple copies among all the species. Characterizing the multigene family evolution of specific AMPs families is crucial due to their up and downregulation regulation has been associated with positive or negative outcomes in the host caused by differential regulation of inflammasome pathways. The results of this study attempt to provide a robust framework for a deeper understanding of pathogen tolerance in bats.

Host Choice Experiment and Genetic Comparison of Bedbugs Infecting Bats and Humans

Clara Castex, Laura Clément, Pierre Perréaz, Benjamin Wolf and Philippe Christe
Department of Ecology and Evolution, University of Lausanne, Biophore, Lausanne, CHE

After its eradication in the 1940's, the bedbug (*Cimex lectularius*) experienced a global resurgence with some populations displaying insecticide resistance. Two lineages of bedbug were highlighted to be associated with human or with bats. From laboratory experiments, bedbugs were shown to be a competent vector for *Trypanosoma cruzi*, the agent responsible for Chagas disease in humans. Therefore, host specialization in bedbugs is important to study to understand the risk of pathogen transmissions between host species. We first tested with bugs either collected from

human dwellings or bat roosts, host choice preference between humans and bats using an olfactometer experiment. Then, we performed a genetic comparison between and among human and bat associated bedbugs using COI and 16S rRNA mitochondrial genes, 12 nuclear microsatellites and knock-down insecticide resistance gene variants. Bedbugs from the host choice experiment display more activity during the minimal activity period of their host (night for humans and day for bats) and the human associated bugs prefer human odor. The median-joining analysis exhibits a clear separation of haplotypes that are not shared between hosts. The analysis of genetic structure reveals two genetic clusters associated with bats and humans. This clear separation is also supported by the knock-down resistance analysis which shows that bedbugs infecting bats have not yet evolved insecticide resistance in contrast to the ones infecting humans. Our study is supporting evidence of host specialization in bedbugs with behavioral differences and patterns of genetic differentiation between the two host species.

Dietary Niche Partitioning and Its Relevance in Understanding Community Structure of a Himalayan Bat Assemblage

Rohit Chakravarty[1,2], Viktoriia Radchuk[1], Shreyas Managave[3] and Christian C. Voigt[1,2]
1 Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU; 2 Department of Animal Behaviour, Institute of Biology, Freie Universität Berlin, Berlin, DEU; 3 Department of Earth and Climate Science, Indian Institute of Science Education and Research Pune, Pune, IND

Elevational gradients are fundamental in understanding the geographical distribution of biodiversity. As climate and vegetation change over short distances across elevations, so do the diversity and community composition of various animal taxa. In a previous study on the diversity of bats across an elevational gradient from 1500–3500 m asl in the Himalaya, we found that species richness and functional diversity (the diversity of traits) decrease at high elevation. Niche theory predicts that increasing species richness in a community can lead to denser packing of the niche space ('niche packing') or an increase in its volume ('niche expansion') depending on the need to partition available resources. While functional traits are used as a proxy for past ecological mechanisms (like interspecific competition or abiotic filtering), the use of dietary markers can enhance our understanding. In this study we test these predictions by investigating dietary niche width and overlap among 26 bat species from seven foraging guilds using stable carbon and nitrogen isotope analysis of wing tissue samples collected in the field. Our preliminary results suggest that edge foraging, open foraging, and flutter detecting bats show high niche overlap, whereas trawling and active-gleaning foragers show low overlap with other assemblage members. The high elevation restricted *Plecotus* spp. appear to be dietary specialists with low overlap with other guilds. We also uncover low niche overlap among guilds at high elevations suggesting that these species partition their dietary niches in a resource poor environment – a pattern not visible using analysis of functional traits alone.

Detection of Listed Bat Species Under Bridges Through the Use of Fecal DNA

Carol L. Chambers[1], Susan Dulc[2], Heather Gates[2], Cori L. Lausen[2], Erin Low[2], Cory Olson[2], Meagan D. Owens[1,3], Daniel E. Sanchez[1,3], Abby Tobin[4] and Faith M. Walker[1,3]
1 School of Forestry, Northern Arizona University, Flagstaff, USA; 2 Wildlife Conservation Society Canada, Toronto, CAN; 3 Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, USA; 4 Washington Department of Fish and Wildlife, Olympia, USA

Detection of listed bat species (i.e., designated endangered by national or international organizations such as the International Union for Conservation of Nature [IUCN]) using bridges is important for wildlife conservation and management. Species that roost under bridges include the Indiana bat (*Myotis sodalis*), a United States (US) federally listed species and the little brown bat (*Myotis lucifugus*), listed endangered by the IUCN and for >10 states and provinces. This roosting behavior puts these species at greater risk when bridges require maintenance or replacement. The ability to inexpensively and efficiently detect species will prove essential to bat conservation as infrastructure projects increase. We determined whether bridges could be used to detect listed bat species. We used guano collected at roosts of 118 bridges in the US and 126 bridges in Canada that were provided to our Species from Feces program. We employed DNA metabarcoding or Sanger sequencing to identify bat species. We detected 16 species or species pairs of which ≥3 species are listed in the US or Canada. We found that, like species accumulation curves and our previous samples in mines, the more bridges sampled, the more species detected. However, even a single bridge sample detected a listed species in 4 of 12 states or provinces. Because use of bridges by bats includes both day and night roosting, monitoring bridges using our non-invasive approach can successfully identify species. Our samples show that this approach is productive in identifying use by bat species, including those that are listed.

Activity Levels of Bat Species at Interstate Highway Sites With and Without Wildlife Underpasses in the Washington Cascades

Jenna L. Chapman and Kristina A. Ernest
Department of Biology, Central Washington University, Ellensburg, USA

Roads force wildlife to navigate degraded and fragmented habitats across the globe, creating barriers to movement and increasing the risk of mortality. This includes bats, whose movements between foraging and roosting habitats may be impeded by roads. Wildlife crossings structures (WCS) are a common mitigation strategy to increase connectivity, but investigation into bat activity in or around these structures is limited. Our goal was to test whether highway locations with WCS had more bat species and higher activity levels than locations without underpasses. Echolocation calls were recorded at locations along Interstate-90 with and without underpasses, and in the adjacent forest. Calls were analyzed across all species and separated into 4 guilds based on species-specific frequency ranges. The same 8 species were detected at all locations. Total bat activity was higher along the highway than the adjacent forest but did not differ between locations with vs. without underpasses. Guild activity followed similar trends, with some exceptions. The 40 kHz guild showed significantly higher activity at underpasses than at locations without them. Confounding variables make interpretation challenging, but this study provides important information on bat activity along an interstate highway in Washington State. We highlight the need for more intensive monitoring efforts to better understand the effectiveness of WCS in reducing the impacts roads have on bats in North America.

Urbanization and Genetic Impoverishment of a Tropical Fruit Bat

Balaji Chattopadhyay[1], Kritika M. Garg[2,3], Rajasri Ray[4], Ian H. Mendenhall[5] and Frank E. Rheindt6
1 Trivedi School of Bioscience, Ashoka University, Sonipat, Haryana, IND; 2 Centre for Interdisciplinary Archaeological Research, Ashoka University, Sonipat, Haryana, IND; 3 Department of Biology, Ashoka University, Sonipat, Haryana, IND; 4 Centre for Studies in Ethnobiology, Biodiversity and Sustainability, Malda, IND; 5 Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore, SIN; 6 Department of Biology, National University of Singapore, Singapore, SIN

Anthropocene has experienced massive biodiversity loss and threat to wildlife in general. Many species are experiencing dramatic decline in genetic diversity and imminent extinction. In many cases however, present methods of reconstructions of demographic past cannot sufficiently

capture the signals of this decline. Rather, comparison of pre-decline and post-decline populations can alleviate this limitation and can provide resolution into the demographic history during the Anthropocene. Availability of genomic data from century old museum samples allows comparison of current and historical genetic diversity, thereby facilitating efforts to explore the impact of Anthropocene on the evolution of natural populations. Bats are particularly important in this regard as they are not only sensitive to climate change but are also under intense scrutiny due to their association with human dominated habitats. Leveraging museum samples from a pre-urbanization population and a recently sampled population (wild-caught) of the Sunda lineage of the short-nosed fruit bat from the island nation of Singapore, genome-wide sequence data was obtained to understand the evolution of this synanthrope in a rapidly urbanized landscape. Comparisons of genetic diversity of pre-urbanized and contemporary populations revealed significant loss in genetic diversity within the contemporary population and signals of a drastic population bottleneck coinciding with the beginning of urbanization of the island nation. The study revealed that even commonly occurring species are not immune to urbanization.

Winter Status and Trends Inform Conservation for WNS-affected Bats

Tina L. Cheng[1], Ashton M. Wiens[2], Amanda Adams[1], Yvonne Dzal[1,3], Bethany R. Straw[4], Brad J. Udell[4], Jonathan D. Reichard[5], Craig K. R. Willis[3], Wayne E. Thogmartin[2], Brian E. Reichert[4] and Winifred F. Frick[2]

1 Bat Conservation International, Austin, USA; 2 Upper Midwest Environmental Sciences Center, U.S. Geological Survey, La Crosse, USA; 3 University of Winnipeg, Winnipeg, CAN; 4 Fort Collins Science Center, U.S. Geological Survey, Fort Collins, USA; 5 Ecological Services, U.S. Fish and Wildlife Service, Hadley, USA

White-nose syndrome (WNS) is an emerging infectious disease in North American hibernating bats that has caused greater than 90% decline in three species. It has been 16 years since WNS first emerged; the disease is now widespread across the US and Canada, with WNS confirmed in 12 bat species and in 75% of US states and Canadian provinces. For over a decade, conservation efforts on WNS have focused on impeding the spread and impact of WNS on bat populations. However, in areas where WNS is not established, long-term strategies that focus on protecting remnant populations to support population recovery are needed. We present analyses being developed by the North American Bat Monitoring Program (NABat), including Bat Conservation International (BCI), to produce species' status and trend reports with winter count data on an annual timescale. We demonstrate how status and trends reports can be utilized to develop and strategize long-term bat conservation strategies. We present BCI's conservation framework to improve WNS survival via enhanced foraging opportunities to increase fat reserves prior to hibernation. We show that bats increase foraging activity at prey patches during fall swarm and spring emergence, supporting the idea that habitat enhancements can increase foraging efficiency during periods of energetic stress. We proposed that NABat status and trends reports are a useful tool to help identify and prioritize species and areas to for conservation actions and studies to deliver protection and restoration activities for remnant populations in North America.

Impacts of Major Roads on Bat Population and Mitigation Measures to Reduce Them

Fabien Claireau[1,2,3], Yves Bas[1], Charlotte Roemer[1], Tiphaine Devaux[1,4], Jean-François Julien[1], Nathalie Machon[1], Benjamin Allegrini[3], Sébastien J. Puechmaille[2,5] and Christian Kerbiriou[1,6]

1 Centre d'Ecologie et des Sciences de la Conservation, Muséum national d'Histoire naturelle, Centre National de la Recherche Scientifique, Sorbonne Université, Paris, FRA; 2 Zoology Institute and Museum, University of Greifswald, Greifswald, GER; 3 Naturalia environnement, Avignon, FRA; 4 Office de Génie Écologique, Saint-Maur-Des-Fossés, FRA; 5 ISEM, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, FRA; 6 Station de Biologie Marine de Concarneau, Muséum national d'Histoire naturelle, Concarneau, FRA

Roads have a multitude of negative effects on wildlife, including their prominent role in habitat fragmentation. Habitat fragmentation particularly affects bats during their nightly movements between roosts and foraging areas. We studied the road-effect zone on bat populations in several sites in France and found an effect of roads on bats up to 5 km and, this can be influenced by roads factors (e.g., traffic). At the local scale, seasons and landscape features may also influence bat behavior and lead to high collision risks (e.g., vegetation density). To reduce the road-effect zone on bats and collision risks, mitigation measures (e.g., bat overpasses) are proposed, but they have rarely scientifically been tested. To strictly test them, we developed two innovative methods: (i) Acoustic Flight Path Reconstruction (AFPR) to characterize bat crossings using acoustic recorders and (ii) Bat Tracking Toolbox (BTT) to characterize bat flight height using a thermal camera. Among mitigation measures studied, we performed a BACI analysis as much as possible. Concerning wildlife crossings, we founded that bat species with high risk of collision crossed the road only at the location of the mitigation measure. Concerning bat overpasses, crossings are more numerous if an overpass is located on a pre-existing bat commuting route and can increase habitat connectivity if they are placed on a narrow commuting route (e.g., hedgerow). Finally, concerning bat flight height (one site), bat overpasses reduce the collision risk for bats after their installation.

Belize as a Testing Ground for Ideas

Elizabeth L. Clare

Department of Biology, York University, Toronto, CAN

Finding appropriate field sites is always a challenge. A flexible well-resourced location and exceptionally knowledgeable local staff make all the difference. These resources, combined with a supportive team of colleagues who can facilitate experiments have made Lamanai, Belize an exceptional field location for trying out new things. Some experiments work, some do not, but Lamanai has become our test ground for ideas. I started visiting Lamanai thirteen years ago and my students and I have taken advantage of the extremely well documented capture, roost, and site records we have built up over the years to try out experimental designs, test new technologies, and explore ideas. In this presentation, I will outline our evolving local photo field guide, which has greatly improved field identifications and our approach to netting. I will discuss unusual ideas that worked, such as testing out protocols to extract DNA, perform a PCR, and sequence the products in the field without access to internet and only minimal laboratory equipment. Ideas that took advantage of knowing what species we were guaranteed to capture, such as sampling bat pheromones, DNA barcoding, and dietary analysis. I will also talk about experiments that just didn't pan out - like flower preference trials and Y-maze mate choice experiments. Finally, I will describe our latest technological testing in Belize, sampling eDNA from the air to assess local bat diversity. In particular, I will demonstrate how the long-term monitoring in Lamanai has made these experiments possible.

Temporal Characteristics of Echolocation Calls in Pregnant and Lactating Big Brown Bats

Alexa C. Clarke[1], John M. Ratcliffe[2] and Paul A. Faure[1]

1 Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN 2 Department of Biology, University of Toronto, Mississauga, CAN

Changes in the foraging behavior of echolocating insectivorous bats have been observed in the wild over the course of pregnancy and lactation. Other mammalian species, including rodents and primates, experience changes in vocal characteristics during pregnancy and lactation. As echolocation is a vital tool for spatial navigation and prey detection in bats, investigating echolocation characteristics from pregnancy through lactation may provide new insight into how reproduction, pregnancy and pup rearing influence vocalizations. We measured changes in mass and recorded echolocation calls of twelve pregnant and three non-pregnant female, wild-caught, big brown bats (*Eptesicus fuscus*), beginning ~6 days before giving birth and ending ~35 days after giving birth, when pups were expected to be weaned. Based on changes in mass, we predicted post-partum females would emit calls of shorter duration and interpulse interval (IPI) compared to calls emitted by the same bat during late-stage pregnancy. Echolocation calls were identified, their start- and end-times marked in SASLab Pro, and the data exported to RStudio to determine changes in temporal features of echolocation in each recording. We calculated mean call duration and IPI for each day a bat was flown, and used a within-subject design to compare call duration and IPI before and after parturition. Preliminary results show a trend for call duration and IPI to decrease after parturition and during lactation, suggesting there are changes in the temporal features of echolocation over pregnancy and lactation that may also differ from non-reproductive (e.g., late summer, early fall) adult female big brown bats.

Towards Understanding the Potential for Offshore Wind to Impact Bats

Jeff Clerc
Normandeau Associates Inc., Gainesville, USA

Historically considered anomalous, recent bat monitoring efforts throughout the Atlantic Offshore Continental Shelf (AOCS) suggest that eastern red bats, hoary bats, and silver-haired bats may regularly travel offshore during the fall migratory period. With wind energy development throughout the AOCS expected to support nearly 30 GW of power production by 2030, there is growing concern that the same species that regularly use the AOCS are those that commonly collide with terrestrial turbines. As we continue to investigate what might be driving offshore bat activity, it is equally critical to investigate how bats interact with novel anthropogenic structures once in the offshore environment. Here we present our findings of offshore bat monitoring, comparing bat activity observed from buoys, boats, and turbine platforms. We further present results related to offshore prey abundance monitoring and examine relationships between prey and bat activity. We highlight novel metrics that in the offshore environment can be used to infer the magnitude of bat interactions with different anthropogenic structures offshore. We then use our data to inform a brief working example that considers the potential for bats to experience sub-lethal energetic consequences as the number of offshore wind turbines in the AOCS grows. Our findings suggest that under certain scenarios as offshore wind energy development increases, bats may experience increased energetic costs and mortality risk.

Bats as Hosts of Important Unicellular Endoparasites

Pablo Colunga-Salas[1,2], Giovani Hernádez-Canchola[3], Estefania Grostieta[2] and Ingeborg Becker[2]
1 Instituto de Biotecnología y Ecología Aplicada, Universidad Veracruzana, Xalapa-Enriquez, MEX; 2 Centro de Medicina Tropical, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, MEX; 3 Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de México, MEX

Some bacteria and protozoan species are important pathogens causing high mortality rates not only in humans, but also in other mammal species including bats. Infectious agents, such as viruses, bacteria, protozoa, and fungi have been reported in the order Chiroptera, but a thorough analysis of zoonotic unicellular pathogens is needed. To address this topic, we conducted an exhaustive search of literature reports on pathogenic bacterial and protozoan infections in bats, in order to summarize the current state of knowledge on these pathogens. From this search, we obtained information on 7 protozoan and 12 bacterial species present in 187 bat species, which were retrieved from 169 articles. Despite all the records, bats are only considered reservoirs for two protozoan species. Thus, more studies are needed to consider bats as reservoirs for bacteria. At North American Society for Bat Research (NASBR) symposia, 17 studies have been presented and discussed, but only two focused on pathogens responsible for the principal causes of death in human populations. More worldwide studies are needed to assess the actual role of bats in public health problems and to help develop conservation measures for bat populations that need to be protected.

Blood-borne: Pathogens in Bats from Central and Eastern Europe

Alexandra Corduneanu[1], Áron Peter[1], Attila D. Sándor[1,2], Andrei Daniel Mihalca[1] and Sándor Hornok[2]
1 Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, ROU; 2 Department of Parasitology and Zoology, University of Veterinary Medicine, Budapest, HUN

Most bats live in dense colonies and are well adapted to various environments, thus they are prone to host a wide range of pathogens, including bacteria and haemosporidia. Regular interaction between bats, other wildlife, livestock or humans can contribute to spillover of infectious agents from bats to other hosts. Studies showed that bats can harbor different blood-borne pathogens that are transmitted by ectoparasites to other hosts. Different species of *Bartonella* spp. and Rickettsia spp. may be present in bats. Thus, the aim of this study was to identify them in blood (250 samples) of different bats species from Central and Eastern Europe. In order to investigate the presence of the specified bacteria, conventional PCR and quantitative PCR was employed, targeting different genes (ITS, gltA, ftsZ) and the results were analyzed both statistically and phylogenetically. We identified different strains of *Bartonella* spp. and *Rickettsia* spp. and the phylogenetic analysis showed that they were closely related to previously described strains from bats. There is a high genetic diversity among *Bartonella* spp. and *Rickettsia* spp. isolates from bats, suggesting an ancestral role for this vertebrate group in the evolution of these bacteria.

Unraveling the Role of the Andes in the Diversification of the Nectar Bat *Glossophaga soricina*

N. Cortés-Delgado[1,2], R. Mason-Gamer[2] and B.D. Patterson[1]
1 Integrative Research Center, Field Museum of Natural History, Chicago, USA; 2 Department of Biological Sciences, University of Illinois at Chicago, Chicago, USA

Glossophaga soricina is a generalist species of nectar bat that occupies multiple habitats and ecosystems. It has one of the widest distributions among Neotropical bats, ranging from Mexico to Argentina. According to phylogeographic studies, *G. soricina* comprises two clades: 1) individuals

from South America east of the Andes Mountains, and 2) individuals from Central America, Jamaica, and the western slope of the Andes (Hoffmann and Baker 2001, Rocha-Dias et al. 2017, Hoffmann et al. 2019). However, the limited sampling in previous studies and the use of a single mitochondrial marker (Cytb), prevent us from making strong inferences about biogeographical patterns. Thus, the main goals of this work are to analyze phylogeographic patterns of *G. soricina* in South America, and to establish the extent to which the Andes act as a barrier for *G. soricina* populations. To this end, UCEs (Ultra Conserved Elements) and mitochondrial genomes are being utilized as genetic markers. Our results do support two main clades of *G. soricina*, as reported in previous studies, but their geographic distributions are different. The two groups are not delimited by the Andes; instead, each group has cis- and trans-Andean distributions.

Offshore Bat Activity Patterns Detected by Vessel-based Acoustic Monitoring

Katelin K. Craven, Nathan A. Schwab, and Derek Hengstenberg
Tetra Tech, Inc. Pasadena, USA

Current understanding of offshore bat activity and behavior is limited. Tetra Tech conducted bat acoustic monitoring within Bureau of Ocean Energy Management's Renewable Energy Lease Areas along the eastern United States. Bat detectors mounted at the top of roving offshore research vessels confirmed presence of four bat species (eastern red bat, silver-haired bat, hoary bat, and big brown bat) during the active season (April–October) from 2018–2021. The results among the different lease areas were highly variable, although detection rates for all species were highest in early August through early November, consistent with migration periods for migratory tree bats. Regression analyses were completed for temperature, wind speed, and date to investigate correlations for the number of bat passes per night with weather data collected from the National Oceanic and Atmospheric Administration's National Data Buoy Center. The regressions for similar studies have yielded nonsignificant positive correlations of temperature with bat activity and a significant negative correlation of wind speed and bat activity. This survey indicates that the Lease Areas are used by non-migratory bat species (big brown bats), as well as long-distance migrants (eastern red bat and silver-haired bat) with the highest detection rates during the fall of the study. Migratory tree bats represented the majority of the total bat passes recorded, with detections spread across the Lease Areas. Although the understanding of offshore bat activity and behavior is limited; migratory tree bats have been the most common species observed offshore, which is consistent with the results of this study.

Does Artificial Roost Design and Placement Affect the Thermoregulatory Behavior of Indiana Bats?

Reed D. Crawford[1], Luke E. Dodd[2], Anna C. Doty[3] and Joy M. O'Keefe[1,4]
1 Program in Ecology, Evolution, and Conservation Biology, University of Illinois at Urbana-Champaign, Urbana, USA; 2 Department of Biological Sciences, Eastern Kentucky University, Richmond, USA; 3 Department of Biological Sciences, California State University, Sacramento, USA; 4 Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign, Urbana, USA

Artificial bat roosts are commonly deployed for conservation and mitigation, but we lack data on bat thermoregulation in these structures. Previous research showed that artificial roost design and landscape placement substantially impact roost temperature. Further, many artificial roost designs weakly buffer temperature extremes due to low thermal mass and traditionally dark paint schemes. The unstable microclimates of artificial roosts could alter thermoregulatory behavior and possibly increase torpor use or instances of hyperthermia and affect energy budgets and survival. At sites in Indiana and Kentucky during the spring and summer of 2021, we used temperature-sensitive telemetry to record the skin temperature of 15 female Indiana bats (*Myotis sodalis*) using rocket-box artificial roosts of 4 designs and solar exposures, as well as bark-mimic roosts. We collected 57 bat days of skin temperature data (3.8 ± 0.7 days/bat); temperatures ranged between 7.3–43.4°C, averaging 27.8°C. Bats used longer duration, deeper torpor in shaded artificial roosts. The effect of box design on thermoregulatory behavior was not readily detectable in any solar exposure. Regardless of roost type, bats in solar-exposed and shaded artificial roosts responded to fluctuations in outside air temperature, indicating that artificial roosts may not buffer bats against daily temperature extremes. Bats used torpor on 80.4% of days and recorded hyperthermic skin temperatures (i.e., >40°C) on 31.5% of days. We recommend further investigation of bat thermoregulatory responses in natural and artificial roosts, and simultaneous measures of roost microclimate and skin temperature to better inform future artificial roost designs that more closely approximate natural roosts.

Open-source Systems for Observing and Monitoring Bats: OpenBatMonitoring (and a Few Birds too)

Paul M. Cryan[1], Brian E. Reichert[1], Bethany R. Straw[1], P. Marcos Gorresen[2,3], Eben H. Paxton3, Mari K. Reeves[4], Josh Guilbert[5], Stephen Mullin[5] and John Yarbrough[6]
1 Fort Collins Science Center, U.S. Geological Survey, Fort Collins, USA; 2 Hawai'i Cooperative Studies Unit, University of Hawai'i at Hilo, Hilo, USA; 3 Pacific Island Ecosystems Research Center, U.S. Geological Survey, Hawai'i Volcanoes National Park, USA; 4 Pacific Islands Fish and Wildlife Office, U.S. Fish and Wildlife Service, Honolulu, USA; 5 Division of Fish and Wildlife, Dept. of Lands and Natural Resources, Commonwealth of the Northern Mariana Islands MNP; 6 National Renewable Energy Laboratory, Golden, USA

We could dispel much of the unnecessary mystery surrounding bats if only they were easier to see in the dark. 'Dark-vision' cameras help us count, classify, and observe behaviors of free-ranging bats, yet such technology is underutilized for bats because of cost, technical complexity, susceptibility to the elements, potential to disturb animals, and required imagery processing effort. The openBatMonitoringProject addresses these issues by leveraging and integrating trends in open-source computing and sensing hardware, computer-vision and deep-learning methods, desktop manufacturing, electronic miniaturization, and the Internet of Things to develop powerful bat observation systems that more people can afford and learn to build themselves. Devices currently being developed and tested include image time-lapsing, video, and acoustic detection systems with associated environmental sensors that cost less than about $200US, are open source, and can run bat detection and classification algorithms in real time. We began our testing with swiftlets in caves in Guam during early spring of 2022 and continued at remote bat and bird caves in the Mariana Islands through autumn. We compare the developing system to our more expensive but well proven thermal surveillance imaging systems for multi-day continuous or timed video monitoring at remote caves and wind turbines. This talk illustrates the failures and successes of the project, with example imagery and count data. New collaboration opportunities abound. OpenBatMonitoring aims to kindle a global community of professional/maker/programmer/tinkerer/citizen scientists creating useful tools for bat conservation, management, appreciation, and public health that are accessible to anyone, anywhere in the world.

Genomics of *Myotis yumanensis* to Inform Statewide Conservation Management and White-nose Syndrome Planning

Joseph Curti[1], Devaughn Fraser[2], Merle Escalona[3], Colin W. Faibairn[4], Samuel Sacco[4], Ruta Sahasrabudhe[5], Will Seligmann[4], Erin Toffelmier[1], Robert Wayne[1], H. Bradley Shaffer[1] and Michael Buchalski[6]

1 Department of Ecology and Evolutionary Biology, University of California Los Angeles, Los Angeles, USA; 2 Connecticut Department of Energy and Environmental Protection, Hartford, USA; 3 Department of Biomolecular Engineering, University of California Santa Cruz, Santa Cruz, USA; 4 Department of Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, USA; 5 DNA Technologies and Expression Analysis Core Laboratory, Genome Center, University of California Davis, Davis, USA; 6 CDFW Wildlife Genetics Research Laboratory, Sacramento, USA

Since the first reference genome of the little brown bat (*Myotis lucifigus*) was published by the Broad Institute in 2011, 44 additional bat reference genomes have been made publicly available. These genomic resources span 11 of the 18 current chiropteran families, predominantly from pteropodid, phyllostomid, and vespertillionid bats. Here we present the first de novo genome assembly for the Yuma myotis bat (*Myotis yumanensis*), generated as a part of the California Conservation Genomics Project (CCGP), a California state-funded initiative with the goal of building the most comprehensive genomic dataset ever assembled for conservation science. The *M. yumanensis* genome was generated using standard CCGP protocols, including Pacific Biosciences HiFi long reads and Hi-C chromatin-proximity sequencing technology. This high-quality reference genome is one of 4 chromosome-level assemblies for bats, and is one of the most complete assemblies available, with a contig N50 = 26.4 Mb (range = 10.3 Kb–31.9 Mb). In addition to this valuable genomic resource, we discuss a simultaneous genome re-sequencing project through CCGP for *M. yumanensis*, which includes the first range-wide genomic assessment for the species. Through these two projects, we will analyze range-wide patterns of genomic variation and geneflow, as well as signatures of local adaptation. The findings from these projects will assist conservation managers in establishing meaningful conservation management units as well as planning for future impacts of White-nose syndrome for the species.

A Seasonal Comparison of Foraging Movements of Pteropus alecto from an Urban and Peri-urban Roost

Adrienne S. Dale[1], Nita Bharti[2], Raina K. Plowright[3], Peggy Eby[4,5], Alison J. Peel5, Tigga Kingston[1] and Liam P. McGuire[6]
1 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 2 Department of Biological Sciences, Center for Infectious Disease Dynamics, Penn State University, University Park, USA; 3 Department of Biological Sciences, Montana State University, Bozeman, USA; 4 School of Biological, Earth, and Environmental Sciences, University of New South Wales, Sydney, AUS; 5 Centre for Planetary Health and Food Security, Griffith University, Brisbane, AUS; 6 Department of Biology, University of Waterloo, Waterloo, CAN

Historically nomadic, black flying foxes (*Pteropus alecto*) traveled hundreds of kilometers across the landscape in search of seasonally ephemeral food resources. Land clearing has decreased native habitat of *P. alecto* in coastal eastern Australia and increased seasonal variability in native food sources, driving flying foxes into continuously occupied roosts in and around urban areas. Urban settings provide consistent resources, so we hypothesized that urbanized bats would forage across relatively short distances, especially as native resources are increasingly unavailable in winter months. We investigated links between resource availability and foraging distances, by tracking 83 adult *P. alecto* from two continuously occupied roosts using GPS-GSM trackers. One roost is in a highly urbanized area, and the other is in a peri-urban area, adjacent to native habitat. We collected 897 bat-nights of data throughout 2019–2021. Although we observed extreme nightly movements of up to 218.1 km, most nightly foraging distances were comparatively short and did not vary seasonally. Bats travelled longer distances when foraging from the peri-urban roost, with individual median track lengths ranging from 6.0–51.9 km compared to 3.0–40.4 km at the more urban roost. Bats from the urban roost predominantly foraged locally in developed areas, while bats from the peri-urban roost displayed a mixed foraging strategy, exploring developed, agricultural, and native landscapes. Understanding foraging movements of urban resident flying foxes can help prevent human-wildlife conflicts and promote coexistence in increasingly urban environments.

Torpor Duration and Wing Damage in Little Brown Bats That Did Not Succumb to White-nose Syndrome

Brooke A. Daly[1], Rodney Foster[1], *Allen Kurta[1] and DeeAnn Reeder[2]
1 Department of Biology, Eastern Michigan University, Ypsilanti, USA; 2 Department of Biology, Bucknell University, Lewisburg, USA

Hibernating populations of little brown bats (*Myotis lucifugus*) typically decrease by 90%, within three years of the arrival of white-nose syndrome and its causative agent, *Pseudogymnoascus destructans* (*Pd*), and declines purportedly are greater at sites with high autumn temperatures. Tippy Dam, a concrete hibernaculum in northern Michigan, is an exception. Although the fungus probably arrived in winter 2014–2015, the overwintering population has remained steady at 20,000–24,000 animals, from 2012 through 2021, even though internal ambient temperature at the start of hibernation exceeded 10°C. To investigate behavior of bats at the dam, we initiated a study of environmental parameters, use of torpor, and fungal-related wing damage in 58 adult male bats during winter 2019–2020. Internal ambient temperature in late October, when all bats began hibernation was 10.8–14.0°C; it decreased to 1.7–3.2°C during February and rose to 5.4–8.7°C in late April, when the bats began to leave. Temperature-sensitive radiotransmitters placed on 19 December and 14 February indicated that average torpor bout length was 17.1 ± 6.9 days, which was similar to previous studies of uninfected bats. Photos of wings trans-illuminated with ultraviolet light indicated that fungal damage increased during winter but was consistently low. Fluorescent tissue amounted to only 0.02 ± 0.02% of the surface of the wings in December, and 0.12 ± 0.18% in February. The bats at Tippy Dam are clearly surviving exposure to *Pd*, with normal patterns of arousal and minimal physical damage, although the mechanism is unknown.

Opening the Genome Frontier and the Future of Bat Diversity

Liliana M. Dávalos
Department of Ecology and Evolution and Consortium for Inter-Disciplinary Environmental Research, Stony Brook University, Stony Brook, USA

Genomics has the potential to reveal the basis for extraordinary bat adaptations, as well as translate these insights into therapeutics of relevance to people and domestic animals, raising the value of global bat biodiversity. Yet, the track record of genetic resources yielding gains in conservation is thin and the many steps required to connect biodiversity to successful commercial applications means past success rarely involves the direct stewards of biodiversity. I analyze the state of bat genomics today as a promising (but risky) knowledge frontier with great potential for sustainable conservation. This potential will only be realized, however, by convening diverse stakeholders worldwide beyond the scientific community. Over the next decade, connecting curiosity-driven genomics to stakeholder-driven objectives over the next decade will be critical to realizing the vision of sustainable diversity in a rapidly changing world.

Plasticity of the Lesser Long-nosed Bat Diet at the Northern Extent of Its Range

Mallory L. Davies[1], Theresa M. Laverty[2], Caitlin P. Wells[1] and Kathryn E. Stoner[1]

1 Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, USA; 2 Department of Ecology and Evolution, University of Chicago, Chicago, USA

The lesser long-nosed bat (*Leptonycteris yerbabuenae*) is a nectar feeding species that serves as an important migratory pollinator. Some populations migrate 1,200 km north each spring from south-central Mexico to the southwestern United States following a hypothesized "nectar corridor" of columnar cacti and agave species. In New Mexico, Palmer's Agave (*Agave palmeri*) is believed to be the most important species in the long-nosed bat diet. However, long-nosed bats have been documented in New Mexico during the spring and fall when flowering Agave sources are extremely limited which may indicate a change in resource use throughout the season. Former studies have indicated that long-nosed bats consume arthropods in low amounts, with intake reported as incidental in most cases. The diet of lesser long-nosed bats, especially in terms of insect consumption at the most northern extent of their range, is not yet fully understood. We investigated how their diet varies within seasons and across years in relation to local flowering Agave density in New Mexico. We collected bat fecal samples throughout the season and, using DNA barcoding, assessed plants and insects in the bats' diet. Among our samples, we confirmed that *Agave* spp. were the only nectar resource plants detected in the lesser long-nosed bat diet. We also found that insect consumption decreased during peak Agave bloom, suggesting that bats may be supplementing their diet with insects during periods of low nectar availability. A better understanding of lesser long-nosed bat diets can inform ongoing Agave restoration and bat conservation efforts.

Trees in European City Streets: Do Bats Care?

Luc De Bruyn[1,2], Lien Gyselynck[2], Sarah Janse[2], Evelyne Kennis[2], Inez Vanhoutte[2], Lisse Verheyen[2] and Ralf Gyselings[1]
1 Research Institute for Nature and Forest, Brussels, BEL; 2 Evolutionary Ecology Group, University of Antwerp, Antwerp, BEL

Urbanization has a major influence on insectivorous bat communities. Although most bat species are negatively affected by urban sprawl, some species can exploit urban areas. Most attention has been paid on foraging areas and (potential) roosting sites. However, bats also must be able to commute between these habitat areas. If these areas are not connected, even the best foraging and roosting sites are useless. In the present study we assess whether trees in the streets can lower (light induced) landscape resistance for commuting bats. To assess bat activity, we drove 10 km transects in 5 different cities in Flanders, Northern Belgium. The transects were selected to cross suburban (detached houses with gardens) and core urban (continuous built-up, street canyons) areas. In both city types, we selected streets with and without trees. Transects (5 times/city) were driven weekly by bike (10 km/h), starting 1 hour after sunset. Bat echolocations were recorded with automatic bat recorders with GPS. Sonograms were identified manually. Overall, 2589 bat passings were recorded. 95% belonged to *Pipistrellus pipistrellus*. The results revealed that significantly more bat passes were recorded in streets with trees in the core city area. This was not the case in the suburban areas.

Sex-biased Migration in the Common Noctule - A Decade of Results

Dina K.N. Dechmann[1,2,3], M. Wikelski[1,2], L. Keicher[1,2], T.A. Wild[1,2,5], M. Teague O'Mara[1,2,4]
1 Max Planck Institute of Animal Behavior, Radolfzell, DEU; 2 University of Konstanz, Konstanz, DEU; 3 Centre for the Advanced Study of Collective Behaviour, Konstanz, DEU; 4 Southeastern Louisiana University, Hammond, USA; 5 Product Development Group Zurich, ETH Zürich, Leonhardstr, Zürich, CHE

Bat migration is rare but of great conservation relevance because of the high levels of risks migrating animals are exposed to. However, the study of bat migration remains challenging mainly due to technological limitations. We have used a multi-technology approach since 2012 to study female-biased migration of the common noctule (*Nyctalus noctula*) in Southern Germany and Switzerland. We have found that while female-biased, males complete moderate (~50 km) movements around the site, and that females show highly variable migration paths, altitudes, and decisions with a few common patterns. Female common noctules at our sites reached the mass necessary for migration in less than a week, and showed no difference in torpor use or foraging behavior from the non-migrating males while preparing for migration. They migrated in relatively short steps of 80 km or less, probably to stop-over and refuel, along the way. The decision to depart from our site was driven by a combination of wind conditions and air pressure, and these are weighted differently across the migration season. There were also indications that changing environmental conditions influence this behavior quite massively as departures from our study site are almost ten days earlier now than in 2012. Understanding migration patterns and routes can help us identify possible challenges of migration for these small insectivores and may help us understand if drastic declines in bat numbers we observed in the last ten years are connected to their migration.

Identifying the Factors Influencing Phylogeographic Breaks in Bats and Other Taxa

Sydney K. Decker, Kaiya L. Provost and Bryan C. Carstens
Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, USA

There is increased recognition that most taxonomic groups, including Chiropterans, contain hidden species-level diversity. One strategy for understanding this diversity is to estimate how genetic diversity within species is distributed across the landscape and identify the environmental and landscape features that contribute to population genetic discontinuities. Evaluating the extent to which intraspecific phylogeographic breaks are predictable based on geographic, ecological, environmental, or landscape features provides valuable clues about potential hidden species which can then be investigated in a more thorough manner. To conduct this analysis, we downloaded mitochondrial data from hundreds of mammal and bird species and identified all intraspecific phylogeographic breaks. The location of phylogeographic breaks across bats, rodents, and birds assessed were not in the same geographic areas so we built a predictive model in order to determine which extrinsic features are predictive of intraspecific genetic discontinuities. Once this predictive model was complete, we explored the extent to which species which contained phylogeographic breaks in their mitochondrial DNA were likely to contain hidden species based on an analysis of genomic data. Brain and body mass were important organismal traits in predicting the presence of phylogeographic breaks in bats while range characteristics such as maximum and mid-range latitude were also important predictors. This work provides an example of how large-scale analyses of phylogeographic patterns can be used as a starting point to understand population structure and species diversity in understudied taxa.

Winter Tree Use by Silver-haired Bats in Southern British Columbia

Emily Marie de Freitas[1], Cori Lorraine Lausen[2] and Erin Faye Baerwald[1]
1 Ecosystem Science and Management, University of Northern British Columbia, Prince George, CAN; 2 Western Canada Bat Conservation Program, Wildlife Conservation Society Canada, Kaslo, CAN

Silver-haired bats (*Lasionycteris noctivagans*) are a tree-roosting species found throughout North America. As a cavity-dwelling species, they are especially dependent on the presence of snags and large, mature trees. This makes them sensitive to silviculture practices because timber harvesting can remove critical roosting habitat. Silver-haired bats are migratory throughout much of their range, however, in the Pacific Northwest region of the North America, some are known to hibernate locally. In British Columbia, Canada, silver-haired bats have been observed visually and acoustically throughout the winter in the southern interior and coastal regions. A unique forested study area has been discovered near a shallow mine in southern British Columbia, where silver-haired bats use the mine, rock crevices, and trees as hibernacula. The use of trees as hibernacula in temperate regions is poorly understood. We sought to investigate and describe use of tree-roosts in the winter by silver-haired bats. We radiotracked 22 silver-haired bats to describe hibernacula across two winter seasons (December–March; 2021 and 2022). We identified and characterized 22 trees used as hibernacula and described the microclimate in seven of these roosts. We compared identified roost trees to a subset of available trees to identify key attributes. Sixty eight percent of all transmittered bats used trees throughout the winter, remaining resident for up to 32 days, and using trees during periods of extreme cold ambient temperatures (-15°C). We conclude that trees provide an important source of winter habitat for this species, and this should be considered when making forest management decisions.

Schools-Based, Science-Based, Participatory Approach to Bat Conservation in Bhutan: Universal Lessons

Tshering Dendup[1] and *Paul J. J. Bates[2]
1 Phuntshothang Middle Secondary School, Samdrupjongkhar, BTN; 2 Harrison Institute, Kent, GBR

Bhutan is committed to protecting its forests and wildlife. However, it has insufficient conservationists to survey, monitor and assess the increasing threats to this globally important biodiversity. We will showcase how Bhutan's schools, currently an under-used scientific resource, can assist in delivering important conservation data, place local communities at the heart of local conservation, and enthuse a new, environmentally aware generation. The project focuses on the role of Phuntshothang Middle Secondary School in promoting the conservation of Deothang Important Bird Area (IBA), which comprises evergreen broadleaf forest and is situated in Corridor 5 of Bhutan's Biological Conservation Complex. The team includes teachers, pupils, Bhutanese conservation organizations, foresters, and international advisors. Outputs will include data on the importance of the IBA for rare, range-restricted bats (and birds); an assessment of threats; and raising awareness and building consensus amongst key stakeholders for conservation action. The project is part of a growing global movement that seeks to inspire children through education and practical involvement to take personal responsibility for their environment and the natural world, including its biodiversity. Meanwhile, it places responsibility on us, the researchers, to deliver scientific data and ideas in a form that is more accessible and understandable to a broad range of users, including amateur and professional scientists, in-country conservationists, and, where possible, bright, interested, and informed children.

Expanding the North American Monitoring Program to Monitor Bat Health in the COVID-19 Era

Luz A. de Wit[1], Amanda Adams[1], Kathy Gerst[1], Nat Goodby[1], Kathryn Irvine[3], Bethany Straw[2], Brian Reichart[2] and Winifred Frick[1]
1 Bat Conservation International; Austin, USA; 2 U.S. Geological Survey FORT; Fort Collins, USA; 3 U.S. Geological Survey Northern Rocky Mountain Science Center, Bozeman, USA

The COVID-19 pandemic has brought stark attention to the need to adopt a One Health approach to wildlife monitoring and natural resource management efforts by recognizing that human health, animal health, and ecosystem health are inextricably linked. Understanding the potential for North American bats to be vulnerable to infection from SARS-CoV-2 is crucial, as susceptibility to infection could have important implications for wildlife health, human health, and conservation efforts. The goal of our project is to expand the capacity of the North American Bat monitoring (NABat) program to conduct bat health surveillance and determine the distribution and occurrence patterns of coronaviruses in bat populations across North America. We aim to sample during the summer and focus on roosts and foraging sites occupied by *Tadarida brasiliensis*, as this species is colonial, has a broad geographic range, and occurs across a gradient of natural to human-dominated landscapes. We also aim to opportunistically sample other species located within the range of *Tadarida brasiliensis*. Collected data will be contributed and integrated with efforts to model bat population status and trends and used in analyses to understand viral diversity patterns of coronaviruses in North American bats and potential risk of human-to-bat transmission of SARS-CoV-2. This work addresses a timely need to understand the vulnerability of bat populations that are already under threat from multiple stressors, including the disease white-nose syndrome (WNS), to the risk of exposure of human-mediated transmission of SARS-CoV-2. This work will help inform wildlife management decisions, conservation efforts, and public health policy.

Airport Expansion and Endangered Bats: Development and Mitigation Near the Indianapolis International Airport

Timothy J. Divoll[1,3] and Joy M. O'Keefe2,3
1 Center for Computation and Visualization, Brown University, Providence, USA; 2 Department of Natural Resources and Environmental Sciences, University of Illinois–Urbana-Champaign, Champaign, USA; 3 Center for Bat Research, Outreach, and Conservation, Indiana State University, Terre Haute, USA

Economic prosperity and globalization are major drivers for the development of international airports. Residential development and aviation-oriented businesses are by-products of airport business models. Among the multitude of planning considerations is the habitat needs of endangered wildlife species in the development zone. We analyzed foraging data from 57 Indiana bats (*Myotis sodalis*) during three time periods of a long-term study at the Indianapolis International Airport (1998–1999: pre-mitigation; 2005–2006: during mitigation, and 2014–2016: post-mitigation). At this site, both developed and forested land covers increased between 1998 and 2016 (34.1% and 3.3%, respectively). Mitigation actions included converting 323 ha of residential lots back to forest, and the creation of a 56-ha wetland and an 85-ha multi-use park. With a weighted compositional approach, we related bat use of landscape cover types to changes in land cover during each period. We then compared competing hypotheses to explain changes in bat foraging space use with an information theoretic approach. With the addition of a major highway interchange within the bat colony's foraging area, bats increased space use, presumable in search of new habitat. In all periods, bats selected for forested habitat; as trees in replanted forest and designated parks aged, bats reduced their foraging ranges. Restoring hardwood forest and setting aside parklands were effective proactive mitigation measures for the colony of Indiana bats near the Indianapolis International Airport and similar actions should benefit other wildlife where human development and habitat needs intersect.

The Influence of Predatory Bats on the Nocturnal Soundscape of the Neotropics

M. May Dixon[1,2,3], Amanda F. Savage[2], Michael J. Ryan[1,2], Gerald G. Carter and Rachel A. Page[2]

1 Integrative Biology, University of Texas at Austin, Austin, USA; 2 Smithsonian Tropical Research Institute, Gamboa, PAN; 3 Ecology, Evolution, and Organismal Biology, Ohio State University, Columbus, USA

The jungle at night is filled with sound from animals moving and calling for mates. Making noise is risky because there are many species of predatory passive gleaning bats that eavesdrop on the sounds made by their prey. How do bat predators influence different groups of nocturnal noise-making prey? Do gleaning bats acoustically partition the night soundscape? To explore these questions, we collected a standardized library of sounds from many of the major groups of night noise-makers: calls from frogs, geckos, katydids, crickets and cicadas, as well as the sounds of frog hopping, rodent rustling, and beetle flight. We then presented these sounds to individuals of 14 species of putative passive gleaning bats and one frugivore, *Artibeus jamaicensis*, and quantified the strength of their responses. Through this study we have confirmed passive eavesdropping in *Lophostoma brasiliense*, identified at least nine animal sounds under selection pressure from bats, and have explored niche partitioning among these nocturnal predators.

Swarming *Myotis lucifugus* Get Fatter After a Decade of White-nose Syndrome, but Not From Increased Hyperphagia

Gwynne Domashinski and Liam P. McGuire
University of Waterloo, Waterloo, CAN

White-nose syndrome (WNS) has devastated temperate hibernating bat populations across North America, but many remnant populations persist. Larger fat stores are associated with an increased likelihood of survival during hibernation, and may indicate an adaptive response to WNS. We hypothesized that WNS has selected for bats that build larger fat stores for hibernation, and predicted that during pre-hibernation swarming bats would gain more mass and forage more intensely compared to the period before WNS arrived in North America. In 2021 we recorded body mass of bats during pre-hibernation swarming, and used plasma triglyceride analysis to quantify foraging intensity, repeating the methods of a study conducted in 2007 prior to WNS. We conducted our study at the same study site (an abandoned mine in eastern Ontario, Canada) and on the same calendar dates as the previous study. From 12 August to 16 September, we collected morphometric data on 571 little brown bats (*Myotis lucifugus*), and collected blood samples from a subset of 150 of those bats. Compared to the 2007 study, adults gained more mass prior to hibernation. In the pre-WNS study subadult bats lost mass through swarming, but we observed no change in body mass through the study period. Thus, both adults and subadults have increased body mass deposition compared to the pre-WNS study. However, plasma triglyceride analysis does not indicate more intense periods of feeding, suggesting other behaviors or physiological mechanisms are responsible for the observed mass increase.

Social Structure Across the Roost Sites of a Critically Endangered Insular Flying-fox

Annabel Dorrestein[1], John Martin[2], David Phalen[3], Karrie Rose[4], David Westcott[5] and Justin Welbergen[1]
1 Hawkesbury Institute for the Environment, Western Sydney University, Richmond, AUS; 2 Taronga Institute of Science and Learning, Taronga Conservation Society, Mosman, AUS; 3 Faculty of Veterinary Science, University of Sydney, Sydney, AUS; 4 Australian Registry of Wildlife Health, Taronga Conservation Society, Mosman, AUS; 5 Atherthon, AUS

Bats are amongst the most colonial mammals, however, the selective pressures underlying their coloniality are relatively understudied. *Pteropus natalis* is a colonial flying-fox, endemic to Christmas Island, a small island in the Indian Ocean. The species consists of one closed, population, rendering it an ideal species to study selective pressures leading to coloniality. In this investigation we assessed the spatiotemporal patterns in social structure of *P. natalis* across its five permanent roost sites, to gain a better understanding of the selective pressures leading to coloniality in this species. Using a combination of census and GPS data, we assessed spatiotemporal patterns in roost dynamics. The results showed that spatiotemporal patterns differed between the five roost sites, with varying compositions and differing peak occupancies. Mating behavior was observed at most roost sites, but only one site had mating as its primary function. Furthermore, only one other roost site served primarily as a maternity site, rendering the Christmas Island flying-fox especially vulnerable to roost site disturbances. Conservation of these sites is thus of great importance for this critically endangered species. These results demonstrate that different roost sites have different functions in *P. natalis* and show that for this species coloniality is primarily driven by important reproductive periods. This study provides insight in spatiotemporal variability in the selective pressures leading to coloniality within a species.

Addition of Two Bat Species into Indian Chiropteran Checklist and a New Cryptic Species Level Lineage

Pilot Dovih[1,2], Balaji Chattopadhyay[1], Kritika M Garg[1], Vanessa Paynter[1], B.R.Ansil[1] and Uma Ramakrishnan[1]
1 National Centre for Biological Sciences, TIFR, Bangalore, IND; 2 Sastra University, Thanjavur, IND

Northeast India rich in biodiversity serves as a corridor for many Palearctic and Indian fauna whose distribution extends into the Southeast Asian region a hotspot for species complex. However, there is high hunting pressure and fast-shrinking forests. It is crucial to assess the biodiversity in landscapes that are threatened by high anthropogenic disturbances and hunting. We conducted a bat diversity survey in Nagaland, India, between the years 2013 and 2015. Using both morphology and molecular genetic approach we were able to identify 14 species belonging to five families and eight genera. Our study has added two more bat species, *Asellicus stoliczkanus*, and *Rhinolophus thomasi*, into Indian Chiropteran checklist while discovering a new cryptic species. Our study implies Northeast India is a hotspot of Chiroptera diversity and potential cryptic diversity of bat species in the region. The sympatric occurrences of the Southeast Asian and south China species in Northeast India could be a hotspot for species complex.

The Transition to Nutritional Independence in an Insectivorous Bat

Jessica M. Dreyer and Gary F. McCracken
Ecology and Evolutionary Biology Department, University of Tennessee, Knoxville, USA

The weaning period in mammals is a highly stressful life stage, and yet relatively little is known about it in wild populations. As younglings leave the safety of nurseries and their mother's milk, their risk of death by predation and starvation increases. We seek to understand more about this transition by studying the dietary shift from milk to insects in Mexican free-tailed bats. We use molecular diet analysis to assess the development of the juvenile insect diet in relation to the diet of adults. Results show that juveniles have a significantly more diverse diet than adults. In addition, most insect taxa are present in similar abundances in juvenile and adult diets with a few taxa that differ significantly. Together, these results suggest that juveniles gain foraging proficiency within a few weeks of fledging but may be less discerning while foraging. Here, we take the first step toward understanding the often risk-fraught transition to adulthood.

Phyllostomid Diversity Distribution: The Role of Niche Evolution and Dispersal Limitation
Leandro Duarte[1], Gabriel Nakamura[1], Vanderlei Debastiani[1], Renan Maestri[1], Marcus Cianciaruso[2], José Alexandre F. Diniz-Filho[2] and *Maria João Ramos Pereira[1]
1 Programa de Pós-graduação em Ecologia, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, BRA; 2 Programa de Pós-graduação em Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Goiás, Goiânia, BRA

Macroevolutionary diversification and dispersal in time and space generate uneven geographic distribution of phylogenetic pools, affecting the imprint left by macroevolution on local species pools. Using a model-based simulation we estimated the strength of adaptation rate along niche evolution and to what extent dispersal limitation influences the distribution of the diversity of the Phyllostomidae. With 222 species known to date, phyllostomids display an array of ecomorphological specializations, showing latitudinal and environmental gradients of richness. Using IUCN maps, we set assemblages based on species incidences in a 110 x 110 km grid. We used a comprehensive bat phylogeny, dated using 24 calibration points along the timespan of the tree, pruned the geographic data, obtaining a dataset of 62% of phyllostomid richness in 1,338 Neotropical assemblages. Phyllostomid entropy of order 1, used as a measure of diversity, was negatively related to temperature seasonality, thus taken as niche condition in our model framework. Based on the species by sites matrix, sites' spatial coordinates, niche condition, and phylogenetic relationships, we estimated the posterior distribution of the adaptative rate of species niche positions and dispersal limitation strength. Niche half-life was 13.9 Myr, indicating high phylogenetic signal of the distribution of entropy across the temperature seasonality gradient. Phyllostomids showed dependency on niche evolution towards an optimum of low-temperature seasonality and high dispersal ability, consistent with the large geographic ranges of most species. Phyllostomids seem to preferably track niche conditions close to their optimum over long distances, instead of quickly adapting their niches towards an optimum condition.

Cave-Dwelling Bat Species as a Reservoir of European Lyssaviruses
Heliana Dundarova[1], Boyko Neov[1], Radoslava Emilova[2], Irina Georgieva[2], Nadya Ivanova-Aleksandrova[2], Rayna Antova3, Krasimir Kirov[4], Jiri Pikula[5] and Jan Zukal[6]
1 Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, BGE; 2 National Centre of Infectious and Parasitic Diseases, Sofia, BGE; 3 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, BGE; 4 Faculty of Biology, University of Plovdiv "Paisii Hilendarski", Plovdiv, BGE; 5 Department of Ecology and Diseases of Game, Fish and Bees, University of Veterinary and Pharmaceutical Sciences Brno, Brno, CZE; 6 Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, CZE

Bats are mammals capable of active flight. This extraordinary characteristic makes then unique within their class and a suitable reservoir for a variety of lyssaviruses. Active surveillance of bat lyssaviruses in Eastern Europe is irregular and information about the Balkan countries e.g., Bulgaria is scarce. Blood samples from 112 bats were taken between 2020–2021 from 6 caves in Bulgaria. Every bat was sampled just one time and released in front of the roost entrance. We used morphological characteristics for the Horseshoe bats and sequencing of the mitochondrial gene for cytochrome b for the Greater mouse-eared bats and Lesser mouse-eared bats. The blocking antibodies in serum against rabies viruses were analyzed with BioPro Rabies ELISA Ab kit (O.K. SERVIS BioPro, Czech Republic). Positive results were detected in 5.35% (6/112) of all samples. In addition to the positive samples, we found 8 samples in which the level of blocking antibodies was slightly below the cutoff threshold (according to the manufacturer's instructions). RT-PCR will be the next step in our study. Our data suggest that accidental contact with bats should be considered as a potential rabies risk in caves. Bats are legally protected in Bulgaria and other European countries that prohibit their deliberate capture and killing. Extensive research on lyssaviruses is necessary to establish the incidence of rabies in different bat species and to clarify whether this is a potential problem for public health following the EUROBATS conservation recommendations.

Habitat Use of Bats Across the Gradient of Urbanization and Seasons
Jessica M. Dwyer, Marianne S. Moore and Jesse S. Lewis
College of Integrative Sciences, Arizona State University, Mesa, AZ

The gradient of urbanization, ranging from low to high development, is a primary driver of landscape change that can affect biodiversity. Animals balance trade-offs in obtaining resources and avoiding anthropogenic disturbances across the gradient of urbanization to maximize their fitness. However, additional research is necessary to understand seasonal variation in how animals respond to urbanization, particularly in arid regions. Our objectives were to evaluate (1) the response of a suite of bat species to urbanization and (2) whether species shifted their response to urbanization across seasons. We predicted that the response of bats to urbanization would differ among species, with some species being more sensitive to urbanization than others. We also predicted that bat species would increase use of moderate and highly urbanized areas in the summer season, where food and water resources were assumed to be greater compared to wildland areas. To test these hypotheses, we used stationary acoustic bat monitors to sample 50 sites across the gradient of urbanization in the Phoenix metropolitan area during four seasons. Consistent with predictions, bats in our study exhibited varying responses to urbanization, with most species exhibiting a negative relationship with urbanization. Counter to our predictions, however, most bat species did not appear to shift their response to urbanization across seasons, indicating that the cost of urbanization outweighed the benefit of obtaining available resources. Results from this study can help inform management plans to conserve bats across landscapes that experience varying levels of urbanization.

Supporting a Unique Running Gait: Mechanics and Physiology of Terrestrial Movement in Vampire Bats
Yvonne A. Dzal[1,2], Teri J. Orr[3], John W. Hermanson[4] and Stuart Parsons[5]
1 Department of Biology and Centre for Forest Interdisciplinary Research, University of Winnipeg, Winnipeg, CAN; 2 Bat Conservation International, Austin, USA; 3 Department of Biology, New Mexico State University, USA; 4 Department of Biomedical Sciences, Cornell University, Ithaca, USA; 5 Science, Technology, and Engineering, University of the Sunshine Coast, Sippy Downs, AUS

The mechanistic understanding of how organismal form and function underpins behavior and ecology holds key insight for explaining spatial gradients in biodiversity. Bats have become so specialized for flight that most bat species have ultimately lost the ability to maneuver on land. Of more than 1400 known bat species, only a handful have opted for a terrestrial lifestyle. Taking a collaborative and interdisciplinary systems approach, we highlight the mechanical, physiological, and cellular mechanisms that underlie the unique running gait of the vampire bat (*Desmodus rotundus*). To determine the energetic requirements of this unique gait, we ran vampire bats on a treadmill and measured their metabolic rate prior to, and following exercise. At the mechanical level, vampire bats recruit their forelimbs instead of hindlimbs for force production at a lower stride frequency than similar-sized mammals. At the physiological level, this unique running gait requires significantly less energy than that of other

running mammals— with vampire bats increasing metabolism 1.5-fold, compared to similar-sized running mammals which increase metabolism 68-fold post-exercise. To determine the cellular mechanisms underlying this energetically-efficient gait we isolated mitochondria from the muscles that vampire bats rely on to produce force while running (pectoralis). At the cellular level, vampire bats exhibit a greater potential maximal aerobic capacity than that of other bats. Collectively, our research in Belize has uncovered substantial adaptations across several levels of organization— mechanical, physiological and cellular— that in part make vampire bats such impressive runners.

A Pilot Study Evaluating Bat-Virus Relationships in Neotropical Bats

Hannah J. Eiseman[1], Phoebe S. Reuben[1], Carlos Carrion[2], Pablo Moreno[2], Julianna Gilson[1], Thalia Williamson[1], William Orrico[3] and Hannah K. Frank[1]

1 Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, USA; 2 Instituto Nacional de Biodiversidad, Quito, ECU; 3 Cummings School of Veterinary Medicine, Tufts University, North Grafton, USA

Bats and humans have a complex relationship. Bats are important for ecosystem function and provide countless ecosystem services upon which humans rely. However, they are also uniquely implicated as reservoirs for a wide variety of zoonotic diseases. Most investigations into the risk of zoonotic spillover have focused on Australia, Asia, and Africa due to the prevalence of previously documented, highly pathogenic viruses in these areas. Comparatively, little research has examined the relationships between viruses and bats in Central and South America. The Neotropics have some of the highest species and ecological diversity of bats in the world and extensive deforestation; this suggests that understanding bat-virus relationships in this region may have important implications for both human and bat health. Indeed, the Neotropics are thought to have most "missing" zoonoses of any global region. We sampled bats in northwest Ecuador across three habitat types (remnant forest, agricultural plots, plots that will be reforested [most of which are abandoned agricultural sites]) to assess viral identity and prevalence in advance of a larger reforestation project. Here we present preliminary data on bat diversity shifts with land use type and lay out our experimental plans regarding viral surveillance. We will use ecological modelling and molecular detection of viruses in non-lethal samples, supplemented with interviews of local residents to understand how infection risk for humans, livestock, and wild bats vary across a mosaic landscape.

Activity of Forest Specialist Bats Decreases towards Wind Turbines at Forest Sites

Julia S. Ellerbrok[1], Anna Delius[1], Franziska Peter[2], Nina Farwig[1] and Christian C. Voigt[3]

1 Department of Biology, University of Marburg, Marburg, DEU; 2 Faculty of Agricultural and Nutritional Sciences, University Kiel, Kiel, DEU; 3 Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU

Globally, an increasing number of wind turbines is being built as a promising approach to reduce carbon gas emissions. However, the availability of suitable construction sites is limited, leading to a gradual expansion of wind energy production into more sensitive ecosystems, such as forests. Consequences for bats in the proximity of wind turbines are still barely understood and may depend on foraging mode, as open-space, edge-space and narrow-space foraging bats depend to varying degrees on forest structures. Therefore, we conducted a two-year acoustic survey in 22 temperate forests of Central Germany and analyzed whether there are shifts in bat activity in relation to wind turbine distance and rotor size. Most notably, we showed that narrow-space foraging bats, which are forest specialists, avoided the proximity of wind turbines in forests, as their activity was reduced over distances of several hundred meters, especially at turbines with large rotors. In contrast, open-space foragers were more active close to wind turbines in late summer, while the activity of edge-space foragers did not change in relation to turbine proximity. Our results are important because they show that also forest specialist bats with low collision risks at wind turbines may still suffer from a turbine-induced habitat degradation. To mitigate the green-green dilemma between bat conservation and sustainable energy production in forests, we advise additional compensation measures to account for a hitherto unknown habitat loss associated with the operation of wind turbines in forests.

Understanding the Winter Hibernation and Foraging Ecology of Red Bats to Inform Prescribed Fire Management

Ashley D. Epstein and Emma V. Willcox

Department of Forestry, Wildlife and Fisheries, University of Tennessee, Knoxville, USA

In the Southeastern U.S., prescribed fire is a tool regularly used by land managers to achieve a variety of management objectives. Prescribed burns in this region are often conducted during winter to best achieve objectives and avoid direct mortality to wildlife. Many bat species hibernate in caves during the winter, reducing their exposure to winter prescribed fire. Eastern red bats (*Lasiurus borealis*, LABO), however, roost exclusively in forests throughout the year and are still present on the landscape when these burns are conducted, making them vulnerable to prescribed fire activities. No studies have examined LABO response following disturbance by fire with regards to roost site selection or foraging activity. With this study we will capture and apply transmitters to LABO in and around stands subject to prescribed burning. Using radio telemetry, we will track bats to roost sites and identify roost characteristics at three spatial scales (i.e., roost site, forest stand, and landscape). We will use full spectrum Song Meter SM4 acoustic detectors to identify bat calls and feeding buzzes as a measure of foraging activity pre- and post-burn. Results from this study will help fill gaps in our knowledge of LABO life history and aid managers in development of prescribed fire prescriptions that conserve this species.

Development of Echolocation and Hearing in the Big Brown Bat

Paul A. Faure[1], Carl E. Lyons[1], Heather W. Mayberry[1,2], Doreen Möckel[1] and John M. Ratcliffe[2]

1 Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN; 2 Department of Biology, University of Toronto, Mississauga, CAN

Big brown bat (*Eptesicus fuscus*) pups are born naked, blind, with closed ears but can fly by post-natal day (PND) 30 and assume an adult-like appearance by PND 45. Newborn pups produce several distinct vocalizations but mainly emit isolation calls (i-calls) which facilitate mother-offspring reunions. Isolated pups emit mostly i-calls during the first 710 days but eventually transition to producing echolocation calls. We have documented morphological, acoustical, neurophysiological, and behavioral changes in developing *E. fuscus* pups. This talk summarizes how the temporal, spectral, and spatial characteristics of pup vocalizations shift from i-calls to downward frequency modulated (FM) sweeps used in echolocation. We then describe changes in the temporal patterning of echolocation calls when pups begin emitting sonar strobe groups, which provides evidence of developmental changes in perception. Using tone-evoked auditory brainstem response (ABR) recordings, we tracked the progressive development and maturation of auditory sensitivity in *E. fuscus* pups from PND 10 to PND 31, with additional ABR recordings at 2 months, 3 months and 1 year of life. Prior to PND 13-16 and when pups were still non-volant, most bats were unable to hear frequencies above 48

kHz; however, sensitivity to higher ultrasonic frequencies increased with age. There was a profound increase in hearing sensitivity in pups across development for sound frequencies between 4 and 100 kHz, with the largest threshold shifts occurring between PND 10 and 19. Notably, these changes occurred near the ages when young bats first begin to fly and echolocate—two important developmental milestones.

Bats and Artificial Lighting Impacts: Creating Best Practice Guidance with Industry Stakeholders in the United Kingdom
Joanna A. Ferguson
Bat Conservation Trust, London, UK.

The Bat Conservation Trust's (BCT) built environment project was set up in 2007 to tackle the challenges this sector presents to the 17 bat species that breed in the United Kingdom (UK). One such challenge is the substantial and wide-ranging negative impact of artificial lighting at night (ALAN) on UK bat species. The potential harm to bats through entombment in or loss of their roosting sites are among the worst impacts, and constitute a breach of UK legislation. Therefore, it is essential that not only are impacts of ALAN on bats and their roosts controlled for, but that bat conservation is promoted through preventative work with industry stakeholders. BCT has developed specific industry guidance on lighting to achieve this. BCT and the Institute of Lighting Professionals (ILP) first collaborated in 2009 to produce guidance on bats and lighting. Further research and changes in technology, particularly the uptake in LED lighting, saw the need for updated best practice guidance. In 2018, BCT and ILP published the second iteration of 'Bats and Artificial Lighting in the UK'. The next year saw BCT's technical symposium on bats and lighting mitigation case studies, attracting lighting professionals, ecologists, local government officials, planners, and bat workers. Building on this strong foundation, the BCT reconvened the bats and lighting steering group for the upcoming third iteration. A focus on multi-disciplinary working and stakeholder engagement is key to ensure guidance is fit for purpose and therefore has the greatest potential uptake by industry to support bat conservation aims.

Roost Site and White-Nose Syndrome Disease Influences on Tri-colored Bat Body Mass in Georgia, USA
Emily A. Ferrall[1,2], Brian J. Irwin[1,3], Katrina M. Morris[2], Jeffrey Hepinstall-Cymerman[1] and Steven B. Castleberry[1]
1 Warnell School of Forestry & Natural Resources, University of Georgia, Athens, USA; 2 Wildlife Resources Division, Georgia Department of Natural Resources, Social Circle, USA; 3 U.S. Geological Survey, Georgia Cooperative Fish & Wildlife Unit, Athens, USA

The tri-colored bat (*Perimyotis subflavus*) was once a common species in the eastern U.S. but has suffered high mortality due to white-nose syndrome (WNS) in the core of its range where it primarily hibernates in caves. In areas without caves, tri-colored bats are known to use road culverts as roosts. *Pseudogymnoascus destructans*, the fungal pathogen that causes WNS, has been detected in culverts in several southeastern states, including Georgia. Prior research has shown that bats with higher body mass at the onset of hibernation have higher probability of surviving repeated arousal events from WNS. Therefore, our objective was to determine if tri-colored bat body mass loss during hibernation varied by gender, hibernaculum type (cave or culvert), year, latitude, and WNS status. We measured bat mass and assigned a WNS wing damage score for 1,217 individuals in early and late hibernation at 41 culvert and 4 cave roosts in Georgia, 20192022. We used linear models to evaluate relationships between body mass loss and the suite of predictor variables. Our results showed that bats utilizing cave roosts lose more mass than those in culverts, and male tri-colored bats lose less mass than female tri-colored bats within each hibernaculum type. Overall, male tri-colored bats roosting in culverts lost the smallest amount of body weight. Understanding which tri-colored bat populations are most at-risk can guide managers on where to focus winter monitoring efforts and potential WNS-treatment trials.

Not All Farms Are Created Equal: Shadier African Cacao Farms Promote a Richer Bat Fauna
Diogo F. Ferreira[1,2,3], Alexandra Darling[3,4], Crinan Jarrett[3,4], Patrick Jules Atagana[3,5], Hermann Taedoumgr[6], Andreanna Welch[7], Hugo Rebelo[1,2,8] and Luke L. Powell[1,2,3,4]
1 CIBIO-InBIO, Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, PRT; 2 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, Vairão, PRT; 3 Biodiversity Initiative, Houghton, USA; 4 Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, GBR; 5 Department of Biological Sciences, Faculty of Sciences, University of Maroua, Maroua, CMR; 6 Consultative Group on International Agricultural Research, Bioversity International, Yaoundé, CMR; 7 Department of Biosciences, Durham University, Durham, GBR; 8 ESTBarreiro, Barreiro Technology College, Polytechnic Institute of Setúbal, Setúbal, PRT

Bats are the second most diverse group of mammals in the world and are known to provide key ecosystems services, with some studies showing that bats can save cacao farmers millions of dollars through pest suppression. Although more that 70% of cacao comes from Africa, no studies have focus on the impacts of cacao management on bat communities in that part of the world. In this study, we investigated how bat communities varied between farms with different levels of shade tree cover and shade tree communities. We sampled bats using 20 ground-level mist-nets across 28 cacao farms over a three-year period in Cameroon. Our GLMMs showed that shade tree cover explained more than 50% and 80% of the variance for abundance and richness of insectivorous bats, respectively. For Shannon diversity, shade tree cover explained 45% while shade tree height explained the remaining variance. Frugivores and nectarivores bats were only positively associated with the presence of fruit shade trees. Finally, bat assemblages varied significantly between high shade and low shade farms, with the former being associated with insectivores while the latter with frugivores. Nevertheless, mixed shade farms showed an intermediary bat community. Our findings highlight that sunny African cacao farms are less able to support a rich community of insectivorous bats, missing some of the rare and specialized species. To counterbalance the expected increase of cacao production in the forthcoming decades, policymakers should adopt wildlife-friendly cacao management systems that maintain bat insectivorous diversity and thus maximize their potential pest suppression services.

Seasonal Variations in the Diet of *Myotis velifer* Using a Molecular Approach
Katheryn V. Fitzgerald and Loren K. Ammerman
Angelo State University, Biology Department, San Angelo, USA

Insectivorous bats worldwide play an essential role as predators in ecosystems and serve as pest control for agriculture businesses. Characterizing diets of specific bat species is difficult using conventional methods that cannot capture detailed dietary information. New technologies have progressed to overcome these challenges, such as high-throughput sequencing. In this study, we used metabarcoding of the cytochrome oxidase I mitochondrial gene to analyze fecal samples of *Myotis velifer* and provide insight into the seasonal variation of diet from a known colony located at Fort Leaton State Historic Site in Presidio, Texas. After filtering sequence reads, we recovered and analyzed 706 unique diet items (UDI) in the diet of *M. velifer*. We found 483 taxa (species and genus level) belonging to 11 insect orders in fecal samples from 66 bats

collected from March to October 2021. Based on our analyses, *M. velifer* experienced seasonal variation in diet. The orders containing the most unique diet items were Diptera (n = 353), Lepidoptera (n = 160), and Blattodea (n = 59). We identified important insect crop pests in their diet and substantial consumption of mosquitoes. Bats captured in June experienced the highest diversity of orders in their diet during the peak maternity season. Females were more abundant than males, indicating that the historic fort may serve as an essential maternity colony.

Overcoming the Challenges and Constraints of Conducting Long-term Acoustic Monitoring Projects in Remote Locations
Jon Flanders1, Jeff Schlueter[2], Matthew McKown[2], Tina L. Cheng[1] and Winifred F. Frick[1]
1 Bat Conservation International, Austin, USA; 2 Conservation Metrics Inc., Santa Cruz, USA.

Passive acoustic monitoring is an effective, non-invasive means of detecting the spatial and temporal trends of echolocating bat species. It has been a vital tool in advancing our understanding of the basic life history traits of many species that Bat Conservation International's Endangered Species Program are trying to protect. The advancement of more cost-effective and scalable acoustic monitoring techniques allows us to deploy a greater number of sensors over extended periods of time. Results from longer-term datasets are extremely valuable for determining how bat populations respond to anthropogenic-induced changes to their environment, informing conservation management decisions, and providing a way to assess the long-term success of mitigation and protection measures. However, scaling acoustic monitoring projects presents its own challenges, especially when survey areas are in remote areas where access (physical and technological) is limited. Here we present case studies from two long-term acoustic monitoring projects, one in the Nimba Mountains, Guinea, and the other in Nyungwe National Park, Rwanda. In Guinea, where three IUCN threatened bats are located, year-round monitoring efforts generate over 20,000 hours of acoustic files per year. Here, we use a multiclass convolutional neural network (CNN) classification model to detect priority species, based on training and cross-validation datasets containing examples of positive sounds for each target species. In Rwanda, where only one priority species is located, data visualization for in-country partners has been a priority to ensure data can be effectively used in conservation management plans, and keep partners engaged and interested in the work.

Karyotypic Stasis and Swarming Influenced the Evolution of Viral Tolerance in a Large Bat Radiation
Nicole Foley
Veterinary Integrative Biosciences, Texas A&M University, College Station, USA

The emergence of COVID-19, Ebola and SARS has urgently placed understanding the status of bats as viral reservoirs as a major focus of global public health initiatives. The coevolution of bats and viruses make resolved phylogenies essential for predicting future disease emergence. Despite this, the phylogeny of Old World Myotis bats is poorly documented. Their conserved karyotype (2n = 44) and swarming behavior is thought to promote interspecific hybridization. Hybridization can act to overwrite the species tree and confound standard phylogenomic analyses. Previous studies have shown that in the presence of hybridization the distribution of phylogenomic signal is non-random and predicted by recombination rate. To this end, we used a novel machine learning approach to infer a recombination map for *M. myotis*, the first for any bat species. Recombination rates and tests of introgression were combined with recently developed locus-tree methods to sample local phylogenomic signal on a genomic scale to infer the species tree. Our results demonstrate widespread introgression with the species tree often limited to as little as 57% of the genome, notably near chromosome centers. Notably, viral interacting proteins were commonly found within the most significantly introgressed genomic regions. Together, our results suggest that the conserved chromosomal architecture and swarming behavior were both key to the success of this mammalian.

Using PIT Tags to Infer Bat Reproductive Status and Parturition Date: Busy Nights During Lactation
Amélie Fontaine[1], Anouk Simard[2], Valérie Simard[2], Hugh G. Broders[3] and Kyle H. Elliott1
1 Department of Natural Resource Sciences, McGill University, Ste Anne de Bellevue, CAN; 2 Ministère de la Forêt, de la Faune et des Parcs, Québec City, CAN; 3 Department of Biology, University of Waterloo, Waterloo, CAN

The population dynamics and life-history traits of small and cryptic species can be challenging to study. In some cases, these issues can be overcome by using Passive Integrated Transponders (PIT tags) to mark individuals and infer behavior. We recorded detections of PIT-tagged bats at the entrance of five maternity roosts from 2017–2021 to evaluate if this system could be used to determine reproductive status, parturition date and time away from the roost of individual bats. To further evaluate the potential of this method, we chose one maternity roost as a case study and investigated factors affecting parturition date and time away from the roost. We were able to estimate reproductive status for most of tagged individuals (63 to 100%) at three of five roosts. Similarly, we were able to estimate parturition date for 42 to 82% of individuals at two of five roosts. The proportion of gestating bats with identifiable bouts away from the roost was also higher at these two roosts (52–93%). Early individual arrival date and warm spring temperature at night led to early parturition dates while long nights, warm temperatures, and heavy rainfall at night increased time away from the roost of gestating females. Through this study, we demonstrated that, with an appropriate set up, PIT tag systems may be useful to infer individual reproductive parameters for female bats, including reproductive status and parturition date. This method can be used to improve understanding of bat population dynamics and, hopefully, population management decisions.

Relationships between Age, Relative Telomere Length, and DNA Methylation in *Pteropus pumilus* and *Pteropus hypomelanus*.
Erika F. Forest[1], Danielle M. Adams[2], Charlyn Partridge[3], Gerald S. Wilkinson[4] and *Amy L. Russell[1]*
1 Department of Biology, Grand Valley State University, Allendale, USA; 2 Department of Biological Sciences, Towson University, USA; 3 Annis Water Resources Institute, Grand Valley State University, Muskegon, USA; 4 Department of Biology, University of Maryland, College Park, USA

Bats are the longest-lived mammalian order relative to body mass, but questions remain about relationships between mechanisms related to aging. The process of telomere shortening, a molecular mechanism highly involved with aging, is of interest in determining how bats age. Relative telomere length (rTL) decreases with age in most mammals, but the relationship between age and rTL is highly variable among the few bat taxa studied to date. More recently, DNA methylation, (DNAm), a type of epigenetic regulation in which methyl groups are added to cytosine-phosphate-guanine (CpG) sites across the genome, has been shown to be highly predictive of age in many species of bats. Our research investigates rTL in the family Pteropodidae and directly compares rTL to DNAm for the first time in bats. We examine the relationship between age, rTL, and DNAm in the long-lived, ecologically important bat species *Pteropus pumilus* and *P. hypomelanus*. We hypothesized that (1) there is a negative linear relationship between age and rTL and (2) rTL is significantly correlated with DNAm at some sites, particularly those previously shown to exhibit age-related change. We found a significant negative linear relationship between age and rTL in *P. hypomelanus*, but no relationship in *P. pumilus*. However, for both species, a high proportion of rTL-correlated CpG sites were also significantly associated with age. Many genes near rTL-

correlated CpG sites in both species control regulatory and developmental processes, suggesting that epigenetic regulation of these genomic regions by DNAm may have an impact on telomere length dynamics in bats.

Strong Selective Signatures of Viruses on Bat Genomes and Immunity

Hannah K. Frank[1,2], David Enard[3], James Ellison[4], Angelica Menchaca Rodriguez[5], Elizabeth A. Hadly[6] and Scott D. Boyd[2]
1 Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, USA; 2 Department of Pathology, Stanford University, Stanford, USA; 3 Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, USA; 4 Poxvirus and Rabies Branch, Centers for Disease Control, Atlanta, USA; 5 Department of Biology, University of Bristol, Bristol, UK; 6 Department of Biology, Stanford University, Stanford, USA

Bats are unique among mammals in their ability to fly and to host and shed numerous highly lethal viruses seemingly asymptomatically, leading to great interest in the adaptations that allow bats to survive these infections. However, the field of bat immunology is still relatively young, and few of the over 1,400, ecologically-diverse species of bats have been studied in depth. We investigated both the innate and adaptive immune system, as well as host proteins targeted by pathogens, of multiple bat species to understand the basis of their unique relationship with pathogens. We present genomic data from over 90 species of bats showing that pattern recognition receptors, specifically Toll-like receptors and RIG-I-like receptors, in bats evolved early to recognize viral pathogens. Comparative genomic analysis demonstrates that bats are under exceptional pressure to adapt to coronaviruses in their ACE2 and DPP4 genes compared to other mammals. Additionally, transcriptomic data from seven bat species show that bats express all three canonical superfamilies of Ig heavy chain V genes, with species-specific diversification and similar CDR3 lengths to those observed in other mammals. Our data suggest that pathogen pressure has shaped bat immunity and evolution differently from other mammals, shaping bats' unique relationship with pathogens.

Anthropogenic Landscape Changes Alter Patterns of Parasitism in Cambodian Bats

Liesbeth Frias[1], Alan Hitch[2], Neil Furey[3], Sophie Borthwick[4], Lena Ch'ng[4], Dolyce Low[4], Awatsaya Pimsai[5], Ith Saveng[6], Chheang Dany[7], Chor Kimashalen[7], Buor Vuthy[7], Yim Raksmey[3], Gavin Smith[4] and Ian Mendenhall[4]
1 Asian School of the Environment, Nanyang Technological University, Singapore, SGP; 2 University of California, Department of Wildlife, Fish and Conservation Biology, Museum of Wildlife and Fish Biology, California, Davis, USA; 3 Fauna & Flora International, Cambodia, Phnom Penh, KHM; 4 Duke-NUS Medical School, Programme in Emerging Infectious Disease, Singapore, SGP; 5 Prince of Songkla University, Princess Maha Chakri Sirindhorn Natural History Museum, Songkla, THA; 6 Royal University of Phnom Penh, Centre for Biodiversity Conservation, Phnom Penh, KHM; 7 Ministry of Agriculture, Forestry and Fisheries (MAFF), Phnom Penh, KHM

Agricultural expansion and urbanization in Southeast Asia have one of the fastest growing rates in the world, and despite of their large-scale footprint on tropical ecosystems, little attention has been given to changes to local biodiversity and ecosystem functioning. Based on field surveys conducted throughout Cambodia between 2014 and 2020, we evaluated the extent to which extensive land conversion in the country has driven changes in bat community composition and shaped helminth transmission processes. Helminth parasites were recovered from the gastrointestinal tract of 451 bat specimens, representing 33 bat species in 14 different habitat types, and categorized morphologically to the species level where possible and to family level where not. Nematodes were the most prevalent parasite group (84%) followed by cestodes (33%) and trematodes (6.3%). Overall parasite species richness was higher in evergreen and deciduous forest, and lower in disturbed and urban habitats. This study represents the most extensive survey yet of bat parasites in Cambodia. Our results indicate that bat helminth communities are affected by land conversion and linked to species-specific differences in terms of bat foraging requirements. The lower number of helminth species detected in bats from urban/agricultural areas might be indicative of a reduced capacity of these anthropogenic habitats to support diverse invertebrate assemblages. Given the information gap regarding bat-helminth dynamics in the region, the systematic collection of bat parasite data provides valuable information to help in establishing biodiversity baselines, identifying rare taxa, and monitoring changes in parasite biodiversity.

A Call to Action to Resolve Barriers to Improve Monitoring and Enable Bat Conservation Globally

Winifred Frick[1,2] and Brian Reichert[3]
1 Bat Conservation International, Austin, USA; 2 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA; 3 U.S. Geological Survey, FORT Science Center, Fort Collins, USA

Globally there is need for coordinated population monitoring for bats at broad spatial and long-term temporal scales to enable informed bat conservation. Advances in open-source hardware and data science infrastructures are on the cusp of revolutionizing our ability to monitor bat populations. Yet, key barriers still exist that currently limit the ways we can use acoustic sampling for monitoring bat populations, including barriers to expanding participation in monitoring efforts beyond professional biologists. Researchers around the world are working to resolve these barriers. We organized this symposium to showcase progress across the data science pipeline: (1) data collection devices: the rapidly advancing technology of acoustic detectors; (2) data transfer realities: so much data, so little bandwidth; (4) data processing: turning sounds into species identifications (with some uncertainty); (5) data analysis: statistics and inferential scope over space and time for bat population monitoring; and (6) decision support: using acoustic monitoring results to inform conservation decisions. The original breadth of presenters in this symposium became limited due to travel difficulties. We will introduce the symposium by sharing key advances made by groups around the world that were unable to attend. We focus on the state of the science, share knowledge and solutions from different regions, and collectively identify next steps to overcome remaining barriers.

Species-specific Effectiveness of an Ultrasonic Acoustic Bat Deterrent Using Experimental Trials in a Flight Cage

Sarah R. Fritts[1], Sara P. Weaver[2], Brogan P Morton[3], Amanda M. Hale[4], Emma E. Guest[1], Brittany F. Stamps[1] and Cris D. Hein[5]
1 Department of Biology, Texas State University, San Marcos, USA; 2 Bowman, San Marcos, USA; 3 Wildlife Imaging Systems, Hinesburg, USA; 4 Department of Biology, Texas Christian University, Fort Worth, USA; 5 National Renewable Energy Laboratory, Arvada, USA

An unintended consequence of wind energy is bat fatalities through collisions with turbines. Ultrasonic acoustic deterrents (UADs) have been designed to create an unattractive air space for bats, thus allowing maximization of energy production. Our objective was to maximize species effectiveness of the NRG Systems-manufactured UAD through experimental trials in a 61 m x 10 m x 4.5 m (L x W x H) outdoor flight cage located in San Marcos, Texas, USA. Specifically, we released wild-captured bats within the flight cage and compared flight distances each bat flew from the UAD between three treatments and control periods and assessed several echolocation characteristics using six acoustic detector microphones.

The three treatments varied in sound emission frequencies: low (20–32 kHz), high (38–50 kHz), and combined (20–50 kHz), and each was interspersed by four-minute control periods. We focused on four species: *Myotis velifer* (n = 50), *Tadarida brasiliensis* (n = 77), red bats (*Lasiurus blossevilli*, *L. borealis*; n = 45), and *Nycticeius humeralis* (n = 37) and conducted trials from July–October 2020 and March–May 2021. All species flew greater distances from the UAD during all three UAD emission treatments than during the control periods. Additionally, results suggest that of the species that altered echolocation during UAD emission. Because the high frequency emission treatment deterred all species, these frequencies likely did not attenuate within the 60-m flight cage. However, sound attenuation may occur at further distances; thus, we are currently expanding the flight cage to continue testing.

Bat Attraction to Very High Voltage Power Lines: A Role for Corona Discharge?

Jérémy Froidevaux[1,2,3], Gareth Jones[3], Christian Kerbiriou[2] and Kirsty Park[1]

1 University of Stirling, Biological and Environmental Sciences, Stirling, GBR;2 Muséum National d'Histoire Naturelle, Centre d'Ecologie et des Sciences de la Conservation, Concarneau/Paris, FRA; 3 University of Bristol, School of Biological Sciences, Bristol, GBR

With the growth of energy consumption demands in modern societies, transmission line networks are expanding worldwide. In Europe, overhead alternating current power lines traverse over 500,000 km and the grid network is expected to grow further. Many studies have highlighted the risks of power lines posed to wildlife ranging from collision to habitat fragmentation, yet the potential effects of power lines on bats largely remain to be tested. In this study, we aimed to assess the responses of insectivorous bats to very high voltage power lines (>220 kV, VHVPL). We implemented a paired sampling design and acoustically monitored bats at 25 pairs, one pair consisting of one forest edge near to VHVPL matched with one control forest edge. Our results revealed that overall bat activity and the activity of *Pipistrellus pipistrellus* and *Barbastella barbastellus* increased with relative humidity at power lines while decreased at control sites. We also observed higher foraging behavior around power lines in wet conditions. These results are broadly consistent with expectations from the 'corona discharges' hypothesis. Corona discharges are electric discharges produced by the ionization of atmospheric air surrounding the conductors and mainly occur at high relative humidity levels. These discharges results in the production of noise but also to the emission of blue and ultraviolet lights that are known to attract nocturnal insects and thus bats. Our work highlights the response of bats to power lines at foraging habitats, providing new insight into the interactions between power lines and nocturnal biodiversity.

Determining Habitat Use and Niche Partitioning of Aerial Insectivores With the Use of Bioacoustics

Brett R.W. Gandy and Erin F. Baerwald

Ecosystem Science and Management Program, University of Northern British Columbia, Prince George, CAN

Bats are notoriously challenging to study because of their nocturnal nature and rapid flight. Identifying sites to study these animals can present barriers to research, particularly in understudied regions, like northern British Columbia. In this study, I used acoustic monitoring at five field sites west of Prince George, British Columbia, Canada, that had variability in the presence of a guild of aerial insectivorous birds (swallows) to determine the activity levels of bats relative to swallow activity. I hypothesized that because swallows are morphologically and ecologically similar to insectivorous bats yet are much easier to find due to their diurnal nature, they could indicate bat presence. I also determined the species composition of bats in the Omineca region of British Columbia because there is a limited amount of data on which species reside in the area. I found acoustic evidence of seven bat species: little brown myotis (*Myotis lucifugus*), western long-eared myotis (*M. evotis*), long-legged myotis (*M. volans*), big brown bat (*Eptesicus fuscus*), silver-haired bat (*Lasionycteris noctivagans*), hoary bat (*Lasiurus cinereus*), and eastern red bat (*L. borealis*). I found that the overall activity of bats was greatest at the habitats with higher swallow use. Additionally, bat species with the greatest morphological and ecological similarities to swallows (hoary bats, silver-haired bats, and eastern red bats) had higher relative activity at sites with high usage by swallows. This study will help guide future research on bat habitat by using indicators that can be identified during daylight hours to identify quality bat foraging habitat.

The Bat Eco-Interactions Database in Action: Where, How, and With Whom Are Bats Interacting?

Cullen Geiselman and Aja Sherman

Bat Eco-Interactions Project, Houston, USA

Bats are critical components to many ecosystems as pollinators, seed dispersers, insect predators in addition to serving as hosts and prey of other species. Scientific studies of their ecological interactions continue to reveal the critical roles bats play in nature and the benefits they provide to human economies. We created the Bat Eco-Interactions Database to catalog published accounts of interactions between bats and other organisms to facilitate scientific research, reduce duplication of effort, and share and visual published data. Each interaction record includes family, genus, and species of each interactor (bat, plant, arthropod, etc.), type of interaction (pollination, visitation, consumption, seed dispersal, transport, prey, predation, roost, host, cohabitation), details of the location (country, habitat type, elevation, GPS), and citation (author, publication, doi, exact text describing the interaction). Search results can be visualized in tables or displayed geographically and are available for csv download. The database is open sourced, free, and updated by its users at www.batbase.org. As of April 2022, >16,000 interactions between 520 bat species and >2,500 non-chiropterans from 114 countries had been gathered from >700 citations. During this talk, we explore geographic, taxonomic, and ecological gaps in the data and discuss plans to link the database with taxonomic treatments to update species names while maintaining data provenance. Further user interface enhancements and expert curation will also be discussed. We invite students and researchers to become part of this online community by submitting publications or adding data directly through the online portal.

Investigating Coronavirus Maintenance and Excretion Dynamics within Bat Populations Toward Improving Our Understanding of Spillover Opportunities

Marike Geldenhuys[1], Muriel Dietrich[2], John L. de Vries[1], Marinda Mortlock[1], Jonathan H. Epstein[1,3], Jacqueline Weyer[1,4,5], Janusz T. Pawęska[1,4,5] and Wanda Markotter[1]

1 Centre for Viral Zoonoses, Department of Medical Virology, University of Pretoria, Pretoria, ZAF; 2 UMR Processus Infectieux en Milieu Insulaire Tropical, Sainte-Clotilde, REU; 3 EcoHealth Alliance, New York, USA; 4 Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases of the National Health Laboratory Services, Johannesburg, ZAF; 5 Department of Microbiology and Infectious Diseases, University of Witwatersrand, Johannesburg, ZAF

A number of novel coronavirus species of public health and veterinary importance have emerged in the first two decades of the 21st century with bats considered as the natural reservoirs for the genetic diversity of coronaviruses. Targeted wildlife surveillance is needed to identify drivers involved in viral perpetuation within natural host populations creating opportunities for interspecies transmission. We review the existing hypotheses for coronavirus epidemiology in bat populations as well as report on the results of two-years of surveillance within a maternal colony of *Rousettus aegyptiacus* in South Africa. Excretory samples from monthly collections were tested for coronavirus RNA and resultant infection dynamics compared to the population demographics to identify important factors for viral maintenance. Three distinct coronavirus genetic lineages were observed, with non-identical temporal excretion dynamics. The study identified near constant shedding from the colony throughout the year, with large excretion peaks during specific times (up to 58% positivity) that coincided with increased infections of young bats, as is suggested following the waning of maternal antibodies. Among adults, higher detection frequency among reproductively active female bats were correlated to lower body conditions, suggesting a metabolic cost or higher susceptibility of infection in pregnant and lactating females. Analysis of recaptured bats suggest that viral clearance may occur within one month. These findings assist in our understanding of coronavirus persistence as well as the identification of higher-risk periods associated with viral circulation in a colony that may be useful in the development of risk reduction strategies for potential zoonotic coronavirus transmission.

The Southwest Bat Hub: Implementing the NABat program in Arizona and New Mexico

Katharine L. Gerst[1], Christen Long[1], Amanda M. Adams[1], Jonathan D. Reichard[2], Brian E. Reichert[3], Bethany Straw[3], Angie McIntire[4] and Winifred F. Frick[1]

1 Bat Conservation International, Austin, USA; 2 US Fish and Wildlife Service, Hadley, USA; 3 US Geological Survey, Ft. Collins, USA; 4 Arizona Game and Fish Department, Phoenix, USA

We established the Southwest Bat Hub in 2021 to unite attempts by state and federal agencies to coordinate data collection to inform population-level understanding of the region's bats. The Southwest Hub serves Arizona and New Mexico (www.southwestbats.org). In the Southwest, there is an urgent need to understand the impacts of threats on bat populations, such as drought, fire and disease. Prior to the establishment of the Hub, the region had low participation in NABat monitoring despite being a hot spot for bat diversity. Monitoring in the first year of the Hub being established has more than doubled prior years efforts, to a total of 65 cells submitting data in 2021. Partners for this project include the USFWS, US Forest Service (USFS), Bureau of Land Management (BLM), Tribal agencies, National Park Service (NPS), and local conservation groups. The Hub aims to facilitate the collection of consistent data and provide data products back to these partners to inform management. The Hub's services reduce the barriers to participation faced by partners, and include equipment sharing, data processing and management, training, and survey coordination and planning. We work with this extensive network of regional partners to ensure NABat's existing standardized data collection protocols are followed in the region. We facilitate the standardized processing of data collected and communicate the results to data contributors and stakeholders. Ultimately, this collaborative approach is necessary to develop robust status and trend modeling outputs to inform the management and conservation of bat populations.

Arousal Behavior in Population of Little Brown Bats, *Myotis lucifugus*, that is Unaffected by White-nose Syndrome

Haley J. Gmutza[1,2], Rodney W. Foster[1] and Allen Kurta[1]

1 Department of Biology, Eastern Michigan University, Ypsilanti, USA; 2 Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, USA

White-nose syndrome is a fungal disease that has decimated populations of hibernating bats across North America since 2006. Tippy Dam, a novel hibernaculum located in Michigan, was hit by the fungus in 2014; however, little brown bats (*Myotis lucifugus*) that overwinter there have not experienced the decline that occurred elsewhere, and the population remains steady at over 20,000 animals. Small ventilation holes within the dam's spillway allow light and bats to enter, and I hypothesized that light filtering through the openings is sufficient for hibernating bats to stay on a circadian rhythm, and that these bats will arouse together, in groups, which is less energetically expensive. High-resolution thermal cameras were placed within the spillway to monitor arousals in two rooms from October 2019 to April 2020. Videos were subsequently cut into frames taken every 5 minutes, and the frame images were analyzed for the contour outlines of awake bats. Peak and mean arousal time was after sunset for early, middle and late hibernation, with peaks and means shifting to later in the night as sunset became later. Maximum aroused cluster size was about 8 bats, and only 14% of total arousals were considered clusters. Although arousal in clusters was not as frequent as expected, bats that hibernate at Tippy Dam are indeed following a circadian rhythm, with most arousals happening at night. Arousals often appeared synchronized within the entire population, but not necessarily in large clusters of adjacent animals.

Utilizing "Bat Blitzes" to Inventory Bat Species Occurrences within National Parks of the Mojave Desert Region

Kimber N. Godfrey and Allen W. Calvert

US National Park Service, Mojave Desert Inventory and Monitoring Network, Boulder City, Nevada

The Mojave Desert Inventory and Monitoring Network conducts long-term research of natural resources within nine National Park units that span the Mojave and Great Basin deserts of Nevada, Arizona, and California. Due to the decline of bat populations across the country; primarily from white-nose syndrome and wind energy development, a need for tracking populations across the network was identified. As part of a larger bat monitoring plan, bat blitzes were initiated to document species occurrences with the network parks. A bat blitz is designed to gather a large number of biologists together to survey multiple locations within a geographic area within a short amount of time. A secondary objective of these blitzes is to provide park biologists with training in bat survey techniques. Between 2540 participants are split up into 35 smaller crews to concurrently sample different sites each night for 34 nights in a row. Capture surveys are utilized with a bat detector deployed during the capture survey period. The first network bat blitz was hosted by Grand Canyon-Parashant National Monument in 2017 where 15 species were detected. In 2018, Joshua Tree National Park hosted the blitz where 13 bat species were detected. Great Basin National Park hosted a blitz in 2019 where 10 species were detected. We plan to resume blitzes this September at Death Valley National Park. The success of these blitzes has increased interest across the region with biologists participating from nine park units along with state agencies and other partners as well.

Chiropterofauna Monitoring in Seven Sites in the Cerrado of Northern Paraguay

Gloria González de Weston[1], María Belén Barreto Cáceres[1], Alberto Yanosky[2] and Nicolás Cantero[3]

1 Programa de Conservación de Murciélagos del Paraguay, Departamento de Biología, Universidad Nacional de Asunción, Asunción, PRY; 2 Estructura Interdisciplinaria de Investigación Socio-Ambiental, Universidad Autónoma de Encarnación, Encarnación, PRY; 3 Wildlife Paraguay, Luque, PRY

Paraguay is in a transitional area between the tropics and the subtropics in South America, where many bat species reach their ranges. The Paraguayan chiroptera is represented by 58 species of six families: Emballonuridae (2), Noctilionidae (2), Phyllostomidae (21), Natalidae (1), Vespertilionidae (15) and Molossidae (17). Paraguayan bat ecology and diversity is poorly known while knowledge about the ecology of bats is increasing through new research techniques, such as acoustic detectors, a less invasive tool that provides original data not obtained through traditional techniques. The aim of the study was to determine the richness of bat fauna in the northern cerrado ecoregion of Paraguay in the Departments of Amambay and Concepción where plantations for commercial industry are introduced. Monitoring of bat species was carried out using two methodologies, direct and indirect in two sampling sessions, during the rainy and dry seasons. In both sampling sessions, for seven nights five mist nests were placed at selected sampling points. To record bat species, an Echo Meter Touch Pro 2 and a Song Meter SM4 BATS-FS connected to an external omnidirectional ultrasonic microphone were used, for active and passive acoustic methods respectively. For the analysis and identification of the recording data, the Kaleidoscope Pro was used. An 81.81% (27) of the species described for the area (33) were recorded. Two species registered by bioacoustics methods are of concern *Peropteryx macrotis* (Vulnerable, VU) and *Saccopteryx leptura* (Deficient Data, DD). Further monitoring may provide additional species and information about bat community in this area.

The PacWest Bat Hub Fosters Collaboration to Implement the North American Bat Monitoring Program

Nathaniel Goodby[1], Christen Long[1], Amanda Adams[1], Jon Reichert[2], Brian Reichard[3], Bethany Straw[3], Bronwyn Hogan[2], Scott Osborn[4] and Winifred Frick[1]

1 Bat Conservation International, Austin, USA; 2 U.S. Fish and Wildlife Service, Washington, D.C., USA; 3 U.S. Geological Survey, Fort Collins, USA; 4 California Department of Fish and Wildlife, Sacramento, USA

We established the PacWest Bat Hub in 2021 to unite attempts by state and federal agencies in California and Nevada to coordinate data collection to inform population-level understanding of the region's bats. The Hub works with its network of partners to effectively implement the North American Bat Monitoring Program (NABat) (www.pacwestbats.org). The creation of the Hub led to a record year of NABat data collection in the region in 2021, with 135 NABat cells of data contributed, as compared to a previous high of 99 cells in 2019. Partners for this project include the US Fish and Wildlife Service, US Forest Service, Bureau of Land Management, Tribal agencies, National Park Service, and local conservation groups. The Hub aims to facilitate the collection of consistent data and provide data products back to its partners to inform management. The Hub's services reduce the barriers to participation faced by partners, and include equipment sharing, data processing and management, training, and survey coordination and planning. The Hub works with its extensive network of regional partners to ensure that NABat's existing standardized data collection protocols are followed in the region. We facilitate the standardized processing of acoustic data collected and communicate the results to data contributors and stakeholders. The network of partners cultivated by the Hub are key in continuing to increase and enable survey efforts in the two states to generate sufficient data to provide both spatial and temporal coverage. Ultimately, this collaborative approach is necessary to develop robust status and trend modeling outputs to inform the management and conservation of bat populations.

Comparing Trends in Activity Versus Occupancy for WNS-affected Bats in the Great Lakes Region

Katy R. Goodwin[1,3], Louis Hunninck[2], Joy O'Keefe[2] and Alan A. Kirschbaum[3]

1 Department of Biological Sciences, North Dakota State University, Fargo, USA; 2 Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign, Urbana, USA; 3 National Park Service Great Lakes Inventory and Monitoring Network, Ashland, USA

The fungal disease white-nose syndrome (WNS) is a major threat to North American populations of hibernating bats. Previous studies document severe declines in some species, but often rely on hibernacula counts or capture data from the eastern United States. In contrast, we assessed bat population trends in the Great Lakes region based on acoustic data and compared two analytical approaches: modeling activity levels versus modeling occupancy probability. We conducted passive acoustic surveys at over 200 sites in nine national parks during five summers (2016–2020). We combined acoustic detection data with site-specific covariates to develop park- and species-specific models for both activity and occupancy. We focused on four species susceptible to WNS: *Eptesicus fuscus*, *Myotis lucifugus*, *Myotis septentrionalis*, and *Perimyotis subflavus*. Model estimates averaged across parks showed strong declines in activity level (calls per detector night) for three species when comparing the first to the last year of surveys. Activity decreased by 89% for *Myotis septentrionalis*, 78% for *Perimyotis subflavus*, and 62% for *Myotis lucifugus*. In comparison, occupancy probability decreased by 41% for *Myotis septentrionalis*, 32% for *Perimyotis subflavus*, and 15% for *Myotis lucifugus*. For *Eptesicus fuscus*, our models estimated an average 15% increase in activity and 8% decrease in occupancy. Our results corroborate studies from other regions and other types of data. When comparing the two modeling approaches, we found more moderate changes in occupancy than in activity. This suggests that although WNS-affected bats are decreasing precipitously across the Great Lakes region, their populations are persisting.

Roost Selection, Roost Availability and Gene Flow Among Culvert Roosts of a Trawling Bat in a Subtropical City

Vanessa Gorecki[1], Ramona Maggini[1], Boyd Tarlinton[1], Caroline Hauxwell[1], Monika Rhodes[2] and Stuart Parsons[1]

1 School of Biology and Environmental Science, Queensland University of Technology, Brisbane, Australia; 2 Goolwa, Australia

Many species of trawling bats roost in concrete culverts under roads. However, little is known about the selection of these artificial sites and how much gene flow occurs among culvert roosts. We investigated culvert roost selection by *Myotis macropus* at two spatial scales and studied gene flow between culvert roosts in a large subtropical city in eastern Australia. We surveyed 365 concrete culverts, identified 23 roosts and collected wing tissue samples from 72 bats. Using generalized additive models, we found the distribution of *M. macropus* roosts in concrete culverts can be predicted at a landscape scale and culvert roosts were a limited resource with only 5.5% of culverts identified as potential roosts. We examined roost selection at the roost scale by comparing roost culverts to available culverts. Roost culverts differed significantly from available culverts and the primary difference was the availability of microhabitat. Culverts containing microhabitat were a limited resource in this urban landscape. We used single nucleotide polymorphisms to study gene flow among culvert roosts located in peri-urban and urban areas. Gene flow was moderate between peri-urban roosts and restricted between urban roosts. We found higher relatedness coefficients between individuals roosting in urban roosts compared to peri-urban roosts, indicating reduced gene flow between urban culvert roosts. This study found that culvert roosts were

limited at two spatial scales and that gene flow was restricted between urban culvert roosts. These findings suggest that disturbance to urban culvert roosts could be a significant impact to an urban population of *M. macropus*.

Niche Partitioning Between North American Migratory Bats
Dana Green[1], Erin Baerwald[2] and R. Mark Brigham[1]
1 University of Regina, Regina, CAN; 2 University of Northern British Columbia, Prince George, CAN

The evolution of long-distance migration has occurred independently in a variety of taxa, and two North American migratory bats are the hoary (*Lasiurus cinereus*) and silver-haired bat (*Lasionycteris noctivagans*). While both species can migrate long distances (>1000 km), they are not closely related and exhibit differences in wing morphologies indicative of foraging behavior. In the Cypress Hills of Saskatchewan, both species co-occur during the summer pupping season, and we catch them in abundance. We have collected data on wing morphometrics, nitrogen and carbon isotopic signatures, and glucocorticoid (GC) levels to explore if migratory bats separate dietary niches and if it potential competition influences physiology. While wing morphology may suggest different adaptations for foraging, preliminary results indicate that the isotopic niches of hoary and silver-haired bats overlap and microscopy of fecal samples indicate similar diets. Additionally, the GC levels in juvenile silver-haired bats are significantly greater compared to any other group. These results may indicate greater competition between the species, in particular for juvenile silver-haired bats.

Urinary Steroids as Reproductive Pheromones: Insights from Endocrine and Behavioral Experiments with *Eptesicus fuscus*
Lucas J. S. Greville[1,2], Tyler Pollock[2], Denys deCatanzaro[2] and Paul A. Faure[2]
1 Department of Biology, University of Waterloo, Waterloo, CAN; 2 Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN

Across mammalian taxa, exposure to sexually mature males can elicit precocious puberty in juvenile females and pregnancy disruption in adult females. Research in mice first demonstrated that both exogenous and male urinary steroids elicit these effects, supporting the notion that steroids can act as mammalian pheromones. This talk summarizes a series of experiments aimed at exploring whether urinary steroids may act as reproductive pheromone in bats. Using the big brown bat (*Eptesicus fuscus*) as a model species, we have addressed this question through radioactive tracers, enzyme-linked immunosorbent assays (ELISA), and behavioral testing. Using tritium (^{3}H)-labelled estradiol (E2) as a radioactive tracer, we previously showed that female big brown bats readily absorb exogenous ^{3}H-E2 applied via cutaneous and intranasal exposure, with radioactivity measured throughout neural, peripheral, and reproductive tissues. Additional experiments with ^{3}H-E2 showed the reliable transfer of estradiol from male *E. fuscus* to cohabitating females. More recently, we explored seasonal patterns in ^{3}H-E2 transfer from males to females at three relevant time points: Autumn (mating season), Spring (female ovulation, ovum fertilization, and implantation), and Summer (maternity colony formation, parturition, and maternal care). Higher levels of ^{3}H-E2 transfer were observed in Autumn and Spring compared to Summer. We report the first urinary steroid profiles in bats with numerous seasonal and sex differences. Lastly, using a Y-maze apparatus, we demonstrate a preference by female bats for the odor of male urine. We conclude by discussing future directions and applications of this research, and its importance in the field of comparative physiology.

Towards a Self-Disseminating Vaccine to Control Vampire Bat Rabies in its Reservoir
Megan E Griffiths[1], Laura M Bergner[1,2], Diana K Meza[1,2], Alice Broos[1,2], Nicolas M. Suarez[1], Ana da Silva Filipe[1], Carlos Tello[3,4], Daniel J. Becker[5], Dan Haydon[2] and Daniel G Streicker[1,2]
1 MRC-University of Glasgow Centre for Virus Research, Glasgow, GBR; 2 Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, GBR; 3 Association for the Conservation and Development of Natural Resources, Lima, PER; 4 Yunkawasi, Lima, PER; 5 Department of Biology, University of Oklahoma, Norman, USA

Vaccination is a powerful tool in combating infectious diseases of humans and companion animals. In most wildlife reservoirs however, achieving sufficient vaccine coverage to mitigate disease burdens remains logistically unattainable. Virally vectored 'transmissible' vaccines which deliberately spread among hosts are a potentially transformative, but still theoretical, solution to the challenge of immunizing inaccessible wildlife. Here, we investigate *Desmodus rotundus* betaherpesvirus (DrBHV) as a candidate vector for a transmissible vaccine targeting vampire bat–transmitted rabies which causes widespread human and livestock mortality in Latin America. We used a combination of deep sequencing on field-collected samples, and computer modelling, to determine its biological and epidemiological suitability as a vaccine vector. Whilst total DrBHV prevalence is >95%, we identified of eleven strains of DrBHV which varied in prevalence and geographic distribution across Peru. The phylogeographic structure of these strains was predictable from both host genetics and landscape topology, informing long-term DrBHV-vectored vaccine deployment strategies. Multi-strain infections were observed in 79% of infected bats and resampling of marked individuals showed strain acquisitions by already infected individuals, implying that pre-existing immunity and strain competition are unlikely to inhibit vaccine spread. Additionally, model fitting using the strain-specific prevalence data suggests that a DrBHV-vectored vaccine can reach a population coverage of >80%, resulting in a 95% decrease in the size of rabies outbreaks. Our results support the development of a transmissible vaccine targeting a major source of rabies in Latin America and show how genomics can enlighten vector selection and deployment strategies for transmissible vaccines.

Indiana Bat Population Response to White-Nose Syndrome Varies with Environmental Conditions and Epidemic Phase
Alexander T. Grimaudo[1], Joseph R. Hoyt[1], Skylar R. Hopkins[2], J. Paul White[3], Joseph A. Kath[4], Gregory G. Turner[5], Bradford J. Westrich[6], Chris Simpson[7], Josh Campbell[7], Daniel R. Istvanko[7], Cory Holliday[8], Rickard S. Toomey[9], Steven C. Thomas[9], William H. Stiver[10], Paul E. Super[10], Ryan H. Williamson[10], Carl J. Herzog[11] and Kate E. Langwig[1]
1 Department of Biological Sciences, Virginia Tech, Blacksburg, USA; 2 Department of Applied Ecology, North Carolina State University, Raleigh, USA; 3 Wisconsin Department of Natural Resources, Bureau of Natural Heritage Conservation, Madison, USA; 4 Illinois Department of Natural Resources, Springfield, USA; 5 Pennsylvania Game Commission, Harrisburg, USA; 6 Indiana Department of Natural Resources, Indianapolis, USA; 7 Tennessee Wildlife Resources Agency, Nashville, USA; 8 Tennessee Chapter of The Nature Conservancy, Granville, USA; 9 Mammoth Cave National Park, Mammoth Cave, USA; 10 Great Smoky Mountains National Park, Gatlinburg, USA; 11 New York Department of Environmental Conservation, Albany USA

Since its emergence in North America, white-nose syndrome (WNS) has caused significant population declines in hibernating bat populations. Environmental conditions within hibernacula, particularly temperature and humidity, are associated with the severity of colony-level declines.

However, host-pathogen coevolution also contributes to colony response and can modify the environmental space in which colonies can persist with WNS. Therefore, as host-pathogen coevolution deepens over time, environmental associations with colony response may change rather than remain static. Here, we pair information on environmental conditions within hibernacula with population datasets to explore the dynamic nature of these associations in the Indiana bat, a species of high conservation concern. We find that Indiana bat colonies displayed variable responses to WNS, with both colony extirpation and stabilization occurring. Immediately following pathogen invasion, environmental dependence of disease resulted in high population declines in the coldest and wettest hibernacula. However, years following pathogen invasion, this association weakens towards the neutral association observed prior to WNS. This suggests that host populations are sensitive to environmental conditions early in the epidemic when the depth of host-pathogen coevolutionary history is at its most shallow point. However, as the epidemic progresses and the host and pathogen extend their coevolutionary history, the breadth of the environmental space in which the host can exist with the pathogen widens, weakening the association between temperature, humidity, and colony response to WNS. Ultimately, this illustrates that environmental contributions to colony response is a dynamic association that varies over time since pathogen invasion and host-pathogen coevolutionary history.

On the Cusp of Adaptive Change: Patterns of Molar Morphological Evolution During the Phyllostomid Radiation

David M. Grossnickle[1], Alexa Sadier[2], Edward Patterson[1], Karen E. Sears[2] and Sharlene E. Santana[1,3]
1 Department of Biology, University of Washington, Seattle, USA; 2 Department of Ecology and Evolutionary Biology, University of California Los Angeles, USA; 3 Burke Museum of Natural History and Culture, University of Washington, Seattle, USA

Adaptive radiations are key to understanding phenotypic evolution and form-function relationships, but there remains considerable uncertainty about their extrinsic and intrinsic drivers. The Phyllostomidae radiation is marked by extensive craniodental adaptations for diverse diets, and we use their molars as a model to investigate the factors that catalyze and/or constrain evolutionary change. Using micro-computed tomography scans of skulls of 125 species of Noctilionoidea (Phyllostomidae and close relatives), we quantified the three-dimensional shapes of first lower molars via geometric morphometrics. The two primary axes of morphological variation reflect relative molar widths and cusp heights, respectively, indicating that these traits may be linked to the early diversification of phyllostomids. Phylogenetic comparative analyses of 3D molar shape further revealed a striking pattern: faunivores' (primarily insectivore) molars exhibit relatively low morphological disparity and slow evolutionary rates, and most omnivores have faunivore-like molars. The molars of faunivores and omnivores occupy a distinct, likely ancestral, region of morphospace. In contrast, the molars of frugivores and nectarivores exhibit faster evolutionary rates and appear to occupy distinct, broad adaptive zones. Sanguivores have extremely derived dentitions and represent an additional morphotype that diverged from the ancestral morphology. These results suggest that during the phyllostomid radiation, strong selective pressures related to shifts to derived diets were necessary to 'free' molar morphologies from the ancestral morphotype, but once free, molars exhibited considerable evolvability, diversifying morphologically in-step with diet.

An Updated Review of Hypotheses Regarding Bat Attraction to Wind Turbines

Emma E. Guest[1], Brittany F. Stamps[2], Nevin D. Durish[3], Amanda M. Hale[4], Cris D. Hein[5], Brogan P. Morton[6], Sara P. Weaver[1] and Sarah R. Fritts[2]
1 Bowman, San Marcos, USA; 2 Department of Biology, Texas State University, San Marcos, USA; 3 ESE Partners, LLC, Austin, USA; 4 Department of Biology, Texas Christian University, Fort Worth, USA; 5 National Renewable Energy Laboratory, Arvada, USA; 6 Wildlife Imaging Systems, Hinesburg, USA

Patterns of bat activity and mortalities at wind energy facilities suggest that bats are attracted to wind turbines based on bat behavioral responses to wind turbines. For example, current monitoring efforts suggest that bat activity increases post-wind turbine construction, with bats making multiple passes near wind turbines. We separated the attraction hypothesis into five previously proposed explanations of bat interactions at or near wind turbines, including attraction based on noise, roost sites, foraging and water, mating behavior, and lights, and one new hypothesis regarding olfaction, and provide a state of the knowledge in 2022. Our review indicates that future research should prioritize attraction based on social behaviors, such as mating and scent-marking, as this aspect of the attraction hypothesis has many postulates and remains the most unclear. Relatively more data regarding attraction to wind turbines based on lighting and noise emission exist, and these data indicate that these are unlikely attractants. Analyzing attraction at the species-level should be prioritized because of differences in foraging, flight, and social behavior among bat species. Lastly, research assessing bat attraction at various scales, such as the turbine or facility scale, is lacking, which could provide important insights for both wind turbine siting decisions and bat mortality minimization strategies. Identifying the causes of bat interactions with wind turbines is critical for developing effective impact minimization strategies.

Seasonal Reproductive Synchrony in Colonies of the *Artibeus jamaicensis* in Southeast Mexico

Edgar G. Gutiérrez[1], Jorge Ortega[1], Diana D. Moreno-Santillán[2] and M. Cristina MacSwiney G[3]
1 Departamento de Zoología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México City, MEX; 2 Department of Integrative Biology, University of California, Berkeley, CA 92697, USA; 3 Centro de Investigaciones Tropicales, Universidad Veracruzana, Calle José María Morelos 44. Centro, C. P. 91000 Xalapa, Veracruz, MEX

In tropical ecosystems, environmental conditions are often less constraining, leading to an increase in the reproductive potential of several species of mammals. One of the strategies to enhance this reproductive potential is to exhibit postpartum oestrus, which is common among different bat families. In the Yucatan Peninsula, we observed for over 2 years two colonies of marked individuals of the Jamaican fruit–eating bat, *Artibeus jamaicensis* to determine their reproductive activity. Females presented postpartum oestrus that allows them to have a second annual parturition. During the peak period of parturition, a marked increase in attempts and successful mating events were observed among the bats roosting within the caves. Births were recorded but in lower proportion in the remaining months of the year; however, no copulation attempts or matings were recorded from October to January in both caves and in both years. A delayed embryonic development after the second birth might explain the continuous parturition events recorded for *A. jamaicensis* in Yucatan.

Differences in Hibernation Strategy of Bats in Relation to Physical Characteristics and Availability of Hibernacula

Ralf Gyselings[1], Luc De Bruyn[1,2], Frank Van Gorp[3], Dirk Swaenen[3], Lucinda Kirkpatrick[2], Alek Rachwald[4], Grzegorz Apoznanski[5] and Tomasz Kokurewicz[5]
1 Research Institute for Nature and Forest, Brussels, BEL; 2 Evolutionary Ecology Group, University of Antwerp, Antwerp, BEL; 3 Natuurpunt, Mechelen, BEL; 4 Forest Ecology Department, Forest Research Institute, Sękocin Stary, Raszyn, POL; 5 Department of Vertebrate Ecology and Paleontology, Wrocław University of Environmental and Life Sciences, Wrocław, POL

Bat hibernation in relation to thermal variability has been addressed in several studies. However, the distinction between long-term variability and short-term variability in temperature has rarely been made. Most studies assume that a higher seasonal variability, giving rise to lower mid-winter temperatures, implies a higher short-term variability. The relationship between both, however, is strongly dependent on structural characteristics of the hibernaculum. We studied the evolution of temperature and temperature variability over the winter season in different types of hibernacula, ranging from underground tunnels to above ground structures, using temperature loggers. The study was conducted in Belgium and Poland, two countries with a different winter climate. We carried out bat surveys in these hibernacula in the beginning, in the middle and at the end of the winter season. Smaller less insulated objects reach generally cold temperatures as the winter prolongs, which in more insulated or underground systems are only reached near the entrance. Thermal variability at these cold temperatures in the latter however is larger. Several species use all types of systems, but with a different phenology. Bats hibernating in generally colder hibernacula tend to hibernate longer. This pattern is consistent over both countries with different winter climates, indicating bats have different hibernation strategies they can use. We discuss the use of different strategies in relation to the physical environment and availability of hibernation sites in the framework of optimal hibernation theory.

Genetic Evaluation of the Distribution and Interactions Between *Lasiurus borealis* and *Lasiurus blossevillii* in the Southwest
Zeinab (Rose) Haidar and Juan Emmanuel Vezquez
Department of Biology, Humboldt State University, Arcata USA

Recognized as having highly dynamic movements and specialized life histories, members of the genus *Lasiurus*, commonly named tree bats, have uncertain and disputed ranges. Several recent accounts of overlap, historic misidentification, and possible phylogenetic variations regarding two species of this genus; western red bat (*Lasiurus frantzii*) and eastern red bat (*Lasiurus borealis*) in California, Arizona, Utah, and New Mexico have cast doubt on our understanding of their distribution, speciation, and assumed spatial allopatry. With the use of genetic sequencing utilizing tissues collected from museum and field specimens throughout California and adjoining states we can infer historic and current distribution and identify genetic variation. Appropriate species classification by region is currently being achieved utilizing mitochondrial DNA, and a more comprehensive analysis at the nuclear and genomic level will be accomplished through lower coverage whole genome sequencing. All samples include morphometrics and pelage records for identifying possible congruence in segregating the species phenotypically in hand. Currently in the first year of our study we have confirmed *Lasiurus borealis* in 4 counties in California since the early 1990's, and one county in Arizona, and have preliminary analysis and conclusively regarding phenotypic differentiation between *L. borealis* and *L. blossevillii*. As our study continues, further analysis and collection will lead to more meaningful and comprehensive results. The results acquired from this study will strengthen our limited understanding of this dynamic group by inferring on their basic biology, their distinctive characteristics, and altogether aid in future conservation and research.

Quantifying Bat Flight Abilities During Natural Pursuit of Insect Prey
Jonas Håkansson[1], Brooke L. Quinn[2], Abigail Shultz[1], Sharon M. Swartz[2] and Aaron J. Corcoran[1]
1 Department of Biology, University of Colorado, Colorado Springs, Colorado Springs, USA; 2 Department of Ecology, Evolution, and Organismal Biology, Brown University, Providence, USA

Bat flight has long been a model system in the study of ecomorphology. However, many predictions, such as the use of wing loading and aspect ratio as indicators of bat flight niche, are based on aerodynamic theory that lacks rigorous empirical validation. Studies of bats in wind tunnels have provided a basis for understanding straight flight of bats, however maneuvering flight has received much less attention. Here, we present our progress on developing and applying methods to quantify the flight of bats exhibiting a range of natural behaviors as they hunt insects. We used high-speed infrared videography to film four bat species hunting insects either in a large flight tent or under natural conditions. We analyzed level turns during these flight bouts by tracking 16 points on the bat's body with markerless automated tracking algorithms based on artificial intelligence using the software package DeepLabCut. This was combined with custom 3-D reconstruction techniques that convert 2-D detections into real world 3-D coordinates. We first show results validating the accuracy of this method by comparing it to traditional tracking techniques involving humans manually digitizing videos. We then show results comparing the maneuvering abilities of bats as they relate to predictions based on their morphology and aerodynamic theory. Preliminary kinematic analysis indicates that bats have a high degree of redundancy in how they perform maneuvering flight, which reflects the complexity of their many-jointed living-tissue flight apparatus. Supported by NSF IOS-1931135 to AC and SS.

Island Endemic Frugivorous and Nectarivorous Bats Show Opposite Patterns of Morphological Extremity
Ronald P Hall and Elizabeth R Dumont
Quantitative and Systems Biology, University of California, Merced, USA

Islands have a long history as a tool for ecologists and evolutionary biologists. As natural experiments, islands have done much to inform our collective understanding of processes such as extinction, colonization, and speciation. The impact of island colonization and subsequent adaptation to local environments is known to have caused both increased dietary specialization and dietary generalization. The circumstances that generate these patterns are specific to the evolutionary history of the colonizing species. The Caribbean's many archipelagos serve as an excellent system to investigate the nature of specialization because they contain many closely adjacent islands that vary in size and habitat structure. Phyllostomid bats exhibit a broad range of dietary strategies and morphological adaptations. Additionally, they have colonized the Caribbean multiple times throughout their evolutionary history. These two factors together make them an excellent organism to study the influence of island colonization on dietary specialization and generalization. Using linear measurements of palate length and width from 82 species as a proxy for morphological specialization, in conjunction with observational dietary data, we found distinct patterns of morphology between mainland species and island endemic species, dependent on the lineage and diet. Specifically, island endemic frugivores from the stenodermatine family are consistently highly morphologically extreme, while island endemic nectarivores from the glossophagine family are consistently less morphologically extreme than their mainland counterparts.

Evidence of Rare Pigment Loss and Genetic Population Divergence in Townsend's Big-Eared Bats
Natalie M. Hamilton[1], Jessica E. Light[2] and Michael M. Morrison[1]
1 Texas A&M University, Department of Rangeland, Wildlife, and Fisheries Management, College Station, USA; 2 Texas A&M University, Department of Ecology and Conservation Biology, College Station, USA

Populations of Townsend's big-eared bats (*Corynorhinus townsendii townsendii*) in the Inyo and White Mountains and the adjacent Sierra Nevada have been monitored as part of a long-term study. This study includes monitoring summer maternity colonies, tagging individuals with Passive Integrated Transponder tags and taking tissue punches from wing and tail membranes for genetic analyses. In the summers of 2020-2021, individuals from maternity roost at Doris Dee Mine presented with notable hypopigmentation patterns – variable patches of white spots on the body and wings (piebaldism). This pattern may be due to environmental causes (i.e., age, injury, chemical interaction) or genetic origin (as a result of inbreeding, low genetic diversity, or genetic drift). It is important to conservation efforts to understand if there are environmental stressors that need to be mitigated or if this population is an independent conservation unit. To explore underlying causes of pigment loss in this colony, we used 9 polymorphic microsatellite markers to compare genetic diversity of this population to other populations of *C. t. townsendii* in our study area. We tested for a recent population bottleneck and genetic population structure between roosts at nuclear and mitochondrial levels. Our analyses reveal that Doris Dee roost exhibits signs of inbreeding and this roost is isolated from nearby colonies. The genetic isolation of Doris Dee is an unexpected result as other roosts within the area appear to be panmictic. Future work examining hibernating colonies and breeding areas can give insight into how this colony has become genetically isolated from nearby roosts.

Spatial and Temporal Patterns of Abandoned Mine Occupancy by Townsend's Big-eared Bat (*Corynorhinus townsendii*)

Laura M. S. Hancock[1], Jason A. Williams[2], Bryan T. Hamilton[3] and Richard E. Sherwin[4]
1 Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, Amherst, USA; 2 Nevada Department of Wildlife, Ely, USA; 3 Great Basin National Park, Baker, USA; 4 Organismal and Environmental Biology, Christopher Newport University, Newport News, USA

Townsend's big-eared bats (*Corynorhinus townsendii*) are widely distributed in the western United States and largely dependent on subterranean roosting habitat (e.g., abandoned mines and caves) in most of their range. However, information about mechanistic roosting associations is largely based on spatially and temporally limited data (e.g., roost site and seasonally specific). Since this species is a conservation priority in much of the U.S., it is critical to understand patterns of roost occupancy, both within and among years, at biologically appropriate spatial scales. To close this knowledge gap, we compiled a database of approximately 3,500 roost surveys (e.g., abandoned mine surveys) conducted between 2006 and 2021 across Nevada. Three hundred-seventy of the sites (10.6%) were occupied by at least one *C. townsendii* individual at the time of survey, indicating day roosting habitat. Additional sites showed probable night roosting or periodic day roosting use by *C. townsendii* as evidenced by presence of guano and/or moth wings. Preliminary statistical analyses (Akaike Information Criterion) indicate that aspect of portal opening and elevation of portal are the best indicators of use. Further statistical analyses will elucidate: 1) if spatial and temporal patterns of occupancy are evident across the landscape, and 2) the relative importance of roost site versus landscape characteristics on predicting occupancy.

Modelling Acoustic Behaviour of Echolocating Bats in Group Flight

Kazuma Hase[1,2], Seiya Oka[3], Tasuku Miyazaki[3], Hiraku Nishimori[4], Masashi Shiraishi[4], Osamu Yamanaka[4], Ken Yoda[2], Kohta I. Kobayasi[3] and Shizuko Hiryu[3]
1 Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN; 2 Graduate School of Environmental Studies, Nagoya University, Nagoya, JPN; 3 Faculty of Life and Medical Sciences, Doshisha University, Kyotanabe, JPN; 4 Meiji Institute for Advanced Study of Mathematical Sciences, Meiji University, Tokyo, JPN

Echolocating bats emit ultrasonic pulses and listen to returning echoes for orientation and prey detection. When bats fly together, calls emitted from group members create acoustically complex situations. Previous work on the eastern bent-winged bat (*Miniopterus fuliginosus*) found bats increased differences in their terminal call frequency when flying in a group, likely to avoid mutual interference. The mechanism(s) of this frequency-adjusting behavior remain unknown. We presented jamming sounds mimicking conspecific echolocation to lone *M. fuliginosus* carrying a telemetry microphone and observed that bats increased the shift in their terminal call frequency as the repetition rate of the jamming stimulus increased. We simulated this frequency-adjusting behavior in response to conspecific echolocation using a leaky-integrator computational model, where each bat increased its terminal frequency by integrating acoustic input from group members. The input was the sum of the acoustic power of all group members, with each emitted pulse attenuated by the directionality and distance to the model bat. When there was no acoustic input, there was no change in the terminal frequency of the model bat. When acoustic input was provided, the model bat was more sensitive when the frequency of the jamming stimulus was lower than the terminal call frequency, as observed in behavioral studies. Simulated bats increased differences in the terminal frequencies of individuals in the group, as observed in real bats. These results suggest that the frequency-adjusting behavior of bats flying in a group, which involves complex audio-vocal interactions and decision making, can be explained by relatively simple rules.

Building Local Conservation Capacity for Bats: A Case Study in Belize

Quentin R. Hays[1,2], Vanessa L. Kilburn[2] and Gliselle Marin[2]
1 Wildlife Program, GeoSystems Analysis, Inc., Corvallis, USA; 2 Toucan Ridge Ecology and Education Society, St. Margaret, BLZ

It is generally accepted that developing long-term solutions for research and conservation needs involves building local capacity. In many of the most biodiverse regions globally, such as the Neotropics, research and management infrastructure may be lacking and training for local conservationists difficult to obtain. The Toucan Ridge Ecology and Education Society (T.R.E.E.S) operates a biological field station in the foothills of the Maya Mountains in the Stann Creek District of Belize, Central America. For more than 10 years T.R.E.E.S has offered educational programs, including training workshops and research internships. Recently, the Programa de conservacion de los murciélagos de Belice (PCMBe) was created at T.R.E.E.S to further the goals of Red Latinoamericana y del Caribe para la Conservación de los Murciélagos (RELCOM), including promoting and stimulating the generation of scientific knowledge that contributes to the conservation of bats and their habitats. Beginning in 2018, biannual Neotropical Bat Capture and Acoustic Survey Techniques Workshops were initiated with PCMBe, with the goal of leveraging the financial support of international attendees to provide gratis training for Belizeans. To date, six workshops have been held and nine Belizeans have successfully completed training, including four that participated in facility-based seasonal internships. In addition, a trainee is now completing a research study examining bat communities in organic versus non-organic agricultural settings in lowland broadleaf forest. Our model provides a template for furthering RELCOM goals and building local conservation capacity for bats in the Neotropics by leveraging the financial support and educational capacity of training workshops.

A Global Review of Phylogeographic Studies on Bats

Giovani Hernández-Canchola[1], Luis D. Verde Arregoitia[2], Pablo Colunga-Salas[3], Yire A. Gómez-Jiménez[4] and Livia León-Paniagua[4]

1 Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de México, MEX; 2 Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Valdivia, CHL; 3 Instituto de Biotecnología y Ecología Aplicada, Universidad Veracruzana, Xalapa-Enriquez, MEX; 4 Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México, MEX

Phylogeography focuses on understanding the mechanisms that have led to the geographic distribution of genetic lineages within species, and studies of mammals have had an important role in its development. Bats are the second most diverse order of mammals; however, they are the subject of fewer phylogeographic studies than less diverse orders of mammals. Herein, we review the global state of phylogeographic bat research. Mitochondrial DNA loci are the most popular molecular markers, and the majority of studies describe geographic patterns of genetic variation. Many phylogeographic surveys were done in the Paleartic (mainly in the family Vespertilionidae), but more species have been studied in the Afrotropics and Neotropics (mainly in Pteropodidae and Phyllostomidae, respectively). Pleistocene climatic change is the main factor that has shaped the genetic diversity of species, but geographical and ecological factors are other important drivers of intraspecific differentiation. More intraspecific phylogeographic studies on bats are needed, but it is also necessary to develop comparative, integrative, and statistical approaches. Bats are excellent models for addressing evolutionary, ecological, and theoretical questions, given their world-wide distribution and their great biological heterogeneity. Annual meetings of the North American Society for Bat Research (NASBR) have contributed to the development of this field of molecular evolution, and we propose some future directions for phylogeographic research on bats.

Molecular Interactions of a Bat Coronavirus With its Natural Host

Isabel Arely Hernández-Dávila[1], Noreen Rapin[1], Darryl Falzarano[1,2] and Vikram Misra[1]
1 Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, CAN; 2 Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, CAN

Coronaviruses related to those that cause Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) have been found in bats leading to the misconception that bats have caused these diseases. While there is considerable research on how coronaviruses cause disease, little is known about the benign relationship of bat coronaviruses with their natural hosts. Our goal is to study how the Myotis coronavirus (Myl-CoV) interacts with its evolutionary host, the little brown bat (*Myotis lucifugus*). Our initial objective is to identify the receptor for Myl-CoV. We hypothesize that the Myl-CoV receptor will bind to one of the common receptors for coronaviruses: aminopeptidase N (APN), angiotensin converting enzyme (ACE2) or dipeptidyl peptidase (DPP4). We predicted the interaction between Myl-CoV and the potential receptors by in silico analysis using HADDOCK Web Server, showing that APN is presumably the Myl-CoV receptor. Since lungs and intestines are the primary site of infection for most coronaviruses and Myl-CoV has only been detected in intestines, we also hypothesized that bat intestines – will contain higher levels of the potential receptor than lungs. Results from qRT-PCR showed that APN and ACE2 transcripts are higher in intestines than lungs of uninfected bats. Moreover, comparison between infected and uninfected bats demonstrated that APN and ACE2 are overexpressed in the Myl-CoV infected bats, suggesting that any of them could be the receptors of the bat coronavirus.

Immediate Response of Bats to Prescribed Fire in the Sumter National Forest

Zebria S. Hicks[1] and Susan C. Loeb[2]
1 Forestry and Environmental Conservation, Clemson University, Clemson, USA 2 U.S. Forest Service, Southern Research Station, Clemson, USA

Prescribed fire is a frequently used management technique in the southeastern United States. Fire can change vertical structure, diversity of vegetation, and insect abundance. To inform this management practice, it is important to understand its impact on species vital to the ecosystem, such as bats. The goal of this study was to determine if prescribed fire has a positive, neutral, or negative effect on bat behavior immediately following prescribed fire. We recorded bat activity after fires conducted February−April 2022 in northwestern South Carolina using Anabat Express ultrasonic detectors. Burned and control sites within hardwood and pine stands were monitored each night for two weeks following prescribed fires. We also collected prey availability at each site using sticky traps. We interpreted an increase in bat activity as a positive effect, while a decrease in activity was seen as a negative effect. We recorded a total of 2,035 calls with 502 in hardwood controls, 228 in pine controls, 472 in hardwood burns, and 1,101 in pine burns. There was no significant difference in mean number of calls per night in burned and control hardwood stands (p = 0.05) but there were significantly more calls per night in burned pine stands than control pine stands (p = 0.05). Insect abundance did not differ significantly between burned and control sites for pine or hardwood stands (p = 0.05). Our data suggest that prescribed fire can have a neutral or positive effect on bat behavior depending on vegetation type more than prey availability.

Hierarchical Multi-method Occupancy Estimates Inform Disease Surveillance from Bats in Cambodia

Alan T. Hitch[1], Neil M. Furey[2], Chor Kimshalen[3], Buor Vuthy[3], Yim Raksmey[4], Sophie A. Borthwick[5], Gavin J.D. Smith[5,6], Chheang Dany[3] and Ian H. Mendenhall[5,6]
1 Museum of Wildlife and Fish Biology, Department of Wildlife, Fish, and Conservation Biology, University of California at Davis, Davis, USA; 2 Fauna & Flora International, Phnom Penh, KHM; 3 Forestry Administration, Phnom Penh, KHM; 4 Centre for Biodiversity Conservation, Department of Biology, Faculty of Science, Royal University of Phnom Penh, Phnom Penh, KHM; 5 Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore, SGP; 6 SingHealth Duke-NUS Global Health Institute, SingHealth Duke-NUS Academic Medical Centre, Singapore, SGP

An important component of disease surveillance is the spatial relationship of pathogen reservoirs. The nexus of disease ecology and vertebrate ecology is the habitat relationship model. We used a hierarchical multi-method occupancy model to model habitat relationships of bats in Cambodia to support disease surveillance efforts. Sites were selected from a stratified random sample based on habitat class. Bats were sampled using mist net arrays and acoustic detectors at 227 sites across Cambodia. Forty-five species were detected using mist net arrays, and 39 species were detected by acoustic detectors. We developed a bat call reference library for identifying anonymous call data to species or species group. We manually vetted acoustic data using Scan'R software and a R-language shiny app 'SZapp'. We estimated detectability for all species and survey method. Detectability varied among species and survey method. Model averaged estimates of detectability were then used to estimate probability of species occupancy by habitat class. Pathogen presence/absence was included as a covariate in the occupancy model and estimates of pathogen probability of occupancy by habitat were calculated. These estimates were used to develop probabilistic risk maps of pathogen prevalence. A hierarchical multi-method occupancy framework is a practical approach to estimating the spatial prevalence of pathogens, and averaged estimates of detectability allow more precise and accurate estimates of occupancy, especially with species where a single survey method only captures a small proportion of the species assemblage.

Coastal Living: Island Habitat Refugia Support Population Persistence of *Myotis septentrionalis*
Samantha Hoff[1,2], Casey J. Pendergast[1,2], Luanne Johnson[3], Elizabeth Olson[3], Danielle O'Dell[4], Carl J. Herzog[2] and Wendy C. Turner[5]
1 Department of Biological Sciences, University at Albany, Albany, USA; 2 New York State Department of Conservation, Albany USA; 3 BiodiversityWorks, Martha's Vineyard USA; 4 Nantucket Conservation Foundation, Nantucket USA; 5 Wisconsin Cooperative Wildlife Research Unit, Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Madison, USA

Since the arrival of white-nose syndrome (WNS) in North America, *Myotis septentrionalis* have experienced widespread population declines (<90%) throughout much of their range, prompting a proposal to reclassify the species as federally Endangered. Despite this, some remnant populations along the Atlantic Coast are persisting with evidence of multi-year survivors and successful reproduction. Our research investigated the mechanisms supporting survival on Long Island NY, Martha's Vineyard MA, and Nantucket MA. We radio-tracked bats during fall to document behavior and conducted acoustic studies and insect sampling to determine seasonal activity patterns and prey availability. Between 2017–2020, we captured 68 *Myotis septentrionalis*, 54 of which were tracked to 85 unique roosts from 547 relocation events. Roost characteristics varied by island, largely reflecting local landscape composition and structure. Over 25% of roosts were anthropogenic structures, with Nantucket and Martha's Vineyard bats using a significantly larger proportion compared to Long Island. Tree roosts were characterized by large diameters, early decay stages, and high percentages of canopy cover. Residency time was significantly higher in anthropogenic roosts (5.3 days vs. 3.6 days) and use of these structures increased as the season progressed. We identified local hibernation in anthropogenic structures, periodic winter activity coinciding with insect presence, and a shorter hibernation season compared to the mainland, which together may have allowed these populations to far better. Given the limitations of winter habitat availability and lack of protection for bats in these structures, our future focus is providing safe hibernation structures to ensure persistence of these remnant populations.

Passive Acoustic Monitoring Yields Informative Bat Population Density Estimates
Meredith L. Hoggatt, *Clarissa A. Starbuck and Joy M. O'Keefe
Department of Natural Resources and Environmental Sciences, University of Illinois at Urbana-Champaign, Urbana, USA

Bat population estimates are typically made during winter, though this is only feasible for bats that aggregate in hibernacula. While it is essential to measure summer bat population sizes for management, we lack a reliable method. Acoustic surveys should be less expensive and more efficient than capture surveys, and acoustic activity data are already used as indices of population size. Although we currently cannot differentiate individual bats by their calls, we can enter call counts, information on signal and detection angles, and weather data into generalized random encounter models to estimate bat density. We assessed the utility of generalized random encounter models for estimating Indiana bat (*Myotis sodalis*) population density with acoustic data collected at 60 total sites in six conservation areas in northeast Missouri, 2019–2021. We tested the effects of year, volancy period, conservation area, and their interactions on estimated density. Volancy period was the best predictor, with predicted density increasing 61% from pre-volancy (83 bats/km2) to post-volancy (134 bats/km2); however, the magnitude of the effect differed by conservation area. We showed that passive acoustic surveys yield informative density estimates that are responsive to temporal changes in bat population size, which suggests this method may be useful for long-term monitoring. However, we need more information to choose the most appropriate values for the density estimation formula. Future work to refine this approach should include assessments of bat behavior and detection parameters and testing the method's efficacy in areas where population sizes are known.

Non-invasive Diet Analysis of Bats in a Productive Agricultural Region Using DNA Metabarcoding
Ann Holmes[1,2], Leila Harris[2], Khyana Yearwood[1], Serra Perry[1], Shayan Kaveh[1] and Andrea Schreier[1]
1 Department of Animal Science, University of California, Davis, USA; 2 Graduate Group in Ecology, University of California-Davis, Davis, USA

Insectivorous bats can provide valuable ecosystem services for agriculture. Conventional diet analysis by fecal pellet dissection is limited to relatively small sample sizes, mostly hard-bodied prey, and requires taxonomic expertise in arthropods. DNA metabarcoding can overcome these limitations and identifies partially digested prey, often with high taxonomic resolution. We analyzed guano samples from a large colony dominated by Mexican free-tailed bats (*Tadarida brasiliensis*) roosting in California's Central Valley agricultural region. Guano was non-invasively sampled twice weekly over 12 weeks throughout pupping and lactation, a crucial period for the survival of pups. DNA was extracted from pooled guano samples and sequenced on an Illumina MiSeq using a COI genetic barcode previously validated in diet analysis of insectivorous bats. With few historical data points on regional bat diets for comparison, our results broadly reflect data from guano dissection showing dipterans (mosquitoes, midges, crane flies, and flies), moths, and beetles as the most frequently detected taxonomic groups. Rarer taxa detected included parasitic mites (Arachnida: Mesostigmata), presumably consumed via grooming, and crickets (Orthoptera: Gyrallidae). Our results provide a higher taxonomic resolution of prey compared with gut dissection, especially for moth taxa. Detection of agricultural pests (moths) and disease vectors (mosquitoes) suggests that bats may contribute to agricultural productivity and help reduce the need for insecticides. A nuanced understanding of bat diets can be used to guide conservation and management of wild populations.

Torpid Metabolic Rate, but Not Evaporative Water Loss, Scales Allometrically in 12 Species of Hibernating Bats
Lily Hou[1], Catherine G. Haase[2] and Liam P. McGuire[1]
1 Department of Biology, University of Waterloo, Waterloo, CAN; 2 Department of Biology, Austin Peay State University, Clarksville, USA

Hibernation has long been recognized as an energetic challenge, but the importance of water balance in hibernation has been increasingly recognized. Hibernators must manage energy and water over weeks or months, including trade-offs in these currencies (e.g., dehydration can trigger energetically demanding arousals). The relative influence of energy and water may drive differences in hibernation strategies, which may be related to differences in body size and surface area among species. As with many other morphological and physiological features, metabolic rate scales allometrically with body size. Evaporative water loss (EWL) during torpor should also scale with body size as it relates to metabolic rate and cutaneous surface area. Using respirometry data collected from 378 individuals across 12 species of hibernating North American bats (body mass: 4.4 to 21.9 g), we assessed the allometric scaling of torpid metabolic rate (TMR) and rate of total EWL. As expected, TMR scaled with body mass (scaling exponent = 0.71), but there was no relationship between rate of total EWL and body mass. Independent of body mass, whole animal rates of water loss during torpor were similar among species. This finding suggests that bats have adaptations that modulate evaporation, likely related to cutaneous water loss which dominates over respiratory water loss in the torpid state. Mass-specific TMR scaled with body mass as expected (scaling exponent = -0.27), whereas the scaling exponent of mass-specific total EWL was -0.82. This suggests that water loss may be relatively more influential on the hibernation strategies of species than energetics.

Investigating the Effects of Wildfire and Urbanization on Bats Within the Mediterranean Ecosystem of Southern California
Dillan J. Hoyt[1,2], Nathan C. Gregory[2,3] and Orly Razgour[1]
1 University of Exeter, Department of Biosciences, Exeter, GBR; 2 Jersey International Centre of Advanced Studies, Channel Islands, GBR; 3, The Irvine Ranch Conservancy, Irvine, USA

The globally rare Mediterranean ecosystem of Southern California is one of the most fire-prone ecosystems in North America, however little is known about the effects of increased wildfire frequency and a rapidly expanding wildland urban interface (WUI) on biodiversity within this ecosystem. We use bats as models to assess how these multiple stressors interact to affect Mediterranean biodiversity, due to their abundance and sensitivity to environmental change. Using bioacoustics, we investigate whether habitat type, urban structures, year since last wildfire and inter-fire intervals influence bat activity and community composition. Time since wildfire had no effect on bat activity and species richness, however generalized linear model selection revealed that the interaction between inter-fire intervals and habitat type best explained bat activity. Roads appeared to have a positive effect on the activity of bats that emit echolocation calls at low frequencies (Fc <33 kHz), whereas several *Myotis* species and *Parastrellus hesperus* activity increased with distance to roads. Bats that echolocate at high frequencies (Fc >33kHz) were most active within woodland habitats than any other habitat type. These results highlight the importance of sustaining a pyro-diverse and heterogenous landscape to promote bat species richness and activity throughout the Mediterranean Type Ecosystem (MTE) of Southern California, and further efforts to investigate the effects of pressures relating to climate change and development on native biodiversity within MTEs are paramount to their protection.

Conserving Bats in East Asia: Species Status and Trends
Joseph R. Hoyt[1], Keping Sun[2,3], Aoqiang Li[2], Zhongle Li[2], Xiaobin Huang[4], Haixia Leng[2], Yue Zhu[2], Muneki Sakuyama[5], Syuuji Yachimori[6], Akiyoshi Sato[7], Yushi Osawa[8], Keiko Osawa[8], Ami Hamada[9], Koji Harashina[9], Toshiki Aoi[9], Yu-Seong Choi[10], Ariunbold Jargalsaikhan[11,12], Munkhnast Dalannast[11], Sun-sook Kim[13], Dai Fukui[14] and Jiang Feng[2,15]
1 Department of Biological Sciences, Virginia Polytechnic Institute, Blacksburg, VA, USA; 2 Jilin Provincial Key Laboratory of Animal Resource Conservation and Utilization, Northeast Normal University, Changchun, CHN; 3 Key Laboratory of Vegetation Ecology, Ministry of Education, Changchun, CHN; 4 School of Basic Medical Sciences, Dali University, Yunnan, CHN; 5 Association of Bat Conservation in Northeast JPN, Morioka, Iwate, JPN; 6 Shikoku Institute of Natural History, Kochi, JPN; 7 Almas Ltd. Co., Saitama, JPN; 8 Bat Study and Conservation, JPN; 9 Department of Agriculture, Iwate University, Morioka, JPN; 10 National Migratory Bird Center, National Institute of Biological Resources, Ongjin-gun, Incheon, KOR; 11 Bat Research Center of Mongolia, Ulaanbaatar, MNG; 12 Department of Biology, Mongolian State University of Education, Ulaanbaatar, MNG; 13 Division of Ecological Applications, National Institute of Ecology, Seocheon, KOR; 14 University of Tokyo Hokkaido Forest, University of Tokyo, Furano, Hokkaido, JPN; 15 Jilin Agricultural University, Changchun, CHN

The conservation of bat species is of paramount importance for the preservation of global biodiversity, the health of ecosystems, and their agroecological significance. Bats face numerous threats including habitat loss, infectious diseases, climate change, and human persecution. Conservation efforts have finite resources which can only be directed towards the most vulnerable species. However, the population status of most bat species remains unknown, making directing these limited resources difficult. There is a high proportion of bat species in East Asia that remain data deficient. Given the numerous threats they face, evaluation of bat population trends is urgently needed. Here we present an assessment of 13 bat species across 146 colonies in East Asia. We find that population trends vary among species and countries. At least one species of bat shows declining populations over the last decade and several other species warrant continued monitoring and further investigation. These findings will help direct much needed conservation efforts and highlight the importance of ongoing bat conservation efforts across this region.

Fruit Bat Migration Matches the Green Wave in Africa
Edward Hurme[1,2,3], Jakob Fahr[1,3], Eidolon Monitoring Network[4], Eric Bakwo Fils[5], C. Tom Hash[6], M. Teague O'Mara[1,7], Heidi Richter[8], Iroro Tanshi[9,10], Paul W. Webala[11], Natalie Weber[1,2], Martin Wikelski[1,2,3] and Dina K. N. Dechmann[1,2,3]
1 Department of Migration, Max Planck Institute of Animal Behavior, Radolfzell, DEU; 2 Centre for the Advanced Study of Collective Behaviour, University of Konstanz, Konstanz, DEU; 3 Department of Biology, University of Konstanz, Konstanz, DEU; 4 Eidolon Monitoring Network, www.eidolonmonitoring.com; 5 Department of Biological Sciences, Faculty of Sciences, University of Maroua, CMR; 6 ICRISAT Sahelian Center, Niamey, NER; 7 Southeastern Louisiana University, Hammond, USA; 8 Department of Biology, Bellevue College, Bellevue, USA; 9 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 10 Department of Animal and Environmental Biology, University of Benin, Benin City, NER; 11 Department of Forestry and Wildlife Management, Maasai Mara University, Narok, KEN

Many migrating animals respond to seasonal changes in the environment and often match peaks in resource abundance. However, it is unclear if and how frugivorous animals use phenological events to time migration, especially in the tropics. The straw-colored fruit bat (*Eidolon helvum*), Africa's most gregarious fruit bat, forms large seasonal colonies through much of sub-Saharan Africa. We hypothesized that aggregations of *E. helvum* match the timing of their migration with phenologies of plant growth or precipitation. Using monthly colony counts from across much of the species' range, we matched peak colony size to landscape phenologies and explored the variation among colonies matching the overall closest phenological event. Peak colony size was closest to the peak instantaneous rate of green-up, and sites with closer temporal matching were associated with higher maximum greenness, short growing season, and larger peak colony size. *Eidolon helvum* seem to time their migrations to move into highly seasonal landscapes to exploit short-lived explosions of food and may benefit from collective sensing to time migrations. The link between rapid changes in colony size and phenological match may also imply potential collective sensing of the environment. Overall decreasing bat numbers along with various threats might cause this property of large colonies to be lost. Remote sensing data, although, indirectly linked to fruiting events, can potentially be used to globally describe and predict the migration of frugivorous species in a changing world.

Effects of Latitude on Bat Foraging Behavior and Nightly Activity Patterns in Western Canada
Camila Hurtado, Erin Bayne and Matina Kalcounis-Rueppell
Biological Sciences, University of Alberta, Edmonton, CAN

Light levels guide the activity times of bats, as their peak activity tends to align closely to the few hours after sunset and before sunrise. Bats at high latitudes face unique challenges associated with limited night length or a complete absence of darkness during the summer months. Some North American bat species have continental ranges that allow us to examine how timing and duration of darkness influence species-specific behaviors. Using acoustic recordings, we are examining the effects of latitude, night length, and landscape cover on overall and species-specific

nightly activity of bats across a 1930 km transect from Southern Alberta to the Northwest Territories, Canada. From May to September 2021, we acoustically sampled bats in a south (49°N) to north (65°N) transect at 112 sites for a total of 699 recording nights. We found that at southern latitudes a characteristic bimodal pattern of activity, with a large peak after sunset and another peak before sunrise, occurred throughout the sampling period. Northern sites had a unimodal pattern of activity, with a large peak happening after sunset, during the longest days of the year but as nights lengthened, towards the end of summer, the activity curves had the characteristic bimodal pattern. We are also examining the difference in foraging site preference across latitudes and predict that bats living further north will spend more time in the edge and darker interior of the forest compared to bats in the south. We acknowledge our partners, and land guardians of the Dene First Nations of Canada.

Quantifying Hibernation Traits to Predict White-Nose Syndrome Impacts on Bats in the Desert Southwest, United States

Hayden K. Hutcherson[1], Jabe A. Kahawaii[1], Heidi J. Kitchel[1], Harrison Tamayo[1], Angela L. McIntire[2] and Marianne S. Moore[1]
1 College of Integrative Sciences and Arts, Arizona State University, Mesa, USA; 2 Arizona Game and Fish Department, Phoenix, USA

As white-nose syndrome (WNS) moves westward across North America, generating baseline datasets of uninfected hibernating bat populations is critical. Despite the imminent arrival of *Pseudogymnoascus destructans* (*Pd*) to Arizona, little is known about bat hibernation in the Southwest. Thus, our study is monitoring hibernating bats in Arizona to increase knowledge and predict potential WNS impacts on these populations. Utilizing passive acoustic monitoring and internal cave surveys from September 2021 through April 2022, we quantified hibernation length, population sizes and compositions of bats in three north-central Arizona caves. To assess microclimate preferences, we continuously recorded relative humidity and temperature within caves using HOBO data loggers, measured conditions adjacent to roosting bats, and estimated body temperatures using thermal imaging (FLIR T540). Hibernation appeared to last from late November through late February, during which time bats roosted at locations with an average of 5.4ºC (range = -0.4ºC13.3ºC) and an average of 46.9% relative humidity (range = 23.0% 68.6%). Hibernating populations were small, ranging from 11 to 40 individuals and clustering activity was only observed in 4% of hibernating bats. Bats may select for specific roost conditions within caves, which we will test once HOBO logger data are retrieved from the field. Results suggest *Pd* could proliferate on some Arizona bats hibernating in colder areas, yet the range of observed roost humidities was lower than optimal for *Pd* growth. Additionally, small population sizes and virtually no clustering activity may keep rates of *Pd* transmission low in Southwest bat populations.

Movements of Banded *Nyctalus lasiopterus* in Southwestern Europe: Conservation Implications

Carlos Ibáñez[1], Sonia Sánchez-Navarro1, Jesús Nogueras[1], Jordi Camprodon[2,3], David Guixé[2], Marie-Jo Dubourg-Savage[4], Ralph David Savage[4], Lionel Gaches[5], Óscar de Paz[6], Pablo T. Agirre-Mendi[7], Joxerra Aihartza[8], Juan Tomás Alcalde[9], Unai Baroja[8], Ana Cordero[10], Roberto de la Peña[11], Jesús de Lucas[12], Daniel Fernández Alonso[13], Juan Luis García- Mudarra1, Inazio Garin[8], Félix González[14], Javier Juste[1], Detlev Kelm[1], Luis Lorente[15], Iñaki Martínez[16], Susana Martínez-Alós[6], Xosé Pardavila[17], Gonzalo Pérez-Suárez[6], Ana G. Popa-Lisseanu[1], Juan Quetglas[1,18], Marisol Redondo[19], Íñigo Sánchez[20], José Manuel Sánchez[21], Godfried Schreur10 and *Elena Tena[1]
1 Departmento de Ecología Evolutiva, Estación Biológica de Doñana, Sevilla, ESP; 2 Grup de Biologia de la Conservació, Centre de Ciència i Tecnologia Forestal de Catalunya, Lleida, ESP; 3 Grup de Recerca BETA, Universitat de Vic-Universitat Central de Catalunya, Barcelona, ESP; 4 Société Française pour l'Etude et la Protection des Mammifères, Bourges, FRA; 5 Conservatoire d'espaces naturels d'Occitanie, Montpellier, FRA; 6 Departamento de Ciencias de la Vida, Universidad de Alcalá, Madrid, ESP; 7 Álava, ESP; 8 Zoologia eta Animalia Zelulen Biologia, University of the Basque Country (UPV/EHU), Bizkaia, ESP; 9 Pamplona, ESP; 10 LUTRA Extremadura, Badajoz, ESP; 11 Madrid, ESP; 12 Delegación de Desarrollo Sostenible de Guadalajara, Junta de Comunidades de Castilla-La Mancha, ESP; 13 Soria, ESP; 14 Museo de la Naturaleza de Cantabria, Cantabria, ESP; 15 Athmos Sostenibilidad, Zaragoza, ESP; 16 Navarra, ESP; 17 Sorex Ecoloxía e Medio Ambiente, Santiago de Compostela, ESP; 18 Secció de Ciències Naturals, Institut Menoquí d'Estudis, Maó, ESP; 19 Centro Montes y Aserradero de Valsaín-Organismo Autónomo de Parques Nacionales, Ministerio para la Transición Ecológica y el Reto Demográfico, Segovia, ESP; 20 Zoobotánico de Jerez, Jerez, ESP; 21 Zaragoza, ESP

From 1999 to 2021, more than 2600 greater noctules (*Nyctalus lasiopterus*) were banded over a large part of the Iberian Peninsula (52% females) and 18% of them were recaptured at least once. Most of the recaptures (97%) took place in the same location of banding with a balanced sex ratio (50% females), which can be explained by the strong phylopatry of this species. The rest of the recaptures showed 1580 km-long movements corresponding to daily foraging journeys along roosting areas with sparse and fragmented forest cover (87% females). Three additional females were recovered more than 150 km from the banding place, likely related to seasonal migratory movements: Girona (Spain) to Occitanie (France), 240 km; Seville (Spain) to Portalegre (Portugal), 237 km; La Rioja (Spain) to Cuenca (Spain), 167 km. The greater noctule is considered as "Vulnerable" in the IUCN Red List and the Spanish and French legislation, and it is considered as "Data deficient" in the Portuguese law. Some of the movements of more than 25 km took place over deforested landscapes with wind farms where high mortality of this species has been detected. Recaptures also provided information on longevity, with one case of at least 14 years old and another eight cases over 10 years. It is urgent to increase the knowledge on the greater noctules and their movement routes in order to reduce mortality and prevent the location of new wind farms.

Telebat: a New System for Long-Term Bat Monitoring at Wind Parks

Fernández Ignacio[1], Bernardino Camousseigt [2] and Ignacio von Unger[1]
1 Myotis Chile, Santiago, CHL; 2 Enel Green Power & Thermal Generation, Santiago, CHL

In Chile, little is known about the relationship between environmental conditions and bat activity at windfarms. In general terms, the only information available was the mortality monitoring reports and records by static devices that had to be analyzed manually, which generated a delay in the delivery of information and the high cost of analyzing a large number of calls. Therefore, the alliance Myotis Chile and Enel Green Power & Thermal Generation created a device with the aim of detecting and identifying bat calls in real time. Also, this information is linked with the environmental parameters, looking for correlations that allow, first to understand and then to predict bat behavior. After two years of research and development, Significant results have been achieved, and the detected information it is uploaded to a digital platform, which can monitor the activity throughout the year in real time, resulting in a successful tool that help to understand and predict the moments with higher risk of collision. This product is already being used in one of Enel Green Power's wind farms, where a large amount of information can be accessed daily, and with a very low monitoring cost. This New Long-Term Monitoring System is called Telebat, will allow us to get a better understanding of the bat behavior near nacelles, in order to implement more efficient and effective management measures to reduce the number of collisions.

Reverse Colonization of Bats from the Japanese Archipelago to Eurasian Continent

Yugo Ikeda[1] and Masaharu Motokawa[2]

1 Department of Zoology, Graduate School of Science, Kyoto University, Kyoto, JPN; 2 Kyoto University Museum, Kyoto University, Kyoto, JPN

Island biology has been exploring the question: Where did the animals come from? Bats are the only vertebrates other than birds that have acquired flight ability, and they often consist as a part of the island ecosystem. In Japan, 35 species of bats are known, and it is highest species diversity among Japanese mammals. Japanese bats are considered to have immigrated from the Eurasian Continent, but counter-immigration from Japan to the continent is unreported. Japanese population of *Rhinolophus nippon*, living widely in Eastern Asia, has also been considered as merely a population immigrated from Eurasian Continent. We investigated cytochrome b and D-loop of mitochondrial DNA of *R. nippon* from Japan, and performed molecular phylogenetic tree construction and divergence time estimation of *R. nippon* in Northeast Asia including the Japanese Archipelago, the Korean Peninsula, and the northeastern China. The results show that *R. nippon* in Northeast Asia have diverged into three clades in the Japanese archipelago after immigration from Eurasian Continent, and one of these clades was found to have reverse colonized the Korean Peninsula and the northeastern China. The results emboss the new question: Where will the animals go to? Some other Japanese bat species also show the similar distribution pattern as *R. nippon*, but they may have different divergence histories. Here we discuss how continental peripheral islands contribute to the creation of biodiversity.

Insights into Bat Diets and Microbiomes– a Community View

Melissa Ingala[1,2], Miranda Dunbar[3], Nancy Simmons[2] and Daniel Becker[4]
1 Department of Biological Sciences, Fairleigh Dickinson University, Madison, USA; 2 Department of Mammalogy, The American Museum of Natural History, New York, USA; 3 Biology Department, Southern Connecticut State University, New Haven, USA; 4 Department of Biology, University of Oklahoma, Norman, USA

Neotropical bat communities are extraordinarily diverse, with some supporting more than 100 sympatric bat species. Each of these species, in turn, interacts with countless non-chiropteran organisms, including the animals and plants that compose their diets as well as the symbiotic microbes that colonize their bodies. Because these interaction networks are so complex, their study requires careful coordination of multiple sources of data and benefits from interdisciplinary areas of expertise. By leveraging the uniquely collaborative environment of yearly expeditions to Lamanai, Belize, we have developed a vastly improved understanding of the basic natural history, ecology, and gut microbiomes of more than 30 species of Neotropical bats. This long-term collection of studies has yielded new molecular tools to profile bat diets in fine taxonomic detail as well as novel information about the various functions that gut bacteria play in bats of different dietary guilds. Insights from these projects reflect multiple levels of biological organization, ranging in taxonomic scale from the entire local bat community to one or a few species of interest (e.g., vampire bats). Future work will expand on these research areas by repeatedly sampling individuals through space and time, allowing us to incorporate a previously intractable temporal component to our analysis of patterns in bat diet and microbiome composition.

To Model or Design Your Way to Defensible Conservation Information on At-risk Bat Populations?

Kathryn M. Irvine[1], Christian Stratton[2], Katharine M. Banner[2], Thomas J. Rodhouse[3] and Brad Udell[4]
1 U.S. Geological Survey, Northern Rocky Mountain Science Center, Bozemam, USA; 2 Montana State University, Department of Mathematical Sciences, Bozeman, USA; 3 National Park Service, Upper Columbia Basin Network, Bend, USA; 4 U.S. Geological Survey, Fort Collins Science Center, Fort Collins, USA

Surveying cryptic, sparsely distributed taxa using autonomous recording units, although cost-effective, provides imperfect knowledge about species presence. Summertime bat acoustic surveys in North America exemplify the challenges with characterizing sources of uncertainty: observation error, inability to census populations, and natural stochastic variation. Statistical uncertainty, if not considered thoroughly, hampers determining rare species presence accurately and/or estimating range wide status and trends with suitable precision. Additionally, the volume of bat acoustic data collected during a survey requires an automated workflow in which proprietary or open-source algorithms assign a species label to each recorded high-quality echolocation sequence. A false-negative occurs if a species is actually present but not recorded and/or all recordings from the species are of such poor quality that a correct species identity cannot be assigned to any observation. False positives for a focal species are a direct result of the presence and incorrect identification of a recording from another species. We introduce our work developing a multi-species count detection model motivated by the idiosyncrasies of bat acoustic data. The count detection model provides unbiased estimates of relative activity and probability of occurrence while simultaneously accounting for false-positive and false-negative detections. Our work creates exciting opportunities for integrating local, short-term and range-wide, long-term acoustic surveys within a cohesive statistical framework. We acknowledge our proposed statistical solutions must be practical and feasible for bat biologists to adopt and in turn operationalize. Our research balances the inherent tension between providing guidance to mitigate sources of error through the design and data processing workflow versus advancing statistical model development.

Building Roost Selection by Synanthropic Bats in Rural Southeastern Kenya

Reilly T. Jackson[1], Paul Webala[2], Joseph Ogola[3] and Kristian M. Forbes[1]
1 Department of Biological Sciences, University of Arkansas, Fayetteville, USA; 2 Department of Forestry and Wildlife Management, Maasai Mara University, Narok, KEN; 3 Department of Medical Microbiology, University of Nairobi, Nairobi, KEN

Many bat species are synanthropic, often occupying structures built by humans. However, little is known about conditions that make bats choose such human structures. Additionally, there is often conflict between bats and humans, leading to human retaliation that may threaten bat health and increase opportunities for zoonotic pathogen spillover. To understand selection parameters, we surveyed 235 buildings in southeastern Kenya in 2021–2022 and recorded features related to their structure and climate important in roost selection. In total, we identified 86 buildings occupied by eight species of bat and 149 nearby control buildings unoccupied by bats. Seventy-seven buildings were occupied by three species of bat, *Cardioderma cor*, *Chaerephon pumilus* and *Mops condylurus*. Using logistic regression models, we found that *C. cor* selected older buildings ($p = 0.0413$) that were less disturbed by humans ($p = 0.0285$) than control buildings. *C. pumilus* selected buildings that were taller ($p = 0.0224$), more cluttered in the interior ($p = 0.0489$), more humid ($p < 0.0001$), and more commonly disturbed by humans ($p = 0.0144$) than control buildings. *M. condylurus* selected buildings with lower levels of disturbance by humans ($p = 0.0003$) compared to control buildings. Our results show that these three species select different factors when determining suitable roosts and likely represent different levels of potential for interactions and conflict with humans. More practically, these findings can be used to guide building design in rural Africa so to mitigate bat-human conflict, ultimately promoting bat health and reducing the risk of zoonotic pathogen transmission.

Automated Detection of Feeding Buzzes in Echolocation Call Recordings
Joel W. Jameson
Wood Environment & Infrastructure Solutions, Wood Canada Limited, Oakville, CAN

Acoustic bat surveys have been widely adopted as a non-invasive means of quantifying bat communities and habitat use. These surveys are often government-mandated to assess impacts of development projects on bats. Despite the abundant acoustic data being collected, this data is underutilized. Analysis is often limited to species classification and, while this may help understand the distribution of bat species on the landscape, it provides little information on habitat function. Feeding buzzes are produced by foraging bats, generally indicating a successful prey capture event, and have historically been used to evaluate foraging habitat quality. Automated identification of feeding buzzes in recordings could benefit conservation by helping identify critical foraging habitat, yet feeding buzzes are difficult to detect as they are of low amplitude and narrow frequency bandwidth. I tested if detection of feeding buzzes in recordings could be automated with bat recordings from Ontario, Canada obtained with three different recording devices. I manually compiled clips containing a feeding buzz, and clips containing another call type. I extracted low-amplitude signals from clips by sequentially scanning narrow frequency windows. I measured parameters describing the temporal patterns of each pulse and rate of pulse production and used linear discriminant analysis to train a predictive model on a subset of the data. The model accurately identified passes with feeding buzzes over 90% of the time. It is therefore possible to automate the detection of feeding buzzes. Automated detection of feeding buzzes will enrich results and conclusions from acoustic bat studies and should be pursued.

A Comparison of the Diet Specialization of Two Forest-dwelling Bat Species: *Barbastella barbastellus* and *Plecotus auritus*
Katarzyna Janik-Superson[1,2,3], Klaudia Burlińska[1], Iwona Gottfried[3], Tomasz Gottfried[4], Błażej Wojtowicz[4], Jakub Lach[2,5] and Dominik Strapagiel[2,5]
1 Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, POL; 2 Biobank Lab, Department of Molecular Biophysics, University of Lodz, Lodz, POL; 3 Department of Behavioural Ecology, University of Wroclaw, Wroclaw, POL; 4 The Polish Society for Bat Protection OTON, Poznan University of Life Sciences, Poznan, POL; 5 BBMRI.pl Consortium, Polish Center for Technology Development PORT, Wroclaw, POL

Western barbastelle and brown long-eared bat are small, sedentary forest bats. We aim to investigate how much the food niches of these bat species overlap and consider, whether conservation of these bats species be favorable to forest management? In our study we applied NGS using the MiSeq illumina platform to investigate *B. barbastellus* and *P. auritus* DNA guano samples (n = 67), collected in July during 20192021 in 21 polish regions. In the diet of *Barbastella*, representatives of 137 genera of insects from 55 families were detected, while in *Plecotus* 154 genera from 67 families were found. The majority of the barbastelle preys comprised Lepidoptera (Noctuidae, Pyralidae and Geometridae). The long-eared bat diet was dominated by Lepidoptera (Noctuidae, Pyralidae and Erebidae), but we also found Diptera (Syrphidae, Tipulidae and Muscidae) and Coleoptera, Blattodea and Hemiptera. The diet of the barbastelle showed a low level of diversity (Shannon index was 1.1 and 2.74 at family and genus level, while in *Plecotus* the values were 3.94 and 9.06). Dietary overlap: 39% of families, and 28% genera and 19% of species were common to the diet of both species. The results of this analysis provide that the barbastelle is more of a specialist predator and will have a greater effect on the fauna of flying insects by selective predation. *Plecotus*, as a generalist, will reduce populations of flying insects but not significantly affect the species composition. Conservation of bats is a more effective strategy for controlling insect pests than large-scale spraying with insecticides.

Project BatCast: Forecasting Emergences as a Vehicle for Conservation and Public Outreach
Aditi Jayarajan[1,2], Caitlin J. Campbell[2] and Hannah B. Vander Zanden[2]
1 Florida Museum of Natural History, Gainesville, USA; 2 University of Florida, Gainesville, USA

The University of Florida bat houses host the largest bat house colony in an artificial roost in the world, housing approximately half a million Mexican free-tailed bats and attracts hundreds of observers weekly. Although the Bat House complex is among the most popular and best-reviewed Gainesville attractions, the residents of the bat houses are poorly understood: their numbers are not closely monitored, and local weather conditions and population fluctuations can dramatically change the number of bats choosing to emerge to forage each evening. To leverage the bat emergences to promote bat conservation and education, we initiated Project BatCast to monitor and study bat emergences nightly in near-real time. This effort leverages paired acoustic and video monitoring with computer vision to predict the nightly timing, duration, and rate of bats emerging each minute. We have trained a neural network to predict the nightly emergences of bats with respect to local weather conditions and plan to generate regular predictions of nightly emergences based on forecasted conditions. We have engaged general audiences from school groups to undergraduate and graduate students by explaining how BatCast works and disseminating information about bat behavior and ecology. We have developed a Twitter account (@uf_bats) to share educational materials about bats and to share forecasted bat emergences. This project produced a novel modeling framework suitable for quantifying and testing predictions about local conditions which estimate bat emergence behavior, as well as represented a cutting-edge virtual and in-person outreach campaign to engage with the broader public.

Converting Abandoned Railroad Tunnels into Bat Hibernacula: Benefiting Bats and Transportation Organizations
Joseph S. Johnson[1], Christopher Staron[2] and *Janette Perez-Jimenez[1]
1 Department of Biological Sciences, Ohio University, Athens, USA; 2 Office of Environmental Services, Ohio Department of Transportation, Columbus, USA

Suitable hibernacula for bats are currently rare in the Appalachian region of the USA. While hibernacula are often degraded by anthropogenic activities, some actions have created winter habitat, fostering opportunities for partnerships. For example, abandoned railroad tunnels often provide winter habitat, and are sometimes publicly owned. Our goal was to locate abandoned railroad tunnels throughout Ohio, the West Virginia panhandle, and western Pennsylvania, USA, evaluate their suitability for bats, and improve habitat where possible. We surveyed 75 tunnels from 2017–2022 and collected data on microclimates, physical dimensions, and use by bats. Six sites (8%) were used by *Myotis lucifugus*, 16 (21% by *Perimyotis subflavus*, and 39 (52%) by *Eptesicus fuscus*. Although *M. lucifugus* were rarely found, tunnels were the only hibernacula known to be used by the species in Ohio. Furthermore, the largest winter colonies of *P. subflavus* in Ohio were found in tunnels. Tunnels occupied by both species were partially sealed and flooded, with internal temperatures that varied by <5 °C during winter. By contrast, *E. fuscus* commonly inhabited tunnels that were unsealed and experienced large temperature fluctuations. Finally, two tunnels were gated by the Ohio Department of Transportation as the start of a conservation program. One site had populations of *M. lucifugus* and *P. subflavus* that were declining and rebounded following gating. The

second was also modified to stabilize internal temperatures. These results highlight the value of abandoned railroad tunnels for bats and provide an example of collaborative stewardship headed by a government transportation authority.

An Analysis of Bat Mitigation Structures on Bridges and Culverts of California
Dave S. Johnston and Kim Briones
Wildlife Department, H.T. Harvey & Associates, Los Gatos, USA

Over 8,000 of California's vehicular bridges are over 50 years old and because many of these bridges with bat populations will need to be replaced, there is a need to better understand the most effective bat mitigation to conserve these existing bat populations. During the summers of 2017 and 2018 we surveyed 61 bridges and culverts distributed throughout California to evaluate the implementation of bat mitigation. We measured the efficacy of using various add-on structures such as Oregon-wedge-style bat boxes, steel bat boxes, and open-top bat boxes as well as cast-in-place day-roosting and night-roosting habitat. Evaluations were made through acoustic surveys, exit counts, and day roost counts. Cast-in-place crevice habitat appeared to be the most successful followed by Oregon wedge-style bat boxes that were attached to bridge/culvert projects. Open-topped bat boxes worked in regions with warm summer nights but not in regions along the coast where summer nights were cool. Five issues were identified as common reasons bat mitigation failed. Off-site bat boxes were almost never occupied by bats, regardless of their design. Night time temperatures and crevice widths for replacement bat habitat for bridges and culverts appears critical to bat occupancy. Bat habitat designs that worked in areas with warm summer nights often did not work along coastal areas where days were warm but nights. Bat mitigation at transportation structures is complex and a thorough understanding of bats' natural history in needed for the best results.

Sequential Attraction of Bats to Wind Farms – A Novel Hypothesis
Kristin A. Jonasson[1,2], Amanda M. Adams[1,3], Alyson F. Brokaw[1,4], Michael D. Whitby[1] and Winifred F. Frick[1,5]
1 Bat Conservation International, Austin, USA; 2 Ecosystem Science and Management, University of Northern British Columbia, Prince George, CAN; 3 Department of Biology, Texas A & M University, College Station, USA; 4 Department of Biological Sciences, Lehigh University, Bethlehem, USA; 5 Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

Wildlife conservation is increasingly beset by unanticipated interactions between animals and human-altered landscapes. An alarming number of bats are killed at wind energy farms each year. Discovery of the behavioral mechanisms underlying collision risk may provide new insights for solutions to reduce bat fatalities. We reviewed the perceptual range of the primary sensory modalities of bats and the propagation of stimuli produced by wind farms. We propose a Sequential Attraction Hypothesis – different mechanisms are responsible for bat attraction to wind farms at a landscape scale, their movement within the facility, and ultimately result in collisions with turbine blades. The distance at which bats use sensory stimuli to execute natural behaviors determines the scale at which different ecological traps act. We present three mechanisms that could explain bat-turbine interactions at each spatial scale. Disruption of stimuli used for long-distance navigation (visual and geomagnetic) could mislead bats. Flight paths within the facility could be channeled by patterns of airflow or resource acquisition (e.g., potential roosts). The escape response likely governs bat behavior just prior to collision with turbine blades. Increasing understanding of the mechanisms of bat-turbine interactions can provide new solutions for the development of effective mitigation measures, which is especially important given rapid growth of wind energy to meet renewable energy goals.

Diversity of Black Flying Fox Gastrointestinal Microbiome is Positively Associated with Inflammation
Devin N. Jones[1], Braden Scherting[2], Adrienne Dale[3], Tamika Lunn[4], Maureen Kessler[5], Liam McGuire[6], Alison Peel[4], Carl Yeoman[7] and Raina Plowright[1,8]
1 Department of Microbiology and Cell Biology, Montana State University, Bozeman, USA; 2 Department of Mathematical Sciences, Montana State University, Bozeman, USA; 3 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 4 Center for Planetary Health and Food Security, Griffith University, Nathan, AUS; 5 Department of Ecology, Montana State University, Bozeman, USA; 6 Department of Biology, University of Waterloo, Waterloo, CAN; 7 Department of Animal & Range Sciences, Montana State University, Bozeman, USA; 8 Department of Public and Ecosystem Health, Cornell University, Ithaca, USA

Bats are reservoirs of important zoonotic viruses, and it is imperative to analyze factors affecting bat health as these may consequently influence viral shedding dynamics. The gastrointestinal tract (GIT) microbiomes of a variety of mammalian species have been shown to impact and respond to mammalian host health in many ways; however, the influence of the bat GIT microbiome on host health and viral shedding dynamics remains to be determined. To improve our understanding, we measured fecal cortisol concentrations, body composition with bioelectrical impedance analysis, quantified blood cell types via blood smears, quantified Hendra virus (HeV) prevalence in captured and roosting black flying foxes (*Pteropus alecto*) and used 16S rRNA sequencing of the V4 region from rectal swabs to determine the *P. alecto* GIT microbiome. We observed no association among GIT microbiome alpha-diversity, body composition, population-level fecal cortisol, or HeV prevalence. By contrast, we observed a positive association between GIT microbiome alpha-diversity and neutrophil:lymphocyte ratios (N:L). Thus, increased GIT microbiome diversity is associated with greater N:L, which may be indicative of inflammation. This trend is the opposite of what is observed in humans, where increased GIT microbiome diversity is associated with decreased N:L. Our study provides evidence that bat GIT microbiomes may influence or respond to host health through interactions with host immune function. Elucidating mechanisms underpinning bat health may ultimately enable us to improve bat health and better predict spillover events.

***Myotis lucifugus* Summer Colony Dynamics in Response to Invasion of White-nose Syndrome in Wisconsin**
Heather M. Kaarakka[1], Joseph R. Hoyt[2], J. Paul White[1] and Kate E. Langwig[2]
1 Wisconsin Department of Natural Resources, Madison, USA; 2 Department of Biological Sciences, Virginia Polytechnic Institute, Blacksburg, USA

The invasion of novel pathogens can have devastating consequences for host populations. Hosts at high densities typically enhance the spread of pathogens relative to those that are scarcer. However, after host populations decline from disease, larger population sizes can help buffer hosts against the negative consequences of lower population sizes (e.g., Allee effects). Since its arrival, white-nose syndrome (WNS) has caused significant declines in cave-hibernating bats in North America. Many bat species form colonies suggestive of survival benefits of grouping behavior. In the absence of disease, large colonies would be expected to be successful, but during pathogen invasion are expected to experience more severe impacts than smaller colonies due to higher transmission rates. We used generalized linear mixed-effect models to assess the effect of population

size and roost colony characteristics on the response of *Myotis lucifugus* summer colonies to arrival of WNS using yearly population growth rates from emergence counts conducted at 39 *M. lucifugus* summer roosts in 2010−2021. We found that prior to the arrival of WNS, large and small roosts grew similarly. However, following the arrival of WNS, smaller summer colonies experienced more severe declines than their larger counterparts, suggesting that Allee effects may be an important consideration in the recovery of *M. lucifugus*. Furthermore, we found that colonies closer to water fared better than those at greater distances, particularly during invasion years, suggesting that identifying and protecting significant *M. lucifugus* summer roosts near major water bodies may be one of the best options for aiding recovery of this species.

Common Ground: The Foundation of Interdisciplinary Research on Bat Disease Emergence

Rebekah C. Kading[1] and Tigga Kingston[2]
1 Department of Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, USA; 2 Department of Biological Sciences, Texas Tech University, Lubbock, USA

Human perturbation of natural systems is accelerating the emergence of infectious diseases, mandating integration of disease and ecological research. We conducted a bibliometric analysis of co-author relationships to investigate cross-disciplinary collaboration between ecological- and infectious disease-oriented bat researchers. Publication metadata were extracted from the Web of Science database on over 5,600 journal articles published between 1950 and 2019. Ongoing analyses are extending this evaluation through mid-2022 to assess how the co-authorship network may have changed following the emergence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). This analysis identified a separation of bat ecologists and infectious disease researchers with few cross-disciplinary relationships. Of 5,645 papers, true interdisciplinary collaborations occurred primarily in research focused on white-nose syndrome (WNS). This finding is important because it illustrates how research with outcomes favoring both bat conservation and disease mitigation promotes domain integration and network connectivity. Just as WNS provides common ground for convergent research, understanding and mitigating other emerging zoonoses with One Health implications, like SARS-CoV-2, involve common challenges that are best met through cross-disciplinary engagement. We advocate for increased engagement between ecology and infectious researchers to address such common causes, and suggest that efforts focus on leveraging existing activities, building interdisciplinary projects, and networking individuals and networks to integrate domains and coordinate resources. We provide specific opportunities for pursuing these strategies through the Bat One Health Research Network.

Sex-Biased Infections and Mortality in a Multi-Host Fungal Pathogen of Bats

Macy J. Kailing[1], Joseph R. Hoyt[1], J. Paul White[2], Heather M. Kaarakka[2], Jennifer A. Redell[2], John E. DePue[3], William H. Scullon[3], Katy L. Parise[4], Jeffrey T. Foster[4], Tonie E. Rocke[5], Ariel E. Leon[5], A. Marm Kilpatrick[6] and Kate E. Langwig[1]
1 Department of Biological Sciences, Virginia Tech, Blacksburg, USA; 2 Wisconsin Department of Natural Resources, Bureau of Natural Heritage Conservation, Madison, USA; 3 Michigan Department of Natural Resources, Baraga, USA; 4 Center for Microbial Genetics and Genomics, Northern Arizona University, Flagstaff, USA; 5 U.S. Geological Survey National Wildlife Health Center, Madison, USA; 6 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

Emerging infectious diseases are a key threat to wildlife and understanding disease dynamics within populations is fundamental for the conservation of impacted species. Sex differences in infection are widely observed across disease systems and may have consequences for host population recovery. We explored sex-biased infections of bat species impacted by an emerging fungal disease, white-nose syndrome (WNS), and evaluated disease-associated differences in mortality between sexes and potential effects on population structure. We collected epidermal swab data from five species of hibernating bats at 43 sites spanning the eastern and midwestern U.S. to characterize infections and host traits over the course of an annual outbreak. We also used radio-frequency identification systems at hibernacula and passive integrated transponders affixed to bats to determine the role of sex-based activity in shaping infection patterns by sex. We found females suffered from more severe infections of the fungal pathogen causing WNS than male conspecifics. In addition, we found females were less likely than males to be recaptured overwinter and accounted for a smaller proportion of populations over time. Notably, female-biased infections were evident by early hibernation, suggesting that sex-based dynamics prior to hibernation may play an important role in shaping WNS outbreaks. Higher fall activity in male bats may enable them to reduce infections through euthermia relative to less active female bats. Higher impacts in female bats may have cascading effects on bat populations and extend the consequences of WNS beyond the hibernation season, such as limiting recruitment and increasing the risk of Allee effects.

Cross-species Infection of Nairovirus and Borrelia species in Bat Population in Zambia

Masahiro Kajihara[1], Yongjin Qiu[1], Changla Katendi[2], Akina Mori-Kajihara[1], Kosuke Okuya[1], Naganori Nao[1], Ryo Nakao[3], Kozue Sato[4], Yoshiki Eto[1], Hayato Harima[1], Hirofumi Sawa[1], Edgar Simulundu[2,5], Daniel Mwizabi[6], Benerd M Hang'ombe[2,7], Hiroki Kawabata[4], Hirofumi Sawa[1,2] and Ayato Takada[1,2]
1 International Institute for Zoonosis Control, Hokkaido University, Sapporo, JPN; 2 School of Veterinary Medicine, University of Zambia, Lusaka, ZMB; 3 Graduate School of Veterinary Medicine, Hokkaido University, Sapporo, Japan; 4 National Institute of Infectious Diseases, Tokyo, JPN; 5 Macha Research Trust, Macha, ZMB; 6 Department of National Parks and Wildlife, The Ministry of Tourism and Arts, Lusaka, ZMB; 7 Africa Centre of Excellence for Infectious Diseases of Humans and Animal, Lusaka, ZMB

It is known that bats harbor diverse microorganisms. Previously, our team detected a novel Borrelia species in Egyptian fruit bats (*Rousettus aegyptiacus*) in Zambia. Kasokero virus (the family Nairoviridae) and Sosuga virus (the family Paramyxoviridae) are also known to be hosted by Egyptian fruit bats in Uganda and cause febrile illness in humans. However, distribution of these viruses in Zambia are totally unknown. In this study, to understand risks of zoonoses from bats, Egyptian fruit bats, striped leaf-nosed bats (*Macronycteris vittatus*), and long-fingered bats (*Miniopterus* sp.) in the Leopards hill cave in Zambia were examined for Nairovirus, Paramyxovirus, and Borrelia infection. Total DNA and RNA were extracted from, in total, 394 archived bat specimens and subjected to genetic screening. The screening revealed that Egyptian fruit bats (n = 7) and long-fingered bats (n = 1) were infected with Kasokero virus, while Sosuga virus was not detected. Nucleotide sequences of detected Kasokero virus genome had approximately 97% homology with those of the strain that caused human infections in Uganda in 1970's. Borrelia was detected in 27% of multiple bat species tested (n = 64/237). Phylogenetic analyses demonstrated that Borrelia in bats formed a monophyletic lineage with the strain from the first patient in Zambia. These findings indicate that Kasokero virus and Borrelia infect multiple bat species in the cave. The present study highlights the risk of Kasokero virus and Borrelia infection in humans from bat population. The frequency of pathogen transmission to humans should also be evaluated by serological survey of residents around the cave.

Comparative Embryology of the Specialized Nasal Turbinals of *Desmodus rotundus* and *Glossophaga soricina*
Alexa D. Kane, Alisa Hutagalung and Laurel R. Yohe
Department of Bioinformatics and Genomics, University of North Carolina, Charlotte, USA

Neotropical leaf-nosed bats (Phyllostomidae) demonstrate a diversity of different feeding strategies and are known to use olfaction to locate their food sources. *Desmodus rotundus* is one of the few mammal species that feed exclusively on blood, therefore they have specialized senses to optimize hunting capabilities, including olfaction. In contrast, *Glossophaga soricina* is a nectarivorous bat with an elongated palate and sticky tongue. By using diffusible iodine-based contrast-enhancing computed tomography (dice-CT) scanning, we obtained 3-dimensional digital models of the olfactory structures of *D. rotundus* and *G. soricina* throughout different stages of ontogeny. These models have allowed for more accurate measurements of the surface area of the olfactory epithelium of the different nasal turbinals. Segmenting the nasal turbinals throughout the embryonic stages across different species gives a better understanding of how each turbinal forms and then subsequently specializes, especially when compared to other species with different diets. Ongoing investigation can provide morphological and genetic evidence for the evolution of highly specialized traits observed in both species.

Impact of Forest Management Strategies on Ozark Big-Eared Bats and their Prey in the Arkansas Ozarks
Gemma L. Keegan[1], Jorista Garrie[1] and Patrick R. Moore[2]
1 Department of Biological Sciences, Arkansas Tech University, Russellville, USA; 2 Environmental Solutions & Innovations, Inc, Cincinnati, USA

The Ozark big-eared bat (*Corynorhinus townsendii ingens*) is a federally endangered subspecies that occurs only in western/north-central Arkansas and northeast Oklahoma. To determine if managed forest stands are preferred by these bats compared to unmanaged stands, we conducted a Year 1 foraging and telemetry study at a maternity colony in the Ozark-St. Francis National Forest in Franklin County, Arkansas. We used VHF transmitters to track 14 bats and obtain triangulated locations used to determine home range and core-foraging areas. These locations will be used to model habitat preferences after Year 2 to determine how prescribed fire and timber-harvest management practices drive selection of foraging habitat. As many bat foraging studies do not investigate prey availability as an explanation for habitat selection, we are incorporating these data into our study with an objective to determine which habitats and management strategies provide bats with the greatest foraging opportunities. We will use defined core-foraging areas and home ranges from the telemetry study to begin insect sampling in summer 2022, assessing prey availability in areas these bats use. Preliminary insect surveys using universal blacklight traps were conducted in 2021 and yielded a mean biomass of 2.6 g ± 1.2 SE for lepidopterans and 3.8 g ± 2.7 SE for coleopterans. Based on preliminary results from 10 sites, we plan to extend the study to include 40 sites and site variables such as prescribed burning, understory and commercial thinning, and regenerative harvest in summer 2022. These data will be presented at the meeting in August.

Insights From Whole Genome Sequences of Madagascar Bat Viruses
Gwenddolen Kettenburg[1], Hafaliana Christian Ranaivoson[2,3], Angelo Andrianiaina[2], Santino Andry[4], Anecia Gentles[5], Amy Kistler[6], Sharline Madera[6], Ny Anjara Fifi Ravelomanantsoa[2] and Cara E. Brook[1]
1 Department of Ecology and Evolution, University of Chicago, Chicago, USA; 2 Department of Zoology and Animal Biodiversity, University of Antananarivo, Antananarivo, MDG; 3 Department of Zoology and Animal Biodiversity, University of Antananarivo, Antananarivo, MDG; 4 Department Entomology, University of Antananarivo, Antananarivo, MDG; 5 Odum School of Ecology, University of Georgia, Athens, USA; 6 Chan Zuckerberg Biohub, San Francisco, USA

Recent advances in bat virus research and the COVID-19 pandemic have led to pronounced efforts to undertake comprehensive studies encompassing the ecology and molecular biology of novel pathogens. Our research incorporates longitudinal sampling efforts and molecular techniques to take a One Health approach to bat virus discovery. Metagenomic Next Generation Sequencing (mNGS) was carried out on fecal, urine, and throat samples collected from endemic Malagasy fruit bats (*Pteropus rufus*, *Eidolon dupreanum*, and *Rousettus madagascariensis*). From these, coronavirus and henipavirus hits were identified in Chan Zuckerberg ID (CZID) that showed significant nucleotide or protein BLAST alignment to coronaviruses or henipaviruses present in NCBI databases. Phylogenies of full sequences and proteins of interest were constructed in concert with bootscan recombination analyses. We describe three novel Nobecovirus sequences (two from *R. madagascariensis* and one from *P. rufus*) and one novel henipavirus (named Angavokely virus, from *Eidolon dupreanum*). These sequences define unique clades that are ancestral to all currently described Nobecoviruses and bat henipaviruses, lending to interesting ecological questions about the timing of the divergence of Madagascar's endemic fauna and their related viruses. We are using these genomic insights to develop more accurate ecological models of bat virus dynamics and population-level persistence. These models will inform public health efforts to develop focused zoonotic disease surveillance and even, possibly, wildlife vaccines. We anticipate continued discovery of more divergent bat viruses from the isolated Madagascar ecosystem, which we will continue to study holistically, using the tools of dynamical modeling, antibody and PCR assays, and virus isolation.

***Corynorhinus townsendii* Prefers Ventilated Hibernation Roosts in Arizona Caves (United States)**
Heidi J. Kitchel[1], Hayden K. Hutcherson[1], Jabe A. Kahawaii[1], Harrison Tamayo[1], Angela L. McIntire[2] and Marianne S. Moore[1]
1 College of Integrative Sciences and Arts, Arizona State University, Mesa, USA; 2 Arizona Game and Fish Department, Phoenix, USA

Corynorhinus townsendii is reported to hibernate in highly ventilated areas within caves and abandoned mines, but there is little specific data regarding this tendency. Understanding how air movement influences hibernacula selection is critical in bettering bat conservation efforts generally but especially as white-nose syndrome (WNS) continues to devastate hibernating populations across North America. High ventilation accelerates evaporative water loss and could cause bats hibernating in these conditions to arouse more frequently to drink, or it could drive the evolution of other water-saving adaptations. Additionally, high ventilation in arid environments could facilitate environment-to-bat transmission of *Pseudogymnoascus destructans*. Thus, our study aimed to begin filling in this knowledge gap. We repeatedly measured wind speed across multiple fixed locations and recorded hibernating bat roost locations in three Arizona caves during winter 2021−2022. We explored our data using non-parametric descriptive statistics and tested for predictors of the observed data using generalized linear models. In two caves and over the entire survey period, nearly 80% of hibernating *C. townsendii* observations occurred in the windiest areas where wind speed ranged from 0−0.9 m/s. Generalized linear models using negative binomial distributions confirmed that wind speed is indeed a significant predictor of *C. townsendii* roost selection during hibernation ($p = 0.0349$). We measured other variables at roost locations, including temperature, relative humidity, and atmospheric pressure. Our completed analysis will account for the impact of these variables on *C. townsendii* roosting preferences and examine how *C. townsendii* preferences may differ from other species roosting in the same caves.

Is a Bat Census Within Reach? Moving Towards a Future of Automated Counting with Emerging Technology
Laura Kloepper[1]
1 Department of Biological Sciences and the Center for Acoustics Research and Education, University of New Hampshire, Durham, USA

Bats are the most abundant mammals on the planet and provide billions of dollars in economic benefit worldwide. Many species of bats, including migratory cave bats like *Tadarida brasiliensis*, concentrate the majority of their population into discrete cave roosts. The timing of both migration and evening emergence can have important implications for agriculture and wind energy. Despite their importance, we know relatively little about the range-wide population of cave bats, largely due to the historical resources needed to assess populations. The recent and rapid explosion of miniaturized, affordable, and automated sensing technology reduces the human effort needed to study animals in remote locations. In my talk, I will highlight some of this technology and propose a framework to conduct automated, daily, range-wide population monitoring of cave bats. With this approach we can not only estimate entire species populations, but also extract life history parameters and reproductive and migratory phenology. With emerging technology, is a continuous global cave bat census within reach?

Social Foraging Behavior and Information Use Linked to Prey Distribution in an Ephemeral Insect-eating Bat
Jenna E. Kohles[1,2,3,4] and Dina K. N. Dechmann[1,2,3,4]
1 Department of Migration, Max Planck Institute of Animal Behavior, Radolfzell, DEU; 2 Department of Biology, University of Konstanz, Konstanz, DEU; 3 Centre for the Advanced Study of Collective Behaviour, University of Konstanz, Konstanz, DEU; 4 Smithsonian Tropical Research Institute, Ancón, PAN

In highly variable environments, where food patches are unpredictable yet shareable, animals can use social information to locate patches more efficiently or more reliably. However, how resource availability fluctuates in space and time can vary in complex ways, and the behavioral strategies animals employ to exploit such resources can also vary, particularly if, when, and where they use available social information. We developed a framework for predicting and characterizing strategies of social information use across taxa, and used it to investigate the foraging behavior of *Noctilio albiventris*. We integrated GPS tracks of simultaneously foraging individuals with the distribution of their aquatic insect prey in two climatic seasons to determine: 1) food availability relative to foraging bout duration, 2) location of social information use, and 3) whether social information use is opportunistic or coordinated. Preliminary results suggest that the insect prey of *N. albiventris* is available in one location for less than the duration of their foraging bouts, they use social information near food patches, and they are flexible in their use of social information, switching between opportunistic and coordinated strategies even within a single foraging bout. Linking foraging behavior, food distribution, and social information is important to understand how ecology shapes social behavior.

Climatic Drivers of Migratory Bat Phenology and Demography
Jennifer J. Krauel[1], Phillip M. Stepanian[2,3], Silke Bauer[4], Felix Liechti4, Charlotte E. Wainwright[2] and Birgen Haest[4]
1 Department of Biology and Microbiology, South Dakota State University, Brookings, USA; 2 Department of Civil and Environmental Engineering and Earth Sciences, University of Notre Dame, Notre Dame, USA; 3 MIT Lincoln Laboratory, Lexington, USA; 4 Swiss Ornithological Institute, Sempach, CHE

The role that weather plays in bat migratory behavior is complex and poorly understood, particularly for long-distance migrants with large geographic ranges. In the case of the Brazilian free-tailed bat, *Tadarida brasiliensis*, bats provide economically important ecosystem services, and yet we lack basic knowledge of resources important to them in much of their range. Recent advances in remote sensing tools permit us to examine drivers of migration phenology and population demography at continental scales. We used weather radar to estimate spring arrival and autumn departure dates and summer and winter population sizes at Bracken Cave, in Texas, USA, from 1995 through 2017. We compared those results to patterns of gridded weather variables across the US and Mexico to identify the weather variables in time and space that best explain variations in the radar-derived dataset. Over the study period, bats arrived earlier in spring, and winter population size at Bracken Cave increased. Tailwinds at high altitudes in spring to the west were linked to earlier spring arrival. High maximum temperatures in summer and autumn in central and northwestern Mexico, respectively, were linked to larger Bracken Cave populations the following summer. Summer precipitation in Oklahoma was associated with later autumn departures, and higher summer maximum temperatures in Oklahoma were linked to larger populations the following winter. Many of these factors are already shifting due to climate change, highlighting the importance of further research.

Social Foraging Trade-offs in *Mollosus rufus* Bats – Revealed Using On-board Microphones
Ksenia Krivoruchko[1], Jens Koblitz[2], Aya Goldshtein[1,3], Antonio Guillén-Servent[4] and Yossi Yovel[1,5,6]
1 School of Zoology, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, ISR; 2 Bioacoustics Network, Neuss, DEU; 3 Wissenschaftskolleg zu Berlin, Berlin, DEU; 4 Instituto de Ecología, Xalapa, MEX; 5 Sagol School of Neuroscience, Tel Aviv University, Tel Aviv, ISR; 6 School of Mechanical Engineering, The Fleischman Faculty of Engineering, Tel Aviv University, Tel Aviv, ISR

Group sensing is supposedly one of the most important social benefits for animals that hunt in a group. But group hunting also comes with a cost. In addition to the increase in competition, group foraging might also impose difficulties on collective sensing, which might deteriorate foraging performance at increased conspecific densities. Therefore, a social foraging trade-off has been suggested in many systems, where elevated conspecific densities improve the overall success of the individual up to a certain threshold, beyond which the success rate declines. We used an improved on-board microphone that allowed us to directly assess individual foraging success, as depicted by the chewing sounds recorded right after echolocation attack sequences. We used this system to study the social foraging trade-off in black mastiff (*Mollosus rufus*) bats that forage on patchily distributed ephemeral prey. Using continuous sound recordings performed on-board freely foraging bats, we could assess the density of conspecifics, the rate of detecting prey and the rate of successful attacks. We could thus separate the performance in searching from prey from the performance in actually catching prey and we could estimate the effect of nearby conspecifics on both of these behaviors. Our results clearly demonstrate the social-foraging trade-off: all of the 11 bats that we monitored were more successful in detecting and hunting prey with some conspecifics nearby, but their performance deteriorated when conspecific density was too high.

Impact of White-nose Syndrome and Local Climate on Reproductive Female Bats in the Southeastern United States
Sarah K. Krueger[1], Trevor G. Walker[1], Sarah C. Zirkle[1], Joy M. O'Keefe[2], Gene Zirkle[3], and Catherine G. Haase[1]
1 Department of Biology, Austin Peay State University, Clarksville, USA; 2 Department of Natural Resources and Environmental Sciences, University of Illinois, Urbana, USA; 3 Environmental Division, US Army Fort Campbell, Fort Campbell, Kentucky, USA

Energetic trade-offs between hibernation and reproduction occur in hibernating bat species to ensure pups are born when forage availability is optimal, yet little is known about how disease impacts reproduction and how these impacts may vary with local climate. White-nose syndrome (WNS) is an infectious disease that disrupts hibernation in bats, leading to premature exhaustion of fat stores. There is evidence of reproductive shifts in areas where WNS has devastated bat populations; however, current research has yet to assess these changes in response to winter duration or local climate. I compiled data from four states and used generalized linear mixed effects models to compare effects of WNS, winter duration, and local climate variables on the number of reproducing females for WNS-susceptible species and two species not affected by WNS. I incorporated the effects of WNS in two ways: presence and absence of WNS and year since WNS was reported. I predicted WNS susceptible species would see a decline in the number of reproductive females, with the effect exaggerated by longer winter durations and inadequate pre-hibernation climate variables. I found that the number of reproductive females in both WNS-susceptible species and species not affected by WNS was positively correlated with pre-hibernation local climate conditions conducive to foraging; however, WNS-susceptible species experienced an overall decline with years since WNS. This overall negative trend of WNS-susceptible species may cause a shift in bat populations, which is critical to understanding the effects of disease on population growth through impacts on reproductive behavior.

Four Bat Species Affected by White-nose Syndrome

Dennis L. Krusac[1], Brian A. Bogaczyk[2], Matthew C. Anderson[3], Brian D. Heeringa[4], Katrina L. Schultes[5] and Scott A. Warsen[6]
1 USDA Forest Service, Atlanta, USA; 2 USDA Forest Service, Milwaukee, USA; 3 USDA Forest Service, Russellville, USA; 4 USDA Forest Service, Washburn, USA; 5 USDA Forest Service, Nelsonville, USA; 6 USDA Forest Service, Wellston, USA

White-nose syndrome (WNS) has caused significant population declines in *Myotis sodalis*, *M. septentrionalis*, *M. lucifugus*, and *Perimyotis subflavus*. To meet its obligations under the Endangered Species Act, the U.S. Forest Service developed a bat conservation strategy (BCS) collaboratively with U.S. Fish and Wildlife Service. The BCS will be implemented on approximately 10,120,000 ha of national forest lands in the eastern United States, and focus management on hibernacula, known or suspected maternity colonies, and high potential habitat for population expansion. Primary, secondary, and tertiary buffers will be established around hibernacula based on species present and abundance within the individual hibernaculum. The higher the abundance, the larger the buffer. During spring staging and fall swarming, certain management activities will be constrained, and others will be prohibited. All known summer roosts will have a 50 m primary roost buffer to protect roost integrity. Each primary roost will also have a secondary roost buffer varying in size up to 1.1 km to protect additional unknown roost trees within the roosting home range. Suspected maternity colonies will be identified when we have a post-WNS capture of a reproductive female or juvenile and we have no roost tree location. Buffers will be established around the capture site varying in size up to 3 km. To protect pups, most management actions are prohibited during the nonvolant period within the primary and secondary roost buffers. Management actions to improve bat foraging and roosting habitat will be implemented across forested landscapes, with emphasis near known occupied habitat.

Effect of Putatively Selected Genomic Loci on Gene Expression in White-nose Syndrome Affected Little Brown Bats

Robert Kwait[1], Sarah Gignoux-Wolfsohn[2], Evan Eskew[3], Malin Pinsky[1], Kathleen Kerwin[1] and Brooke Maslo[1]
1 Department of Ecology, Evolution and Natural Resources, Rutgers, The State University of New Jersey, New Brunswick, USA; 2 Smithsonian Environmental Research Center, Edgewater, USA; 3 Department of Biology, Pacific Lutheran University, Tacoma, USA

Some *Myotis lucifugus* populations in the northeastern United States are showing signs of recovery after initial mass mortality events caused by white-nose syndrome (WNS). Population increases appear to be driven, in part, by rapid natural selection acting on standing genetic variation. In support of this hypothesis, several single nucleotide polymorphisms (SNPs) putatively under selection by WNS have been discovered in this species. In addition, WNS survivors exhibit differences in hibernation-related behavior and physiology relative to individuals prior to disease emergence. However, the mechanistic links between genotype and phenotype of surviving bats remain unclear, in part because the discovered SNPs are in areas of the genome that do not affect protein structure. Therefore, these genetic variants are likely to affect gene expression. Here we tested whether alleles associated with resistance to WNS create phenotypic differences by altering gene expression. We genotyped 146 individual *M. lucifugus* collected from both before and after WNS emergence and compared gene expression levels across the transcriptome between WNS-resistant and WNS-susceptible genotypes within wing tissue. We found multiple changes in gene expression related to selective SNP loci. Two of the identified genes have been linked to immune function in other non-bat species, and several others were associated with transcriptional regulation and chromatin remodeling. Although the function of genes can vary between tissue types and species, this provides evidence that the genes putatively under selection impact transcription patterns in wing tissue. Elucidating the mechanistic effects of these genes could suggest how some bat populations are recovering from WNS.

NASBR Origins 1970-2022: From an Informal Gathering to a Scientific Society

Gary G. Kwiecinski[1] and G. Roy Horst[2]
1 Department of Biology, University of Scranton, Scranton USA; 2 8578 US Highway 11, Potsdam, USA

The annual meetings of the North American Society for Bat Research (NASBR) have served as a prominent worldwide forum for the presentation of, and discussion about, research and conservation on bats. NASBR was founded in 1970 as an informal meeting at which individuals with a special interest in bat research could share, discuss, and develop ideas. Before 1999, the sole purpose was to hold an annual meeting for the dissemination of recent findings about bats. In 1999, NASBR became a formal society governed by a Board of Directors, with a constitution and by-laws. Since its inception, the society has grown from a regional meeting to an international scientific organization. This presentation summarizes the primary changes that have occurred along the way and highlights some of the major events over the past half century. Data will include summaries of NASBR annual meetings and joint meetings with the International Bat Research Conferences (IBRC), and Awardees.

I'm Listening, Who Is It? Acoustic Monitoring of Two Colonies of Cave Bats in Republic of Congo

Morgane Labadie[1], Serge Morand[2], Mathieu Bourgarel[1,3] and Hélène De Nys[1,3]
1 ASTRE, CIRAD, INRAE, University of Montpellier, Montpellier, FRA; 2 CNRS – IRD, FRA; 3 ASTRE, CIRAD, Harare, ZWE

We conducted a project to study how the ecology of cave-dwelling insectivorous bats (habitat selection, ecological niche overlap with other species, reproduction) is influenced by seasonal changes in their environment, in order to better understand the ecology of the transmission of their viruses in relation to risks of emergence of coronaviruses in the Republic of Congo. Currently, we are monitoring two caves (Boundou Cave and Mont Belo Cave) with colonies of cave-dwelling insectivorous bats in the Niari Department of the Republic of Congo. We have set up a passive

acoustic monitoring protocol at the entrance of each cave, with environmental sensors inside and outside the caves. Using these protocols, we aim to answer to what extent seasonal variations may affect the richness, abundance, and composition of cave-dwelling insectivorous bat communities. We used the *Tadarida* classifier (Roemer et al., 2021) to sort the sounds (approximately 684,333 audio files) and then we used the method of Revilla-Martína et al. (2020) to quantify the activity and abundance of species in the two caves. We present the first preliminary results of the acoustic component with approximately 120 days over 8 months with the presence and activity of at least 4 families of insectivorous bats (Hipposideridae, Vespertilionidae, Mioniopteridae, Rhinolophidae). These results can be used to better understand the movement dynamics of cave bats and potentially help identify ecological factors that can promote viral dynamics.

Variation in Host Pathogen Shedding and Abiotic Factors Influence the Environmental Reservoir of *Pseudogymnoascus destructans*

Nichole A. Laggan[1], Katy L. Parise[2], J. Paul White[3], Heather M. Kaarakka[3], Jennifer A. Redell[3], John E. DePue[4], William H. Scullon[5], Jeffrey T. Foster[2], A. Marm Kilpatrick[6], Kate E. Langwig[1] and Joseph R. Hoyt[1]

1 Department of Biological Sciences, Virginia Polytechnic Institute, Blacksburg, USA; 2 Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, USA; 3 Wisconsin Department of Natural Resources, Madison, USA; 4Michigan Department of Natural Resources, Baraga, USA; 5Michigan Department of Natural Resources, Norway, USA; 6 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

White-nose syndrome has had devastating effects on hibernating bat populations across North America. *Pseudogymnoascus destructans*, the fungal pathogen that causes white-nose syndrome in bats, is known to persist for long periods of time in the environment, which can result in widespread infection and mortality. Factors that affect the environmental reservoir include pathogen input from bats and environmental factors influencing pathogen persistence. Differences in pathogen shedding among bat species can lead to some individuals contributing more to overall environmental contamination and increase the intensity of infections in high use areas. The influence of both host and environmental factors on environmental pathogen distribution are rarely examined together and remains an important outstanding question. Here we examine a range of different environmental conditions and the amount of fungal pathogen, Pseudogymnoascus destructans, shed by different bat species. We observe heterogeneity in pathogen shedding by host species and find that a highly abundant species (*M. lucifugus*) has the greatest contribution to environmental contamination. However, we do not find this relationship in a more infected, but less abundant species (*M. septentrionalis*). Additionally, we identify that some environmental conditions pose a higher risk to hibernating bats as these conditions harbor greater amounts of pathogen. Our results show that both variation in pathogen shedding by hosts and abiotic factors influence the extent of the environmental reservoir.

Tricolored Bats Overwinter in Box Culverts in an Arkansas Region Without Caves

Anneka Lamb[1], Roger W. Perry[2] and Virginie Rolland[1]

1 Department of Biological Sciences, Arkansas State University, Jonesboro, USA; 2 Southern Research Station, USDA Forest Service, Hot Springs, USA

In southern Arkansas, records of tricolored bat (*Perimyotis subflavus*; PESU) captures exist for summer but not for winter because this region lacks caves where winter surveys for PESU are typically conducted. However, PESU may overwinter in culverts as reported in neighboring states. Therefore, our objective was to determine which (if any) culverts in this region are used as winter roosts by PESU. We conducted winter surveys of road culverts in 17 southern Arkansas counties between November 2020 and March 2022. Through ground-truthing efforts (96 culverts) and a three-day culvert blitz (193 culverts), we found 11 culverts being used by PESU. Additionally, PESU occupancy increased with culvert length (slope = 0.04 ± 0.01), although other culvert-level factors (i.e., water depth, flow condition, culvert height) did not have a significant effect. These preliminary findings indicate that PESU remains present in the winter in southern Arkansas. In winter 2022−2023, we plan to continue monitoring identified culverts used by PESU along with unoccupied culverts to describe roost-switching patterns and determine landscape- and roost-level factors that make a culvert suitable for wintering PESU in southern Arkansas.

Changes in Host-Pathogen Dynamics Following the Invasion of a Novel Pathogen of Bats

Kate E. Langwig[1], Alexander T. Grimaudo[1], Skylar Hopkins[1], Macy J. Kailing[1], Nichole Laggan[1], J. Paul White[2], Jennifer A. Redell[2], Heather Karaakka[2], John DePue[3], Carl Herzog[4], Katy L. Parise[5], Jeffrey T. Foster[5], A. Marm Kilpatrick[6] and Joseph R. Hoyt[1]

1 Fralin Life Sciences Institute, Department of Biological Sciences, Virginia Tech, Blacksburg, USA; 2 Wisconsin Department of Natural Resources, Madison, USA; 3 Michigan Department of Natural Resources, Houghton, USA; 4 New York Department. of Environmental Conservation, Albany, USA; 5 Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, USA; 6 Department of Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, USA

The invasion of pathogens to new regions has caused widespread population declines and driven species to extinction. The emergence and establishment of white-nose syndrome (WNS), a fungal disease of bats, provides an opportunity to examine disease dynamics across a gradient of pathogen invasion to understand the multitude of factors that contribute to host-pathogen coexistence. We used individually-based bat infection data collected over the 10-year period of WNS invasion and establishment to address the question: How have host-pathogen dynamics changed since the arrival of WNS, and how do they contribute to host-pathogen coexistence? We find that both changes in the environment and host traits contribute to the persistence of bats with WNS. First, temperature-dependent growth of the fungus selectively removed bats roosting at the warmest temperatures and resulted in a population-level shift toward cooler roosting conditions. The preferential survival of bats at the coolest temperatures resulted in overall reductions in pathogen growth on bats. However, bats also evolved host traits that facilitated their survival, including the development of resistance that allowed them to further reduce fungal growth and increased their survival. Interestingly, the importance of specific traits (e.g., body condition) appeared to change with disease phase such that some traits appear important in surviving the initial epizootic but their importance diminishes as the pathogen establishes. Collectively, our results suggest that bat survival in the face of global change will likely require rapid adaptation and a more comprehensive understanding of factors that aid in population health.

Ecological Drivers of Disease Adaptation in Bats: Influences of Order and Sympatry

M. Elise Lauterbur and David Enard

Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, USA

Disease drives much of mammalian evolution. Ecological conditions influence disease exposure, but environmental interactions are complex. By using genomic disease adaptation as evidence of past pathogen exposure, we examined the ecological conditions correlated with disease in bats

and other mammals. To understand the magnitude and type of genomic disease adaptation, we identified virus interacting proteins (VIPs) in over 250 mammalian genomes. We developed a metric of disease adaptation using positive selection on VIPs relative to that on similar control genes. By combining this metric with ecological data from WorldClim and IUCN range maps, we used multivariate phylogenetic regressions to determine the ecological variables most associated with adaptation in VIPs. Genome-wide adaptation is the most significant predictor of VIP adaptation. Order is also a significant predictor, but bats do not have more strongly significant adaptations at VIPs than do other mammalian orders. Within bats, the number of sympatric bat species has a strong effect on VIP adaptation, as do other ecological characteristics with varying effects among viral families. Because ecological factors influence genomic disease adaptation differently across orders, intrinsic life history traits such as metabolism and life span may be of similar importance. To increase our power to detect ecological influences independent of intrinsic traits, we are sequencing *Myotis* bats in western North America. A relatively recent radiation, these species share similar genomes but inhabit many different environments. These genomes will enable us to better understand the most important ecological and life history traits driving disease adaptation, past, present, and future.

Bad Omens or "Just Like Chickens": Perceptions of Bats Among a Namibian Pastoralist Community

Theresa M. Laverty[1,2,] Tara L. Teel[3], A. Archie Gawusab[4] and Joel Berger[2,5]
1 Department of Ecology and Evolution, University of Chicago, Chicago, USA; 2 Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, USA; 3 Department of Human Dimensions of Natural Resources, Colorado State University, Fort Collins, USA; 4 Sesfontein, NAM; 5 Wildlife Conservation Society, Bronx, USA

While relatively little is known about bats across much of Africa, globally, many bat populations are in decline due to human activities. Successful bat conservation efforts, therefore, depend on both ecological studies and research on human-bat relationships. To address these knowledge gaps about African bats and their interactions with humans, we used semi-structured interviews of pastoralists in northwestern Namibia to assess local experiences with, attitudes toward, and cultural stories about bats. Our research was conducted in conjunction with an ecological study on Namib Desert bat distributions, thus allowing for a broader understanding of the social-ecological dynamics of human-bat interactions in this region. Though only 65% of interviews were able to correctly identify bats from photographs, 100% classified these species as bats when provided with an additional description of “animals that fly at night.” A majority (77%) of interviews expressed positive attitudes toward bats and over a third (38%) provided cultural stories, offering detailed reports of myths and common meanings assigned to bats. Of those stories, 12% indicated that bats brought good luck or good rains, and 84% specified that bats represented bad luck or omens of injuries, death, disease, or lack of rains. While the primary threats of habitat loss and bushmeat hunting were never mentioned in our interviews, the influence of negative cultural stories on individual behavior could pose challenges for future bat conservation initiatives. This qualitative approach combined with ecological research may be valuable for assessing cross-cultural relationships between humans and understudied wildlife in other remote areas.

Fast and the Fierce Three: Ecological Opportunity and Evolution of Large Leaf-nosed Bats in Solomon Islands

Tyrone H. Lavery[1,2,3], Devon DeRaad[1] and Rob G. Moyle[1]
1 Biodiversity Institute and Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, USA; 2 Negaunee Integrative Research Center, Field Museum of Natural History, Chicago, USA; 3 Fenner School of Environment and Society, The Australian National University, Canberra, AUS.

Rates of diversification can be much faster on islands than on mainlands, and geographic isolation is widely accepted as a major driver in this via allopatric speciation. However, vacant niches and novel ecological opportunities can also play important roles. The Solomon Islands archipelago in the South-west Pacific supports a diverse and highly endemic bat fauna, including the widespread diadem leaf-nosed bat (*Hipposideros diadema*), and the larger endemic fierce leaf-nosed bat (*H. dinops*). We used an integrative approach to assess relationships between these two species using genome-wide RADseq data, microsatellite genotyping, measurements of craniodental variables and echolocation call recordings. *Hipposideros dinops* is immediately distinguishable from *H. diadema* based on non-overlapping differences in body size alone. However, the two cannot be distinguished at a species level using genetic data. Moreover, our sequencing results have uncovered an unusual pattern whereby the three genetic clades corresponded to three different islands we sampled, but each clade contained samples of both *H. diadema* and *H. dinops*. Microsatellite data indicated syntopic populations in the same cave do not interbreed and echolocation call frequencies to not overlap between the two forms. “*Hipposideros dinops*” has potentially evolved on at least three separate occasions in Solomon Islands. This large-bodied bat possesses morphological features that could allow predation of terrestrial vertebrates. We postulate repeated development of larger forms could have partially been enabled by vacant niches for targeting nocturnal vertebrate prey, and driven by the close links between prey selection, echolocation call frequency, and body size in *Hipposideros* bats.

Recognizing the Importance of Community Livelihoods in Advancing Conservation Measures for Endangered Pollinating Bats

Kristen Lear, Ana Ibarra, Dan Taylor, Mylea Bayless, Kevin Pierson and Jon Flanders
Bat Conservation International, Austin, USA

Pollinators are critical for functioning ecosystems and economies around the world, but anthropogenic pressures combined with climate change are pushing many species to the brink of extinction. Bat Conservation International (BCI) has established an Agave Restoration Initiative to protect and restore healthy, functioning ecosystems that support local livelihoods and protect nectivorous bats in the US Southwest and Mexico. By working with a diverse set of partners, this initiative builds strong local support in key areas that enables us to identify culturally and environmentally suitable sites and strategies for agave restoration actions. These actions are not only necessary to create resilient foraging corridors for migratory movements of nectivorous bats, but also to support local community enterprises through investment in local infrastructure (community greenhouses), business opportunities (wildlife-friendly products), and sustainable livelihoods (investment and training in sustainable agricultural and ranching techniques). With insights from ethnoecological and livelihoods research with rural Mexican communities and agave harvesters, we have identified opportunities for enhancing synergies and reducing trade-offs between livelihood and bat conservation goals. Incorporating local forms of knowledge has allowed us to challenge conventional ecological assumptions about the effects of local land uses on agave populations, allowing for the development of more ecologically effective and socially ethical forms of bat conservation. In addition, BCI is developing justice, equity, diversity, and inclusion (JEDI) frameworks for engaging with local communities. This collaborative and transdisciplinary approach allows us to set ambitious goals that enhance climate resiliency of natural ecosystems, improving local livelihoods and saving bat species from extinction.

Bat Coronavirus Transmission Dynamics and Evolution on a Tropical Island
Camille Lebarbenchon, Axel Hoarau, Léa Joffrin, Marie Köster, Gildas Le Minter, Muriel Dietrich, and Patrick Mavingui
Université de La Réunion, UMR Processus Infectieux en Milieu Insulaire Tropical, Inserm, CNRS, IRD, Saint Denis de La Réunion, REU.

Coronaviruses (CoVs) are commonly detected in bats, worldwide. Although some of these viruses may represent a threat for livestock and humans, alpha- and beta-CoV diversity has been shaped by a long coevolution with their associated bat host species. Current knowledge on the drivers involved in bat CoVs shedding, transmission, and molecular evolution in bat populations, remains nevertheless limited. We investigated transmission patterns and genetic diversity of an alpha-CoV associated to a Molossid species (*Mormopterus francoismoutoui*) endemic to Reunion Island. Based on the collect of >2800 fresh feces collected during five consectutive years in a maternity colony, we report the prevalence of bats shedding CoVs. For instance, we show a high repeatability of CoV shedding pulses, with up to 78% of positive bats, during the aggregation of juveniles. We also identified coinfections with Paramyxovirus and Astrovirus in 1% of the positive samples, without evidence of interactions between viruses. Finally, partial sequencing of the Spike gene provided further information on virus evolution within and between seasons.

Acoustic Survey of Bat Populations in the Wichita Mountains Wildlife Refuge, Oklahoma
Dana N. Lee, Ricky Trent Jr. and Matt J. Van Sant
Cameron University, Lawton, USA

Which species of bats are present in the Wichita Mountains Wildlife Refuge (WMWR), Oklahoma is not well known. Therefore, our objective was to establish a more complete record of the diversity of bats present within the refuge. We placed ultrasonic recording devices at eight locations within WMWR from April–November 2021 in an effort to determine species richness at each site. Noise files were removed and the remaining recordings were analyzed in Sonobat v 4.0. Batch summary reports included likelihood of presence values for each species. If the likelihood of presence was > 0.9 we accepted the identified species as present within the site. We performed manual verification of individual classifications if the species had a likelihood of presence < 0.9. We report the detection of *Myotis velifer*, *Nycticeius humeralis*, *Lasiurus borealis*, *Lasiurus cinereus*, *Eptesicus fuscus*, *Lasionycteris noctivagans*, *Tadarida brasiliensis*, *Antrozous pallidus*, *Corynorhinus townsendii*, and *Nyctinomops macrotis*. We detected each of these species, except *E. fuscus* and *N. macrotis*, at all eight locations. *Parastrellus hesperus* or *Perimyotis subflavus* was also detected at every location, but these two species could not be differentiated manually or by Sonobat. Species richness patterns at two of the locations appear to be impacted by excessive heat and drought. Next steps in this study should include mist net surveys to capture and more confidently document the presence of each species within WMWR. This will also enable us to record more detailed information including population sizes and to monitor for the presence of white-nose syndrome.

From Sodium to LED Lights – Impacts on Bats and Insects in Singapore
Kenneth Lee[1], Deon Lum[1,2] and Joanna Coleman[1,3]*
1 Department of Biological Sciences, National University of Singapore, SIN; 2 Department of Earth and Environmental Sciences, University of Manchester, Manchester, GBR; 3 Department of Biology, Queens College at the City University of New York, Queens, USA

Motivated by sustainability and budgetary concerns, many cities are replacing high-pressure sodium (HPS) streetlights with light-emitting diode (LED) lights. Yet, knowledge of how these retrofits affect wildlife is inadequate and inordinately based on studies in dark, non-urban areas in the temperate zone. Our study focused on bats and insects in Singapore, the only fully urbanized tropical nation and the world's most light-polluted one. We compared bats (acoustic monitoring) and insects (sticky traps) between HPS- and LED-lit streets. The retrofit affected insects – they were less diverse and abundant at LED than at HPS lamps. But light type did not affect bats, except *Saccolaimus saccolaimus*. On HPS-lit streets, its activity increased with traffic noise and rainfall; on LED-lit streets, the opposite happened. If LED lights are less attractive to insects, then retrofits may reduce their mortality at artificial lights. This has potential implications for their bat predators. We attribute the lack of a generalized impact on bats to the fact that the most common species we recorded are urban adapters and they were mainly using our study streets to commute, not hunt. Besides, urban-adapted bats, especially in a highly urbanized and brightly lit city, must be at least somewhat light-tolerant. Do our findings give the green light for LED retrofits in other tropical and light-polluted cities? We suggest proceeding cautiously. Indeed, our study highlights how ecological impacts are contextual. Many bats are not urban-adapted, and their responses to LED retrofits are poorly known, as are responses of phytophagous bats in the tropics.

Contrasting *Myotis lucifugus* Central Place Movement at a Maternity Roost and Swarming Site Using Automated Telemetry
Jade Legros[1,2], Anouk Simard[3,2], Kyle H. Elliott[1,2] and Liam P. McGuire[4]
1 Natural Resource Sciences Department, McGill University, Montreal, CAN; 2 Quebec Centre for Biodiversity Science, Montréal, CAN; 3 Ministère des Forêts, de la Faune et des Parcs, Quebec, CAN; 4 Department of Biology, University of Waterloo, Waterloo, CAN

Life history of many bats involves roosting and foraging in central places, including maternity colonies and swarming sites/hibernacula. Given the importance of these central places, we studied small-scale changes in spatial and temporal movement patterns of endangered *Myotis lucifugus* at a summer maternity roost (June; n = 23 females) and during swarming at a hibernaculum (September; n = 13 females, 20 males) ~110 km apart in Quebec (Canada). We predicted bats would visit the maternity roost more often than the hibernaculum, leading to smaller home ranges in summer than during swarming. Bats were continuously tracked at the maternity roost and hibernaculum with a network of 10 automated telemetry towers surrounding the focal site, supplemented with manual telemetry. As predicted, bats visit the maternity roosts more often (80% of days) than the hibernaculum (22% of days). Revisitation rate varied among individuals, but there was a clear sex bias in hibernaculum revisitation rates. Females revisited the hibernaculum on average 12% of days and at most 66% of days, whereas several males revisited 90% of days or more. We observed repetitive individual movement patterns each night and while females at the maternity roosts stayed in a radius of ~5 km from the maternity roost, we recorded both males and females at > 10 km from the hibernaculum during swarming. These results indicate changes in spatial and temporal use of central places by *Myotis lucifugus* according to the time of the year and sex. Further analyses will evaluate differences in habitat selection at both sites.

Abundances of Flying-foxes at Roosts Linked to Past Patterns of Vegetation Greenness
Pia E. Lentini[1,2], Kylie Soanes[2], Shona Elliot-Kerr[2] and Brendan A. Wintle[2]
1 School of Global Urban and Social Studies, Royal Melbourne Institute of Technology University, Melbourne, AUS; 2 School of Ecosystem and Forest Sciences, University of Melbourne, Parkville, AUS

In recent decades, flying-fox roosts (or "camps") have increasingly become established in Australia's cities and towns, while urban camps have also become larger and more permanent. Because of the impacts associated with some camps, such as noise and smell, they can be the source of significant community concern, particularly when they suddenly increase in size. Hence, better predictions of how and when these changes might occur could help management of potential human-wildlife conflicts. However, to date the flowering and fruiting of perennial Eucalyptus and other key forage species that are thought to drive flying-fox movements has been difficult to predict, particularly over very large scales. Here, we analyzed whether vegetation greenness could act as an indicator of future flowering or fruiting events, and in turn changes in the number of flying-foxes at individual roosts across the east-coast of Australia. We did this using a national-scale, remotely-sensed phenology dataset and quarterly count data of the four mainland Australia flying-fox species from 241 individual roosts. We constructed correlative models of the relationship between the greenness of woody vegetation surrounding the roosts in moving three-month windows in the lead-up to the counts, and the number of bats recorded in those counts, creating separate models for roosts occurring in temperate, subtropical, and tropical regions. While the success of this approach varied depending on species and region, we found that in general higher vegetation greenness in the 10 months prior was correlated with greater numbers of bats being recorded in the counts that followed.

Astrovirus Transmission Between Bats and Small Terrestrial Mammals on Reunion Island

Rachel Leong, Axel Hoarau, Victoria Carcauzon, Marie Köster, Pablo Tortosa and Camille Lebarbenchon
Université de La Réunion, UMR Processus Infectieux en Milieu Insulaire Tropical, Inserm, CNRS, IRD, Saint Denis de La Réunion, France.

Astroviruses (AstVs) are commonly detected in bats and birds worldwide. These viruses are responsible for acute gastroenteritis in children, and cause diseases in livestock, poultry, and domestic pets. Frequent cross-species transmission events have been documented for AstVs, indicating limited host specificity. Current knowledge on the drivers and the extent of such cross-species transmission events remains limited. We investigated AstV diversity and evolution in bats and terrestrial small mammals on Reunion Island, a small tropical island located in the Western Indian Ocean. We collected biological material from 3428 Free-tailed bats (*Mormopterus francoismoutoui*) and 258 small mammals (e.g., rats, mice), and tested for the presence of the AstV RNA-dependent RNA-polymerase (RdRp) gene, with a pan-AstV semi-nested polymerase chain reaction assay. The AstV RdRp was detected in 59 bat samples (mean detection rate ± 95% confidence interval: 1.7% ± 0.4%), 50 *Rattus norvegicus* samples (67% ± 10%), 40 *Rattus rattus* samples (27% ± 7%) and six *Mus musculus* samples (16% ± 12%). Phylogenetic analysis revealed a large genetic diversity of viruses. In particular, AstVs detected in bats were closely related to viruses previously described in birds and small mammals. The AstVs detected in rats and mice clustered in two major lineages, including viruses previously detected in bat guano. Our study reports the circulation of a large diversity of AstVs on Reunion Island, with limited host restriction.

How Bat Activity Is Affected by Wind Turbine Proximity and Blade Rotation Speed?

Camille Leroux[1,2,3], Christian Kerbiriou[1,2], Isabelle Le Viol[1,2], Nicolas Valet[3] and Kévin Barré[1,2]
1 Centre d'Ecologie et des Sciences de la Conservation, Muséum National d'Histoire Naturelle, Centre National de la Recherche Scientifique, Sorbonne Université, Paris, FRA; 2 Centre d'Ecologie et des Sciences de la Conservation, Muséum National d'Histoire Naturelle, Station de Biologie Marine, Concarneau, FRA; 3 Auddicé Biodiversité, Roost-Warendin, FRA

Wind turbines have been documented to have antagonist effects on bats by either repulsing them or attracting them, leading potentially to habitat loss or to increased mortality risks, respectively. Today the nature of the effect and the underlying mechanisms remain highly confusing. This lack of knowledge makes the prediction of wind turbine impacts nearly impossible, as well as the implantation of adequate mitigation measures. We therefore aim to identify determinants of the nature and range of bat response to wind turbine proximity. We recorded bat activity across 361 entire nights at 154 sites at hedgerows along a gradient of distance from 10 to 1500 m from wind turbines in Brittany (France) in June. For each sampled night-site, we collected variables likely to explain bat responses to wind turbine proximity such as nightly mean blade rotation speed of the nearest wind turbine and wind turbine features as well as weather and environmental variables. We found that bat activity at hedgerows was affected by both wind turbine proximity and blade rotation speed. However, we did not find significant interaction between these terms, suggesting the involvement of other mechanisms. In addition, we identified key factors driving the nature of these effects. Our results highlight the crucial need for a multifactorial approach when studying and predicting wind turbine impacts. They also reveal that an oversimplified approach could lead to misleading conclusions regarding wind turbine impacts (i.e., collisions or habitat losses) and thus to inadequate mitigation measures which could seriously affect local populations.

Decreasing Light Pollution is Key in order to Increase the Value of Urban Areas for Bat Conservation

Daniel Lewanzik[1], Tanja M. Straka[1], Julia Lorenz[1], Lara Marggraf[1], Silke Voigt-Heucke[1], Anke Schumann[1], Miriam Brandt[1] and Christian C. Voigt[1]
1 Department of Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU

Global change, including urbanization, threatens many of the >1,400 bat species. Nevertheless, certain areas within highly urbanized cities may be suitable to harbor bat populations. Thus, managing urban habitats could contribute to bat conservation. Here, we established evidence-based recommendations on how to improve urban spaces for the protection of bats. In a team effort with >200 citizen scientists, we recorded bat vocalizations up to six times over the course of two years at each of 600 predefined sites in the Berlin metropolitan area. For each species we identified the preferred and non-preferred landscape features. Our results show that artificial light at night (ALAN) had a negative impact on all species; even on species previously considered 'light tolerant'. For some species, ALAN had the largest effect sizes among all environmental predictors. Canopy cover and open water were especially important for bat species that forage along vegetation edges and for trawling bats, respectively. Occurrence probability of species foraging in open space decreased with increasing distance to water bodies. Our study shows that despite the many negative impacts of urbanization on wildlife, urban environments can harbor bat populations if certain conditions are met, such as low levels of ALAN and access to vegetation and water bodies. Our findings allow inferences on how to manage urban spaces in a bat-friendly way. We recommend limiting ALAN to the minimum necessary and maintaining and creating uninterrupted vegetated corridors between areas with high levels of canopy cover and water bodies, in which ALAN should be entirely avoided.

Wildlife Crossing Structures Aid Bats with a High-risk Collision to Cross the Road Safely

Célia Lhérondel[1], Cédric Heurtebise[2], Thibaut Ferraille[1], Philippe Chavaren[2], Benjamin Allegrini[1] and *Fabien Claireau[1,3]
1 Naturalia environnement, Avignon, FRA; 2 VINCI Autoroutes – Réseau ASF, Vedène, FRA; 3 Centre d'Ecologie et des Sciences de la Conservation, Muséum National d'Histoire Naturelle, Centre National de la Recherche Scientifique, Sorbonne Université, Paris, FRA

Roads have a multitude of negative effects on wildlife, including their prominent role in habitat fragmentation. Habitat fragmentation particularly affects bats during their nightly movements between roosts and foraging areas. In order to increase habitat connectivity, wildlife crossing structures have been implemented. These structures are mainly monitoring for larger mammals but their functionality for bats is rarely tested. We studied, during three consecutive years, two wildlife overpasses located in woodland habitats in France, and used two new innovative methods: the first was the Acoustic Flight Path Reconstruction (AFPR) to characterize bat crossings using acoustic recorders and the second was the Bat Tracking Toolbox (BTT) to characterize bat flight behavior using a thermal camera. Among the two wildlife crossing structures, we performed a Control-Treatment sampling plan. Among the 160,000 bat passes, we obtained over 700 bat crossings: 70% of bat crossings were located at the treatment site and 30% were located at the control site. Moreover, species with a high risk of collision with vehicles, crossed the road only at the locations of the wildlife structures. Concerning the flight behavior, we found that bats used mainly the wildlife overpass for crossing the road. Very few bats used the wildlife crossing structure for foraging: 9% of bat trajectories. Our study also demonstrates that AFPR combined with BTT are a useful approach to evaluate mitigation measures.

Lunar Chronobiology in Bats is Altered by Light Pollution

Han Li[1], Pauline Allen[1], Saige Boris[1], Samantha Lagrama[1], Jade Lyons[1], Christina Mills[1], Pauline Moussi[1], Casey Nichols[1], Carter Tacosik[1], McKenzie Tsaousis[1], Nyzaya Livingston Wilson[1], Kevin A. Parker[2] and *Matina C. Kalcounis-Rueppell[3]
1 Department of Biology, University of North Carolina Greensboro, Greensboro, USA; 2 Parker Ecology LLC, McMinnville, USA; 3 Department of Biological Sciences, University of Alberta, Edmonton, CAN

The timing of behavior, and habitat associations, of nocturnal animals can be influenced by light. Lunar phobia in bats, for example, describes the response of bats to the lunar cycle with reduced activity on nights with full moons. The prevalence of artificial light at night (ALAN) has been recognized as a source of environmental pollution. The interaction between ALAN and the lunar cycle on bat behavior is important for understanding anthropogenic effects on bats. We combined a decade (2012–2021) of acoustic monitoring data collected in North Carolina, USA, to investigate the relationship between bat activity, lunar cycle, and ALAN in temperate insectivorous bats. We examined whether the amount of lunar illumination affected species-specific nightly activity and whether hourly bat activity patterns varied between nights with different moon phases. We also investigated if the relationship between bat activity and the lunar cycle might be altered by ALAN. We found that seven bat species showed activity variation across nights in relation to the amount of moon illumination and that ALAN interacted with that relationship in five of the bat species. We found delayed bat activity patterns on nights with a full or waxing moon in seven species, and ALAN altered that pattern in four species. There are multiple mechanisms through which moonlight affects bats that include both their predators and prey. We show that ALAN can mask moonlight and alter the environment for nocturnal animals such as bats.

Using the North American Bat Monitoring Program (NABat) for Multi-City Comparison Studies of Urban Bats

Han Li[1], Matina C. Kalcounis-Rueppell[2], Katherine Etchison[3], Katrina Morris[4], Emily Ferrall[4], Jennifer Kindel[5], Susan Loeb[6], Bethany R. Straw[7] and Brian E. Reichert[7]
1 Department of Biology, University of North Carolina Greensboro, Greensboro, USA; 2 Department of Biological Sciences, University of Alberta, Edmonton, CAN; 3 North Carolina Wildlife Resources Commission, Asheville, USA; 4 Georgia Department of Natural Resources, Social Circle, USA; 5 South Carolina Department of Natural Resources, Anderson, USA; 6 Southern Research Station, U.S. Forest Service, Clemson, USA; 7 Fort Collins Science Center, U.S. Geological Survey, Fort Collins, USA

Urbanization alters natural habitats for human's needs and creates new ecological niches. Studies have shown that bats respond to urbanization in a species-specific manner. However, most previous urban bat studies were conducted in a single city or via meta-analyses due to logistic constraints. There is a lack of empirical comparisons across species among cities. Thus, it is still unclear whether species that share similar ecological characteristics respond to urbanization in a similar way or whether different cities affect each species' response. The North American Bat Monitoring Program (NABat) provides a platform for collaborative continental-scale monitoring. Over 5% of NABat high priority cells overlap with large metropolitan areas in the United States. Several NABat survey protocols allow bat monitoring in highly urbanized areas. This presentation demonstrates how data collected and shared via NABat can be used to answer ecological questions of urban bats. Specifically, we investigated two questions: 1. whether city size and urban green/blue space availability and connectivity affected species richness in the city in relation to the regional species pool; 2. whether the most common species in the city was also the most common species in the adjacent non-urban areas. Our current results based on data from the southeastern United States showed that adequate urban green/blue spaces in a city could provide suitable habitats for most species. However, the community composition was likely altered. We hope this presentation will serve as a call of collaboration via the NABat database and look forward to more collaborators continent-wide.

Genomes Reveal the Evolutionary History of *Myotis* Bats

Thomas Lilley
University of Helsinki, Helsinki, FIN

The *Myotis* are a diverse and widespread genus of bats within the family Vespertilionidae. The origin of the genus has been placed in South-East Asia, from where species have colonized all continents apart from Antarctica. Recent studies have shown that radiation, especially in the Americas, has been rapid. This is reflected in the rampant phylogenetic conflict among *Myotis*, resulting from incomplete lineage sorting and introgressive hybridization with blurred species boundaries particularly at the mitochondrial level. We hypothesize that species belonging to clades with lower diversification rates show less discordance between nuclear and mitochondrial phylogenies. We seek to explore this using an extensive genomics dataset, from 240 individuals, representing over 70 species of *Myotis* distributed globally. The resulting data is being used to construct phylogenetic hypotheses from a variety of different genetic markers, to explore phylogenetic conflict, biogeographic histories and diversification shifts. To date phylogenies have been constructed from whole mitochondrial genomes and ~3000 single copy nuclear loci. Our results provide the first insight into the large-scale evolutionary history of *Myotis* using a gene-based approach, and elucidate the confounding results based on mitochondrial data within clades where speciation has been rapid, and occurred recently. By examining the evolutionary history of *Myotis* in greater detail and using a variety of datasets we will develop a better understanding of not only the relationships, but also the factors driving their evolutionary, diversification and biogeographic patterns.

Night at the Museum: How Frozen Tissue Collections Can Drive Genomic Studies

Burton Lim

Royal Ontario Museum, Toronto, CAN

The importance of museum collections has been reiterated during the covid-19 pandemic with frozen tissue samples becoming a valuable resource for research on bat genomics and their association with coronaviruses. In particular, using liquid nitrogen for flash-freezing tissues is important for preserving high molecular weight DNA that is needed for newer technologies of genome sequencing. The Royal Ontario Museum is used as an example for the relevance of biobank repositories and different genomic approaches to investigate the evolution of bats, including collaboration on the Bat1K initiative to obtain the genomic sequences of >1,400 species. A recent publication identified gene losses associated with the molecular adaptations to blood feeding in the common vampire bat by comparing its genome with those of closely related species. Another technique based on genomic data to survey single nucleotide polymorphisms (SNPs) was used to hypothesize the phylogenetic relationships in mastiff bats and the discovery of cryptic species. In addition, RNA can be extracted from tissues frozen in liquid nitrogen as done for a transciptome study that investigated the role of ecological factors in the evolution of bat visual opsin genes.

Trypanosomes, Babesia, and Non-tuberculous Mycobacteria in Palearctic Bats

Petr Linhart[1,2], Hana Bandouchova[1], Jan Zukal[3,4], Jiri Pikula[1], Vojtech Baláž[1], Tomas Heger[1], Vendula Kalocsanyiova[1], Aneta Kubickova[1], Monika Nemcova[1], Jana Sedlackova[1], Veronika Seidlova[1], Lucie Veitova[1], Anton Vlaschenko[5], Renata Divinova[4] and Jan Votýpka[6,7]
1 Department of Ecology and Diseases of Game, Fish and Bees, University of Veterinary Sciences, Brno, CZE; 2 Department of Animal Protection and Welfare and Veterinary Public Health, University of Veterinary Sciences, Brno, CZE; 3 Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZE; 4 Department of Botany and Zoology, Masaryk University, Brno, CZE; 5 Bat Rehabilitation Center of Feldman Ecopark, Kharkiv, UKR; 6 Department of Parasitology, Faculty of Science, Charles University, Prague, CZE; 7 Institute of Parasitology, Biology Centre, Czech Academy of Sciences, České Budějovice, CZE

Bats are exposed to a number of stressors potentially affecting their health. Interestingly, bats are known to be resistant to certain pathogens, such as viruses, and even considered a natural reservoir of some pathogens important in human medicine. Little is known about the influence of many potentially pathogenic agents in bats. Here, we analyzed the presence of blood parasites (trypanosomes and babesia) in the blood of hibernating Noctule bats (*Nyctalus noctula*) and spleen, liver and heart collected from cadavers of several Palearctic bat species and also non-tuberculous mycobacteria (NTM) in the gut and organs collected from cadavers. In captive Noctule bats, analysis of hematological and biochemical parameters was performed using iSTAT analyzer. Blood samples and/or organs were tested for presence of trypanosomes and babesia by nested PCR and the presence of non-tuberculous mycobacteria in the gut contents, lungs, liver and spleen was analyzed by conventional PCR. A high prevalence of trypanosomes (dominant was *Trypanosoma dionisii*, lower prevalence was in *Trypanosoma vespertillionis*) was observed; however, there was no effect of trypanosomes on blood parameters. In contrast, *Babesia vesperuginis* was associated with statistically significant effects on acid-base balance parameters during hibernation, when babesia-positive animals developed metabolic acidosis. Although insects are mentioned as one of the possible sources of NTM, the prevalence of mycobacteria in our samples was sporadic.

Winter Activity of Tricolored Bats Hibernating in Subterranean and Aboveground Sites in the Southeastern U.S.

Susan C. Loeb[1], Eric A. Winters[1], Rebecca L. Brown[2], Jessica Anderson[3], Makayla Ferrari[4], Thomas McElroy[5], Andrew J. Edelman[3] and Christopher T. Cornelison[4]
1 US Forest Service, Southern Research Station, Clemson, USA; 2 Department of Forestry & Environmental Science, Clemson University, Clemson, USA; 3 Department of Natural Sciences, University of West Georgia, Carrollton, USA; 4 Department of Molecular and Cellular Biology, Kennesaw State University, Kennesaw, USA; 5 Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, USA

Although the fungus that causes white-nose syndrome (WNS), *Pseudogymnoascus destructans*, is found throughout much of the southeastern U.S, the disease and significant declines have been limited to the northern and more mountainous regions of the southeast. Tricolored bats (*Perimyotis subflavus*) in the southeast often over-winter in aboveground hibernacula such as culverts, bridges, and trees, and bats that use these above-ground roosts often have greater activity during winter, which may decrease their susceptibility to WNS. Our objective was to measure winter activity of bats using subterranean hibernacula, such as caves and tunnels, and aboveground hibernacula such as culverts and bridges to determine the factors associated with winter activity. We used acoustic detectors to measure activity of tricolored bats in four underground hibernacula and seven culverts or bridges in Georgia, Alabama, and South Carolina during winter 2020−2021. We detected tricolored bat activity outside all structures during the winter with the greatest activity being recorded at the bridges. Activity was positively associated with mean outside temperatures but not internal temperatures. Although the effect of structure type (subterranean versus aboveground) on activity levels was not significant, there was a significant interaction between structure type and hibernation period. Activity outside culverts was higher during early hibernation (November−December) than mid (January−February) hibernation, but seasonal differences did not occur in subterranean hibernacula. Higher activity outside above ground hibernacula during warmer periods early in the season may allow these bats to build up greater fat reserves and consequently have greater survival if infected by the *P. destructans*.

Temporal and Geographic Variation in the Diet of *Myotis ciliolabrum* from National Parks in the Southwest

Ashley E. Loehn[1] and Ernest W. Valdez[2]
1 Department of Biology, University of New Mexico, Albuquerque, USA; 2 U.S. Geological Survey Fort Collins Science Center, Department of Biology, University of New Mexico, Albuquerque, USA

Myotis ciliolabrum is distributed across the western North America, ranging from Canada to Mexico. This species is known to feed on flying insects above waterways, but likely feeds in other habitat types. Although there is some information on the diet of *M. ciliolabrum*, many of these studies are either outdated, do not include an adequate number of samples, or do not differentiate this species from its close relative, *Myotis californicus*. Based on earlier studies, it has been suggested that these bats are either beetle or moth specialists. We believe that *M. ciliolabrum* may consume prey opportunistically and feed on a wider variety of insects. To test this hypothesis, we examined the feeding habits of *M. ciliolabrum* netted near water sources at national parks across the Southwest. To date, have analyzed 134 guano samples collected from bats caught, between 2000 and 2021, at El Malpais National Monument, Mesa Verde National Park, Guadalupe Mountains National Park, and Pecos National Historical Park in New Mexico, Colorado, and Texas. From our analysis, we found that *M. ciliolabrum* consumed beetles and moths but also wasps, caddisflies, lacewings, antlions, and true bugs. It appears that some insect prey were taken opportunistically, such as caddisflies. This varied diet may reflect the seasonal and geographic availability of these resources. From our study, we hope to fill information gaps related to the feeding

behavior of *M. ciliolabrum*, which may be important towards future conservation efforts, such as those related to impacts associated with white-nose syndrome and changes in climate.

Long-Term Acoustic Monitoring Reveals Seasonal Activity of Bats in South-Central New Mexico
Christen Long[1], Shawn Thomas[2], Ted Weller[3] and Amanda Adams[1]
1 Science Department, Bat Conservation International, Austin, USA; 2 Conservation Department, Bat Conservation International, Austin, USA; 3 Pacific Southwest Research Station, USDA Forest Service, Arcata, USA

Most monitoring programs are typically conducted during a single season when animals are easiest to detect. As a result, species richness estimates and relative abundances may be biased toward periods when biologists sample. We conducted stationary acoustic monitoring for bats for five years during all seasons of the year at White Sands Missile Range (WSMR) in south-central New Mexico. We used the NABat sampling schema to select areas within WSMR. However, instead of following the 4-night sampling period recommended by NABat, we monitored for extended periods of time throughout the year. This allowed us to generate a more comprehensive and season-specific species list for WSMR as well as compare species presence and activity levels at WSMR among seasons. We documented the presence of at least 17 species of bats at WSMR and we classified each species as common (n = 4), resident (n = 8), or rare (n = 5) according to the number of echolocation recordings identified. Rare species were represented by a total of just 24 detections, with at least one species confirmed each year. We detected 58% of the rare species in 2018 when we monitored for the greatest number of nights throughout the year. This emphasizes the importance of long-term monitoring for documenting species richness throughout the different seasons.

Temporal and Geographic Patterns of Dental Morphological Variation in Noctilionoidea
Camilo López-Aguirre[1], John M. Ratcliffe[2] and Mary T. Silcox[1]
1 Department of Anthropology, University of Toronto Scarborough, Toronto, CAN; 2 Department of Biology, University of Toronto Mississauga, Toronto, CAN

Noctilionoid bats went through one of the most extensive ecomorphological diversifications among mammals, for which dietary adaptations have been identified as a key driver. Several studies have considered the form-to-function link in the ecomorphological diversity skeletal of this bat superfamily. Yet, the variation in aspects of dental morphology, and their relationship to ecology and geography, remain unresolved. We quantified the multidimensionality of dental morphology of 110 species using dental topographic metrics and phylogenetic comparative methods to understand temporal and geographical patterns and their possible drivers. For our temporal analysis, we tested for the effects of evolutionary kinship, diet and body size; for our geographical analysis we tested for the effects of range overlap, diet, latitude and age of divergence. We found multiple bursts of morphological diversification through time, each affecting different morphological traits. Evolutionary rates of most morphological traits evolved independently, although some traits showed concordant changes suggesting they formed evolutionary modules. Several significant shifts in adaptive regimes were found within the family Phyllostomidae. Focusing on congeneric species pairs, our geographic analysis revealed a significant effect of diet, range overlap and age of divergence in the magnitude of morphological divergence. Moreover, we found diverging latitudinal trajectories of morphological distances between sympatric and allopatric species pairs, but no significant effect of latitude in our models. Overall, our results reveal a complex process resulting from multiple interacting mechanisms driving ecomorphological diversification and support the general interpretation of diet as a major driver of evolution in Noctilionoidea.

Bat Player: Evaluation of a Low-Cost Bat Lure for Bat Research and Monitoring
Adrià López-Baucells[1], Adrià Ortega Castaño[1], Laura Torrent[1], Maria Mas Navarro[1] and Xavi Jordà Sanuy[2]
1 BiBio, Natural Sciences Museum of Granollers, Granollers, ESP; 2 Centre Nacional de Microelectrònica, Barcelona, ESP

Bat monitoring programs have faced several challenges to be as comprehensive as possible and collect systematic information about as many species as possible. However, many bat species remain elusive on all continents, extremely hard to detect, and hardly studied. The use of bat lures to broadcast acoustic bat stimuli and attract bats to mist nets or harp traps has increased in the past years due to recent technological advances and developments in open science. However, the elevated cost of these devices and the lack of knowledge regarding their use have hampered a more extended use amongst bat researchers, especially in developing countries. In this study, we evaluated the performance of a low-cost bat lure (Bat player), as a proof-of-concept, designed to broadcast sounds at sample rates of up to 384 kHz, combined with harp traps, to capture rare forest-dwelling bats. We also tested the contribution of the expert eye in terms of survey effectiveness compared to the efficiency of the bat lures. The bat lure greatly improved capture rates when used in open spaces (non-transitory), especially for some species, and was highly biased toward males. However, the expert eye beat the bat lure's efficacy under specific survey conditions (clear pathways or wildlife crossings), turning its advantage highly specific. We demonstrated the value and potential of the Bat Player (user-friendly, easily portable and highly autonomous, supplied with standard AA batteries), which could potentially optimize bat surveys where the conservation status of rare species needs to be further explored.

Food vs Roost Resources: Assessing the Causes of the Endangered Myotis capaccinii Decline in NE Iberia
David López-Bosch, Estel Blanch-Ojea and Adrià López-Baucells
BiBio Research Group, Natural Sciences Museum of Granollers, Granollers, ESP

The long-fingered bat (*Myotis capaccinii*) is one of the most threatened European bat species according to the IUCN. This species presents a combination of characteristics that makes it unique among all European bats: it has an endemic Mediterranean distribution, it roosts exclusively in caves and underground sites, and it hunts using a trawling technique, which makes its distribution very linked to riverine habitats. While the decline of its population has been reported throughout its range, the actual causes of the population decrease are unknown in many areas. In the summer of 2021, a project was set to conduct the most concise study on the long-fingered bat biology in Catalonia (NE Iberia). The project's main objectives were to assess the status of the breeding population and to study aspects of its biology that could explain its current threatened status. We conducted breeding roost counts using non-invasive methodologies, assessed the distribution of the species around nursery colonies during the breeding period, compared the diet of the long-fingered bat and the sympatric sister species, the Daubenton's bat, using metabarcoding, and studied two citizen-science methods for accounting trawling bat activity and their use as ecological indicators. We found that, of all nine historical breeding colonies in Catalonia, only three had a current breeding population, while no differences in the diet of both trawling species was found. The study highlights the importance of underground roost systems for the species, pristine riverine forest habitats, and the potential of using trawling bat activity as an ecological indicator.

Henipavirus Dynamics and Transmission in *Pteropus* Bats

Tamika J. Lunn[1], Remy Brooks[1], Trent Bushmaker[2], Liam Chirio[1], Dan Crowley[3], Adrienne S. Dale[4], Peggy Eby[5], Caylee Falvo[3], Amandine Gamble[6], Andrew Hoegh[3], Peter Hudson[7], Devin N. Jones[3], Maureen K. Kessler[3], Jamie O. Lloyd-Smith[6], Wyatt Madden[3], Hamish McCallum[1], Liam McGuire[4], Vincent J. Munster[2], Olivier Restif[8], Manuel Ruiz-Aravena[3], Kirk Silas[1], Racheal Smethurst[1], Ina Smith[9], Kwe C. Yinda[2], Raina K. Plowright[3] and Alison J. Peel[1]

1 Centre for Planetary Health and Food Security, Griffith University, Brisbane, AUS; 2 Rocky Mountain Laboratories, National Institute of Health, Hamilton, USA; 3 Department of Microbiology and Immunology, Montana State University, Bozeman, USA; 4 Texas Tech University, Lubbock, USA; 5 School of Biological Earth and Environmental Sciences, University of New South Wales, Sydney, AUS; 6 Department of Ecology and Evolutionary Biology, University of California Los Angeles, Los Angeles, USA; 7 Eberly College of Science, Pennsylvania State University, State College, USA; 8 Department of Veterinary Medicine, University of Cambridge, Cambridge, GBR; 9 Australian Animal Health Laboratory, East Geelong, AUS

A major challenge for the design of pre-emptive actions for wildlife zoonoses emerges from the very nature of cross-species transmission as a multilayered process. Prevalence of infection in reservoir hosts is the most used metric to assess infection risk. This is commonly estimated by classifying specimens as positive or negative to pathogen presence based on detection of viral genomic material. However, in many cases these viral genomic fragments may be an overestimation of infectious virus, therefore decoupling the presence of pathogen from the risk of transmission. We undertook a multi-faceted investigation of Hendra virus shedding in *Pteropus* bats –combining insights from virus isolation data with longitudinal shedding, and integrating measures of viral load and prevalence– to target patterns in infectious shedding. We show that periods of high viral load in bats aligned with Hendra virus spillover risk, irrespective of prevalence, and suggest that previously observed low-intensity shedding may not reflect excretion of infectious virus or align with spillover risk. By recognizing the potential for non-infectious shedding, and accommodating viral load into estimates of prevalence, we provide an indication of the spillover risk posed by infectious bats. Understanding the amount of virus potentially available for recipient hosts as a key determinant of the probability of spillover will be crucial for developing effective and targeted strategies for managing exposure risk. Incorporation of viral load into longitudinal studies of virus excretion could better inform periods and places of higher spillover risk and would be a valuable addition to other longitudinal bat surveys.

Relative Influences of Environmental, Historical, and Spatial Factors on Beta Diversity of Japanese Bats

Takahiro Maki[1], Nozomi Sannomiya[1], Toshihide Hirao[2] and Dai Fukui[3]

1 Graduate School of Agricultural and Life Sciences, University of Tokyo, Tokyo, JPN; 2 University of Tokyo Chichibu Forest, University of Tokyo, Saitama, JPN; 3 University of Tokyo Hokkaido Forest, University of Tokyo, Hokkaido, JPN

Determining how bat diversity has been shaped is one of the key challenges in mammalogy and provides fundamental information for bat conservation. At the metacommunity scale, the community structure is mainly determined by representative three processes, niche-based, spatial, and historical processes. The factors determining the community structure of bats have been intensively studied in the New World, however, they have been less studied in the Old World, especially in Asia. In our study, the relative contribution of the three processes on structuring assemblages of bats in Japan was investigated. The bat distribution data were collected from 1,501 pieces of literature and assigned to the First Standard Grid (FSD) of Japan (approximately 6400 km^2). As niche-based environmental factors, current climate, geographical topology, and land use were implemented into the models. As spatial factors, the variables calculated from Moran's eigenvector maps were implemented. As historical factors, past climate and the Tsugaru strait which is considered as one of the most influential biogeographical borders in the Japanese archipelago were used. The relative contributions of the three processes were examined by variation partitioning with distance-based RDA. The fraction of the three processes totally explained 58% of the variation in assemblage composition of Japanese bats. The pure fraction of the niche-based environmental process significantly affected the composition of the bats and the other pure fraction did not have significant effects. Our result suggests that the patterns of bat assemblages in Japan are driven by a niche-based process involving the current environment.

Breaking the Cultural Divide for Better Subterranean Conservation

Stefano Mammola[1,2]

1 Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, Helsinki, FIN; 2 Molecular Ecology Group, Water Research Institute, National Research Council, Pallanza, ITA

Caves are the colliding point of diverse scientific cultures. Since the 19th century, geologists, meteorologists, ecologists, and anthropologists have wandered in the darkness of caves, populating the specialized literature with a wealth of fascinating scientific ideas, hypotheses, and stories of adventurous explorations. On paper, this diversity of viewpoints is an asset, and indeed caves are increasingly regarded as ideal model systems to answer broad-in-scope and general scientific questions. More often, however, these diverse disciplines fail to exchange ideas with each other. In terms of conservation efforts, this may come at a cost. It is not unusual, for example, that conservation interventions designed for a specific organism (say, a cave-roosting bat) overlook carry-over effects on other ecosystem components (say, the arthropod fauna or some geological dynamic). A cross-pollination of ideas among researchers from different scientific backgrounds would enhance the implementation of conservation interventions able to embrace the entirety of the subterranean ecosystem. Therefore, we have to confront a central question: How can we effectively break this cultural divide? Some possible ways forward include: i) limiting discipline-specific jargon in our everyday writing; ii) exposing ourselves to other scientific disciplines; iii) broadening our reading habits outside our niche expertise. These are just preliminary ideas, and there is not a single prescription that will work in all cases. However, when considering that the first author of this abstract is a spider expert who was invited to give a talk at the International Bat Research Conference, it appears we are moving in the right direction.

Identifying Landscape Use and Key Resources for Livingstone's Flying Foxes in Comoros

Isabella Mandl[1,2], Jon Flanders[2] and Hugh Doulton[3]

1 Department of Botany and Biodiversity Research, University of Vienna, Vienna, AUT; 2 Bat Conservation International, Austin, USA; 3 Dahari, Mutsamudu, COM

The Comoros archipelago, located in the Mozambique channel has suffered from one of the highest rates of deforestation in the world since the 1980s. Nearly all accessible surface area on the island of Anjouan has been converted from cloud forest to agroforestry or agricultural land. The present study investigates how the endemic and Critically Endangered Livingstone's flying fox (*Pteropus livingstonii*) copes with this habitat loss by investigating its use of the landscape and identifying key resources, such as feeding areas. Long-term GPS-tracking of multiple individuals since

2019 revealed that the bats' ranges cover all major landscape classes as they visit forested, agroforestry, and agricultural areas. The different landcover classes are utilized differently; the flying foxes visit agricultural lands only to feed (and temporarily roost) in individual tree clusters that have been left standing in-between fields. Their permanent day roosts on the other hand are located in agroforestry and forested areas. These results indicate that natural, forested habitat is important for the bats' survival but also illustrate the need for protection of remaining clusters of native trees throughout the landscape as a critical food source.

Exploring Noninvasive Methods to Assess Body Condition in Live Bats

Mary Beth Manjerovic[1,2], Michelle L. Green[3], Anna C. Dilger[4], Rachel M. Santymire[2,5], Jean M. Mengelkoch[6], Joyce E Hofmann[6] and Nohra E Mateus-Pinilla[6,7]

1 Department of Biology, Virginia Military Institute, Lexington, USA; 2 Lincoln Park Zoo, Chicago, USA; 3 Department of Integrative Biology, University of South Florida, St. Petersburg, USA; 4 Department of Animal Sciences, University of Illinois, Urbana-Champaign, USA; 5 Department of Biology, Georgia State University, Atlanta, USA; 6 Illinois Natural History Survey, Prairie Research Institute, University of Illinois, Urbana-Champaign, USA; 7 Departments of Pathobiology, Animal Sciences, and Natural Resources and Environmental Sciences, University of Illinois, Urbana-Champaign, USA.

Bats infected with *Pseudogymnoascus destructans* often are found with depleted fat stores reinforcing the hypothesis that the fungus disrupts normal hibernation physiology. Developing a noninvasive method to assess body condition more accurately in living bats is critical to address hypotheses that connect white-nose syndrome and overwinter survival across different species and environments. We used bats from The Illinois Natural History archived, rabies negative collection to assess the reliability of a noninvasive MRI technique to quantify fat and muscle mass in adult male and female big brown bats (*Eptesicus fuscus*), little brown bats (*Myotis lucifugus*), silver-haired bats (*Lasionycteris noctivagans*), and Eastern red bats (*Lasiurus borealis*). We found little difference between males and females, but seasonal variation was more pronounced in big brown bats compared to little brown bats with the former adding significantly more fat in months leading up to winter. Our findings suggest MRI technology is a valid method for determining fat and muscle mass in live bats and has applicability not only to questions relating to disease ecology and management but also to understanding impacts of changing environments.

Winter Bat Activity: The Role of Wetlands as Food and Drinking Reservoirs under Climate Change

Maria Mas[1,2], Carles Flaquer[1], Xavier Puig-Montserrat[1,3], Xavier Porres[4], Hugo Rebelo[5,6,7] and Adrià López-Baucells[1]

1 Biodiversity and Bioindicators Research Group, Natural Sciences Museum of Granollers, Catalonia, ESP; 2 Centro de Investigación Ecológica y Aplicaciones Forestales, Universitat Autònoma de Barcelona, Catalonia, ESP; 3 Galanthus Association, Catalonia, ESP; 4 Ebro Delta Natural Park, Generalitat de Catalunya, Catalonia, ESP; 5 Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus de Vairão, Universidade do Porto, Vairão, PRT; 6 Centro de Investigação em Biodiversidade e Recursos Genéticos, Instituto Superior de Agronomia, Universidade de Lisboa, Lisboa, PRT; 7 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus de Vairão, Vairão, PRT

Bat arousals during hibernation are related to rises in environmental temperature, body water loss and increasing body heat. Therefore, bats either hibernate in cold places or migrate to areas with mild winters to find water and insects to intake. During winter, insects are relatively abundant in wetlands with mild climates when low temperatures hamper insect activity in other places. However, the role of wetlands to sustain winter bat activity has never been fully assessed. To further understand bat behavior during hibernation, we evaluated how the weather influenced hibernating bats, assessed the temperature threshold that increased bat arousals, and discussed how winter temperatures could affect bat activity under future climate change scenarios. The effects of weather and landscape composition on winter bat activity were assessed by acoustically sampling four different habitats (wetlands, rice paddies, urban areas and salt marshes) in the Ebro Delta (Spain). Our results show one of the highest winter bat foraging activities ever reported, with significantly higher activity in wetlands and urban areas. Most importantly, we found a substantial increase in bat activity triggered when nocturnal temperatures reached ca. 11 °C. By contrasting historical weather datasets, we show that, since the 1940s, there has been an increase by ca. 1.5 °C in winter maximum temperatures and a 180% increase in the number of nights with mean temperatures above 11 °C in the Ebro Delta.

Genomic Mechanisms Contributing to Adaptive Host Response to White-nose Syndrome

Brooke Maslo[1], Robert Kwait[1], Sarah Gignoux-Wolfsohn[2], Evan Eskew[3], Maarten Vonhof[4], Malin Pinsky[1], Craig Willis[5], Brooke Hines[6], Carl Herzog[7], Alyssa Bennett[8] and MacKenzie Hall[9]

1 Department of Ecology, Evolution and Natural Resources, Rutgers, The State University of New Jersey, New Brunswick, USA; 2 Smithsonian Environmental Research Center, Edgewater, USA; 3 Pacific Lutheran University, Tacoma, USA; 4 Western Michigan University, Kalamazoo, USA; 5 University of Winnipeg, Winnipeg, CAN; 6 Hines Ecological, USA; 7 New York Department of Environmental Conservation, Albany, USA; 8 Vermont Fish and Wildlife, Essex Junction, USA; 9 New Jersey Division of Fish and Wildlife, Lebanon, USA

The magnitude of population-level declines in bats affected by white-nose syndrome (WNS) varies among species, likely based on a combination of physical, genetic, and behavioral factors. Although devastated by early outbreaks of WNS, little brown bat (*Myotis lucifugus*) populations appear to have stabilized in recent years. Several studies have investigated the potential for rapid evolution in this species, and to date, nearly 100 single nucleotide polymorphisms (SNPs) putatively under selection by WNS have been discovered. In contrast, Indiana bats (*M. sodalis*) exhibit a different and opposite pattern of annual survival following WNS exposure, with relative mild but persistent annual population declines. This trend suggests that WNS may be a weaker selective force on Indiana bats than on little brown bats. If so, demographic recovery of infected Indiana bat populations by resistant individuals is unlikely, and this species may require different, more intensive conservation interventions to promote recovery. We conducted an analysis of genomic changes in *M. sodalis* populations before and after exposure to WNS. We performed low-coverage whole-genome sequencing of 330 wing biopsy punch samples gathered from five different regions before and after the onset of WNS. We then performed a genome wide scan for selection comparing SNPs between pre- and post-WNS samples for each region to examine changes in allele frequency coinciding with WNS emergence. We compare the number, location, and putative function of candidate SNPs with those identified in *M. lucifugus,* and we quantify the strength at which selection is acting upon them.

Fatal Attraction? Elevated Bat Activity at Wind Turbines and Implications for Planning Policy

Fiona Mathews[1], Suzanne Richardson[2], Paul Lintott[2,3], Theo Economou[4] and David Hosken[5]

1 School of Life Sciences, University of Sussex, Falmer, UK; 2 Biosciences, University of Exeter, Exeter, GBR; 3 University of West of England, Bristol, GBR; 4 College of Engineering, Mathematics and Physical Sciences, University of Exeter, Exeter GBR; 5 Centre for Ecology and Conservation, University of Exeter, Exeter, GBR

Bat casualties at wind farms are a pressing concern given the continued expansion of this form of renewable energy generation. Although individual bats have been observed approaching wind turbines, and fatalities frequently reported, it is unclear whether bats are actively attracted by, are indifferent to, or are repelled by the turbines at large wind-energy installations. In this study, we assessed bat activity simultaneously at paired turbine and control locations on each of 23 British wind farms using broadband acoustic detectors. The research focused on *Pipistrellus* species, which were by far the most abundant bats recorded at these sites. *Pipistrellus pipistrellus* activity was 37% higher at turbines than at control locations, whereas *P. pygmaeus* activity was consistent with no attraction or repulsion by turbines. Given that more than 50% of bat fatalities in Europe are *P. pipistrellus*, these findings help explain why Environmental Impact Assessments conducted before the installation of turbines are poor predictors of actual fatality rates. They also suggest that operational mitigation (minimizing blade rotation in periods of high collision risk) is likely to be the most effective way to reduce collisions because the presence of turbines alters bat activity. Prediction of future risks prior to construction, though helpful in guiding locations away from highly sensitive locations, cannot be relied upon as a means of avoiding impacts on *P. pipistrellus* since this species is not only widespread but also appears to alter its behavior in response to turbine presence.

Foraging Patch-use and Interindividual Interactions When Multiple Bats Compete Based on Echolocation and Social Call Analysis

Kana Matsuoka[1], Kiho Fujii[1], Emyo Fujioka[1,2,] Dai Fukui2 and Shizuko Hiryu[1]
1 Faculty of Life and Medical Sciences, Doshisha University, Kyotanabe, JPN; 2 Graduate School of Agricultural and Life Sciences, University of Tokyo, Tokyo, JPN

In the optimal patch-use model, foragers are assumed to attempt to maximize energy intake rate. In this study, to elucidate the patch-use strategy of echolocating bats in the wild, we measured echolocation sounds emitted by Japanese large-footed bats, *Myotis macrodactylus*, using a 16ch microphone array system surrounding a pond where they come to forage one after another. The results showed that in 63% of cases when multiple individuals competed for a foraging patch, bats left the patch earlier than the bats that arrived to forage alone later. The tendency to leave earlier was more pronounced when the number of captures was high. Since foraging of multiple individuals in an environment with reflections from the water surface is likely to have a high cost of acoustic interference, it is considered that individuals who have sufficiently foraged will leave the patch to avoid interference. We then therefore focused on the social calls to understand the interaction between individuals as they enter and leave the patch. As a result, we identified two types of social calls from a 45-min sound sequence that were clearly different in structure from echolocation calls, one a repeated 'trills' (n = 7) and the other a long-duration sound (n = 5). The former calls were observed when the bat was being chased by another bat, suggesting it is associated with avoidance behavior. The latter calls were often measured when the bats were leaving the patch, suggesting that the bats were most likely communicating information about the patch.

Looking into the "Magic Well" – a Glimpse from 40 Years with Brazilian Free-tailed Bats

Gary F. McCracken
Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, USA

Karl von Frisch, who won a Nobel Prize in 1973 for discovering the "dance" of honeybees, called honeybees a magic well - the more he learned about them, the more he was rewarded with surprising and exciting discoveries. In 2001, sixty-three years after discovering that bats use ultrasound to avoid obstacles and catch flying insects, Don Griffin borrowed the magic well metaphor to describe studies of echolocation in bats - no matter how much was learned about how bats find their way in the dark, there was more to discover. Forty years ago, I chose to study Brazilian free-tailed bats because their nursing behavior challenged basic concepts in evolutionary biology. With that paradox resolved, my students and I, along with many others, have continued to work with these bats as they became our magic well, providing new questions and unexpected discoveries. As we begin this joint meeting of the 19th IBRC and 50th NASBR, I reflect on the contributions that studies of Brazilian free-tailed bats have made to our knowledge of numerous aspects of bat biology. With Brazilian free-tailed bats as my guide, I explore where we've been, what we know, and challenges and opportunities for future research, as we all look into the magic well of bats. As Brock Fenton, who discovered that "bats don't read the literature", has asserted "the bats, themselves are the magic well".

Bats Flying at High Altitudes

Gary F. McCracken[1], Ya-Fu Lee[2], *Erin H. Gillam[3], Winifred Frick[4,5], and Jennifer Krauel[1]
1 Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, USA; 2 Department of Life Sciences, National Cheng Kung University, Tainan, TWN; 3 Department of Biological Sciences, North Dakota State University, Fargo, USA; 4 Bat Conservation International, Austin, USA; 5 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

At the second North American Symposium on Bat Research, the first reported use of radar to study flight behavior in bats confirmed that Mexican free-tailed bats (*Tadarida brasiliensis mexicana*) fly at altitudes over 3,000 m above the ground. The reasons for these high-altitude flights were unclear, and it was assumed that the bats flew this high to commute to favorable foraging sites. Large numbers of insects now are known to utilize favorable winds at altitudes of hundreds to thousands of meters aloft to assist their long-distance movements. Dietary analyses and deployment of bat detectors to altitudes up to 1,100 m confirm that Mexican free-tailed bats alter their behavior to feed heavily on these insects, many of which are major agricultural pests. Next generation radars confirm the movements and high-altitude intersection of bats and insects. Doppler weather radars continuously monitor and archive information on the emergence and dispersal of bats, providing long-term data on the bats' ecology, behavior, and estimates of population sizes. Bat species regularly fly to high altitudes on all continents where they occur, and many of these bats are confirmed or suspected of feeding on migratory insects. The high-altitude habitat remains poorly known, as are the physiological adaptations, behaviors, and sensory cues that bats use to meet the challenges and opportunities of flying at high altitudes. Advancing technologies should continue to aid future research to investigate the high-altitude frontier and make discoveries about the ecology and behavior of bats aloft.

Guano Among Bat Species from Two Regions Shows Influences of Geography and Diet on Bacterial Community

Thomas McElroy[1], Shannon Whitney[1] and Lydia Moore[2]
1 Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, Kennesaw, USA; 2 Palmetto Bluff Conservancy, Bluffton, USA

Studies of bat guano have shown that the diversity and structure of associated microbial communities can be related to factors such as host phylogeny, life history and reproductive stage, geography, and diet. Many insectivorous bat species in the southeastern U.S. have generalist diets that may shift seasonally to take advantage of abundant prey species or maximize caloric intake. Seasonal shifts in prey availability or consumption should be reflected in a guano microbiome change. We also expected to detect distinct guano microbiomes within species. Within species, distinct microbial communities related to geography, and finally life history and reproductive stage. We compared the bacterial communities in bat guano collected directly from five species and two regions of the USA. Guano was collected opportunistically during netting events from May to October from the Appalachian foothills (Rome, GA), and the coastal plain (Bluffton, SC). DNA was extracted from 160 samples. DNA elutions were pooled for samples based on collection time and species ID. We sequenced the 16S rDNA barcode regions (V3, V4). Qiime2 was used to filter reads and assign taxonomy (green genes reference classifier). The bacterial community detected in the Rome samples showed a seasonal shift related to diet shift in big brown bat and red bat samples. Samples from Rome had greater bacterial diversity among species; whereas, samples from Palmetto Bluff were more similar to each other. Overall geography and diet were important factors related to the diversity and structure of the guano bacterial community.

Migration Ecophysiology: The Influence of Heterothermy in Migrating Bats and Birds
Liam P. McGuire
Department of Biology, University of Waterloo, Waterloo, CAN

Migration has long fascinated biologists and the public alike. There are many examples of small-bodied migrants that make amazing journeys each year, leading to the inevitable question: “How do they do it?” As a graduate student interested in bat migration, there was little literature on which I could rely, and instead I used migratory birds as a model to ask the question “What can birds tell us about the migration physiology of bats?” In the years since, my group has conducted studies of migrating bats and consistently identified the role of heterothermy as a key difference between the way bats migrate and typical bird migration models. We have incorporated the idea of torpor-assisted migration into optimal migration theory models and empirically tested those models to demonstrate that the use of torpor affects many aspects of migration including fuel storage and stopover duration. By using daily torpor, bats reduce the influence of inclement weather or poor habitat quality encountered at stopover along the migration route. These energy savings may explain regional-scale wandering movements that we have observed using the Motus Wildlife Tracking System as torpor-assisted migration precludes the requirement for extended refueling stopovers in high-quality habitat. The importance of torpor-assisted migration in bats led us to reevaluate heterothermy use by migrating birds, and in ongoing work we have demonstrated that many also use heterothermy during migration, albeit to a lesser degree. The question has now become “What can bats tell us about the migration physiology of birds?”

Efficient and Repeatable Data Pipeline for Continental-scale Passive Acoustic Surveys
Matthew W. McKown[1], Olivia Vasquez[1], Kerry Dunleavy[1] and Winifred F. Frick[2,3]
1 Conservation Metrics, Inc. Santa Cruz, USA; 2 Bat Conservation International, Austin, TX, USA; 3 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, CA, USA

Steady advancements in wildlife sensor capabilities and automated classification techniques have made it possible to expand the spatial and temporal scale of wildlife surveys in recent years. The North American Bat Monitoring Program (NABat) has embraced these advances to create a continental scale acoustic survey effort to monitor the status and trends of the 47 bat species found in the United States and Canada. Here we discuss a collaboration between Conservation Metrics, Bat Conservation International, and the NABat Program to create a rigorous, standardized, and efficient workflow for processing large volumes of acoustic survey data from across the United States. Since 2019, we have processed 18,407 NABat survey nights from 1,218 locations within 343 GRTS Cells located in 35 States and have uploaded the acoustic data files and classification results to NABat. Our workflow includes a series of error checks to clean data before it is processed, batch embedding of metadata into files using the Guano standard, species classification with both SonoBat and Kaleidoscope Pro software, and manual vetting of an optimized subset of species predictions. Results from this processing workflow have contributed to related research projects to improve the statistical analyses of NABat data and to the creation of a new Machine Learning bat species classification model. We see this work as part of a larger emerging opportunity to improve global-scale biodiversity monitoring efforts by enabling the efficient generation of standardized species detection data from sensor-based surveys for bats, other terrestrial mammals, birds, frogs, and insects.

Fluid-preserved Bat Museum Specimens Retain Original Stable Hydrogen Isotope Signatures: Implications for Migration Research
Edward D. Medeiros[1], Liam P. McGuire[2], Fred J. Longstaffe[3], Richard Stevens[4] and *Erin E. Fraser[1]
1 School of Science and the Environment, Memorial University of Newfoundland, Grenfell Campus, Corner Brook, CAN; 2 Department of Biology, University of Waterloo, Waterloo, CAN; 3 Department of Earth Sciences, University of Western Ontario, London, CAN; 4 Department of Natural Resources Management, Texas Tech University, Lubbock, USA

Stable hydrogen isotope techniques are widely used to assign probable areas of origin to migratory animals, including bats. Latitudinal gradients in the stable hydrogen isotope composition (2H) of meteoric water make this system well-suited to studies of long-distance aerial migrations. In studies of bat migratory systems, analyses of fur - a keratinous tissue - are common. Fur samples may be taken from museum specimens and the specimens selected are usually dry study skins. Many museum specimens, however, are stored in fluid preservative and the effects of fluid preservation on the stable carbon and nitrogen isotope compositions of various tissues are well-studied and may be significant. We know of no similar investigations on the effects of fluid preservation on the 2H of keratinous tissues. We hypothesized that preservation in fluid does not alter the 2H of bat fur and investigated using a two-pronged approach with bat specimens from the Museum of Texas Tech University. We (i) placed 5 *Perimyotis subflavus* carcasses in each of three common preservatives (formalin, ethanol, and isopropyl alcohol), sub-sampling fur over the following six months and (ii) compared the 2Hfur of dry and fluid-preserved *Sturnira lilium*, *Dermanura tolteca*, and *Carollia sowelli* that had been collected at matched locations between 50 to 30 years previously. We found no differences in the 2Hfur following fluid preservation over the short or longer term. We conclude that fluid-preserved museum specimens are a useful source of samples for future stable hydrogen isotope investigations of bat migration.

Global Assessment of the Effectiveness of Conservation Actions for Subterranean-roosting Bat Species
Melissa B. Meierhofer[1], Joseph S. Johnson[2], Janette Perez-Jimenez[2], Fernanda Ito[1,3], Paul W. Webela[4], Sigit Wiantoro[5], Enrico Bernard[3], Krizler C. Tanalgo[6], Alice Hughes[7,8], Pedro Cardoso[9], Thomas Lilley[1] and Stefano Mammola[9,10]

1 BatLab Finland, Finnish Museum of Natural History Luomus, University of Helsinki, Helsinki, FIN; 2 Department of Biological Sciences, Ohio University, Athens, USA; 3 Laboratório de Ciência Aplicada à Conservação da Biodiversidade, Federal University of Pernambuco, Recife, BRA; 4 Department of Forestry and Wildlife Management, Maasai Mara University, Narok, KEN; 5 Museum Zoologicum Bogoriense, Research Center for Biosystematics & Evolution, National Research and Innovation Agency, Bogor, IDN; 6 Ecology and Conservation Research Laboratory, Department of Biological Sciences, College of Science and Mathematics, University of Southern Mindanao, North Cotabato, PHL; 7 Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Yunnan, CHN; 8 Center of Conservation Biology, Core Botanical Gardens, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Yunnan, CHN; 9 Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, Helsinki, FIN; 10 Molecular Ecology Group, Water Research Institute, National Research Council, Pallanza, ITA

The conservation of subterranean-dwelling bats is a challenging endeavor, involving the need to account for multiple anthropogenic threats and their combined effects. Yet, current knowledge on effective conservation measures is far from organized and exhaustive. To identify the effectiveness of conservation and management interventions, and to understand to what extent actions overlap those employed for other taxa, we conducted a systematic review of peer-reviewed and grey literature focused on subterranean-dwelling bats. From the papers that statistically tested interventions, we extracted all associated statistical measures to perform a meta-analysis. Our results indicate that although gating is routinely applied, its effectiveness is not clear and is rarely tested despite their frequent construction. Restoration efforts and disturbance reduction had a positive effect on bat populations and bat behavior, respectively, but were rarely tested in the literature. Decontamination had a negative effect on pathogens, particularly with studies focused on reducing fungal spores associated with white-nose syndrome. Finally, although the trend was positive, the effectiveness of monitoring techniques on bat populations are unclear and rarely tested. Startlingly, only 4% of the bat studies simultaneously consider other organisms. However, there are similarities in the interventions mentioned with all organisms. If we take care to consider other organisms when applying interventions, we may successfully take those taxa under our wing through our efforts to conserve bats.

Bugs, Berries, and Blood: Diet and Heterothermy

Katelyn C. Miller, Miranda Dunbar
Biology Department, Southern Connecticut State University, New Haven, USA

Torpor is a well-known energy-saving technique used by some endotherms to survive in cold, food-scarce environments. Perhaps unexpectedly, recent studies show heterothermy is also used in warm, tropical and subtropical climates. While incredibly diverse, Neotropical bats have received less research attention as it pertains to their thermoregulatory capabilities. Our experiment explores how body size and diet affect torpor in Neotropical bats. As part of my undergraduate honors thesis, we will capture bats in neotropical forests of Belize to sample adult, nonreproductive insect-, fruit-, and blood-feeding species. Bats will be housed individually and allowed to rest 812h overnight at ambient temperature, ensuring they are postabsorptive and in the resting phase of their circadian rhythm prior to experimental trials. We will measure rectal temperature before and after inducing torpor by placing bats in an environmental chamber for up to 2 h at 12 ˚C. After experimental trials, bats will be allowed to reacclimate, drink water and eat their natural food source before being released at their capture site. We predict that smaller bats will go deeper into torpor regardless of diet because they are less able to retain heat, and insectivorous and vampire bats will go deeper into torpor due to their greater basal metabolic rate differentials and nutritive quality of food. Our work contributes to the growing body of knowledge regarding heterothermic diversity and will provide insight into the evolutionary significance of torpor.

Foraging Activity at Vernal Pools in the California Floristic Province

Shahroukh Mistry[1,2], Leandra C. Boodoo[1], Colleen A. Hatfield[1] and Donald G. Miller III[1]
1 Department of Biological Sciences, California State University, Chico, USA; 2 Department of Biological Sciences, Butte College, Oroville, USA

The California Floristic Province is a global biodiversity hotspot with over 3,500 plant species, sixty percent of which are endemic. Vernal pools are one of the most unique and vital components within this Mediterranean ecosystem. These ephemeral seasonal wetlands, depressions that flood during winter rains and are dry throughout the remainder of the year, are home to numerous endemic and listed species. This habitat has been under significant stress, with over ninety percent lost due to human activities, primarily agriculture. Vernal pools are comprised of open waters with abundant insects, yet this habitat has not been well studied for bat activity. We examined foraging activity of bats at vernal pools of the Vina Plains Preserve in Tehama County using acoustic recorders for several months and analyzed the calls for species identification as well as feeding buzzes. The Mexican free-tailed bat, *Tadarida brasiliensis*, was the dominant species at this site comprising over ninety percent of all identified recordings, and *Myotis* spp. accounted for most of the other calls. Bats were present at vernal pools throughout the year with the highest activity during the spring and autumn, and lowest activity in the hot and dry summer. About half of the recordings included feeding buzzes, and buzzes were significantly higher at the vernal pools compared to a control grassland site one km from the pool, suggesting that these seasonal wetlands are an important habitat for bat foraging.

Evaluating Temporal and Spatial Distribution of Leptonycteris yerbabuenae on the Barry M. Goldwater Range East

Ronald J. Mixan, Emily H. Scobie and *Bradford J. Milbrandt
Arizona Game and Fish Department, Phoenix, USA

The lesser long-nosed bat (*Leptonycteris yerbabuenae* (LLNB)) has recently been delisted under the Endangered Species Act (ESA), and is listed as a species at risk on the Barry M. Goldwater Range East (BMGR East) located in southern Arizona. We detected the first LLNB roost on BMGR East during routine monitoring efforts in May 2016, which represented a 22 km northern range extension. We designed a study to further understand the spatial and temporal distribution and habitat use patterns for LLNB on BMGR East. We focused on two primary methods including evaluation of potential LLNB acoustic calls across five long-term towers on BMGR East, and tracking individual LLNB with the use of store on-board GPS transmitters. Acoustic monitoring results varied across sites, with the majority of LLNB calls recorded at two sites. The highest number of calls were recorded in 2017, with the lowest recorded in 2016 and 2018. Our acoustic records document the arrival and departure of LLNB at the extreme northern end of their range, and any changes in spatial use that may occur. We deployed a total of 21 GPS transmitters at a maternity roost located 24.7 km from the BMGR East boundary in July, 2019 and again in July, 2021. The six recovered GPS transmitters revealed varying average distances traveled per night from 12.3 km to 67 km. From these fixes, we did not observe LLNB utilizing washes as travel corridors, and observed more or less straight-line movements to and from foraging areas.

Penang's Bats and Their Conservation Status: An Update Since 2000

Mansour Saad Abuqasim Mohamed[1,2], Nur-Izzati Abdullah[3,4], Lee-Sim Lim[4] and *Nurul-Ain Elias[1]
1 School of Biological Sciences, Universiti Sains Malaysia, Penang, MYS; 2 Department of Zoology, Faculty of Science, Sebha University, Sabha, LBY; 3 Department of Social Informatics, Graduate School of Informatics, Kyoto University, Kyoto, JPN; 4 School of Distance Education, Universiti Sains Malaysia, Penang, MYS

The composition of Penang's bat community has not been compiled since the 1980s. We expected a local extinction among bat species due to the current changes in Penang's landscape. Therefore, bat surveys by harp trapping and mist netting were conducted between November 2014 and December 2019 to update the community of bats on this island. A total of 2152 individual bats from 25 species and seven families were captured. This survey added seven species from the previous study on the island part of Penang, Malaysia. Based on literature and a recent survey, Penang listed 46 species of bats from seven families. The mainland area recorded 38 species, while the island had 33 species. *Coelops frithii*, *Myotis ater*, and *Myotis siligorensis* were the three species of bats only recorded on the island. A few species of bats were no longer recorded in Penang after the year 2000, including *Pteropus vampyrus*. According to the International Union for the Conservation of Nature (IUCN) and the Peninsular Malaysia Red List of Mammals, two-thirds of the bats in Penang are classified as Least Concern, with three species classified as Near Threatened (*Kerivoula intermedia*, *Myotis ridleyi*, and *Dyacopterus spadiceus*). The rest of the species have a mixed conservation category (Data Deficient and Vulnerable) either at global or national level. Continuous bat monitoring at different landscape gradients and increasing public awareness of bats are the main focus for bat conservation in Penang.

Functional Diversity of African Bats is Influenced by Elevation

Ara Monadjem[1] and Adam Kane[2]
1 University of Eswatini, Kwaluseni, SWZ; 2 University College, Dublin, IRL

Bats represent a speciose and globally widespread mammalian group, making them valuable subjects for macroecological research. Species richness typically responds negatively to elevational gradients, with some taxa showing a mid-elevational peak before declining at higher elevations. In this study, we examine the influence of elevation and bioclimatic variation on species richness and functional diversity of bats surveyed at 98 localities across sub-Saharan Africa. At each locality, we listed bat species together with elevation and environmental variables. We then compiled morphological, functional and habitat traits for each bat species. We used RLQ and fourth-corner analysis to relate species traits to environmental factors, and generalized least squares to create models relating functional diversity to environmental factors. Species richness declined monotonically with elevation and was significantly lower in upland sites (> 1600 m) compared with lowlands. Functional richness mirrored species richness. In contrast, functional evenness, divergence, and dispersion all increased with elevation. Furthermore, the functional group "edge foragers" increased with increased range in daily temperature and declined with isothermality, while "fruit bats" showed exactly the opposite associations. Open-air foragers, in contrast, declined with increased rainfall. An increase in evenness at upland sites demonstrates that bat assemblages here comprise species that are more uniformly separated on functional traits compared with lower sites, while increased divergence suggests the presence of more specialist species compared with the lowlands. This study demonstrates a link between the functional diversity of African bat communities and elevation, drawing attention to the importance of incorporating metrics from other components of biodiversity.

Climatic Niche Differentiation Illuminates Biogeographic Patterns in Caribbean *Eptesicus fuscus*

Pedro I. Mônico[1], Camilo A. Calderón-Acevedo[1,2] and J. Angel Soto-Centeno[1,3]
1 Department of Earth and Environmental Sciences, Rutgers University, Newark, USA; 2 Department of Environmental and Forest Biology, The State University of New York College of Environmental Science and Forestry, Syracuse, USA; 3 Department of Mammalogy, American Museum of Natural History, New York, USA

The Caribbean archipelago had a complex climatic and geologic history. Evolutionary processes like ecological release, genetic drift, and reproductive isolation act to promote population diversification or speciation in the biodiversity of these islands. Thus, a signature of divergence in suitable habitats among populations should be evident. We used Ecological Niche Models (ENMs) to examine the habitat suitability for Caribbean and mainland populations of a generalist bat in North America, *Eptesicus fuscus*. Considering the wide distribution, complex natural history, and the genetic and morphological variation observed among populations, we suspect that the taxonomic diversity of *E. fuscus* could be underestimated. Our ENM approach revealed a wide niche breadth for some populations of E. fuscus, but high levels of niche specialization in others, like in the island of Hispaniola where suitable habitats for *E. fuscus* seem to be structured primarily at high elevations. We also found that suitable environmental conditions of *E. fuscus* from the Caribbean more closely resemble conditions of Florida than those in Mexico. Given that closely related taxa are more likely to retain similar niche occupancy, this could indicate that Caribbean *E. fuscus* could have originated from a Florida population. Our results provide evidence of niche differentiation between populations of *E. fuscus* in the Caribbean. Allied with previous morphological assessments and future phylogeographic analyses, our research could unveil the tempo and mode of evolutionary processes and biogeography of *E. fuscus* in this region.

Bat Diversity and Natural Pest Control in Afrotropical Forests and Agroecosystems

Cecilia M. Montauban[1], Adam J. M. Devenish[1], Ivana Budinski[2], Nathaniel N. D. Annorbah[3], Evans E. Nkrumah[4], Helen L. Taylor-Boyd[5], Andreanna J. Welch[6] and Joseph A. Tobias[1]
1 Department of Life Sciences, Imperial College London, Ascot, GBR; 2 Department of Genetic Research, Institute for Biological Research "Siniša Stanković", Belgrade, SRB; 3 Department of Biological, Physical and Mathematical Sciences, University of Environment and Sustainable Development, Somanya, GHA; 4 Department of Wildlife and Range Management, Kwame Nkrumah University of Science and Technology, Kumasi, GHA; 5 Biological and Environmental Sciences, University of Stirling, Stirling, GBR; 6 Department of Biosciences, Durham University, Durham, GBR

Increasing agricultural production to meet rapidly growing demand for food is driving widespread conversion of natural habitats to arable land. Safeguarding biodiversity while improving food security of local communities remains a key global challenge, especially in regions such as Sub-Saharan Africa, where the population is expected to double by 2050. To develop sustainable solutions that work for nature and humanity, we need to understand how we can harness natural regulation processes like pest control. Bats are widely regarded as a major predator of crop pests, yet little is known about them in African agroecosystems. We investigated the role of bats as natural pest consumers across a land-use gradient, from intact forest to cropland, in two contrasting Afrotropical systems, Zambia and Ghana. A total of 2151 bats of 61 species were captured across

four field seasons between April 2021 and March 2022. From these individuals, 1517 fecal samples were collected, of which 1180 are from insectivorous bats. By gathering data on species diversity, morphological and acoustic traits, and diet, we examine land-use change effects on their taxonomic and functional diversity, trophic networks, and pest control services. Preliminary results show that bat species richness and functional diversity varies across the gradient, with different patterns of occurrence and land-use change effects in Zambia and Ghana. By combining ecological and metabarcoding dietary data, including the identification of agricultural pests in their diets, we aim to improve the knowledge of ecosystem services Afrotropical bats provide in human modified landscapes, and how habitat changes affect them.

Low Tendency to Arouse from Torpor following Nontactile Disturbance in Desert Hibernating Bats (Arizona, USA)
Marianne S. Moore[1], Hayden K. Hutcherson[1] and Angela L. McIntire[2]
1 College of Integrative Sciences and Arts, Arizona State University, Mesa, USA; 2 Arizona Game and Fish Department, Phoenix, USA

The high tendency of bats to arouse from torpor when disturbed by human activities is documented for many species. This costly response is one reason for declining bat populations and underlies the design and implementation of long-term management programs protecting imperiled species (e.g., the endangered *Myotis sodalis*). Here we show a potentially different phenotype for tendency to arouse after a nontactile disturbance in bats hibernating in the desert Southwest (Arizona, USA). On 150 occasions, we opportunistically collected repeated thermal images (FLIR T540) of hibernating bats in three north-central AZ caves while collecting data for a larger study on winter ecology and physiology that uses only nontactile methods. Species included *Corynorhinus townsendii*, *Parastrellus hesperus*, *Eptesicus fuscus*, and *Myotis* species. Bats were located during internal cave surveys and an initial thermal image was collected immediately whenever possible. We captured a maximum of eight images (i.e., time points) up to six hours after our initial observation of each bat. Across all time points, we found that <5% of bats increased surface body temperatures above ambient. These results were generated during surveys involving up to six researchers using multiple pieces of equipment, though we kept our movements as efficient and quiet as possible. We hypothesize that desert populations may be generally less apt to arouse during hibernation to conserve body water, a trait that could also lower sensitivity to disturbance.

Foraging Ecology of an Ozark Big-eared Bat Maternity Complex in Western Arkansas
Patrick R. Moore[1], Gemma Keegan[2], Jorista Garrie[2], Pedro Ardapple[3], Mathew Anderson[4] and Benjamin J. Merritt[1]
1 Environmental Solutions & Innovations, Inc, Cincinnati, USA; 2 Biological Sciences Department, Arkansas Tech University, Russellville, USA; 3 United States Fish and Wildlife Service, Conway, USA; 4 United States Forest Service, Russellville, USA

The Ozark big-eared bat (*Corynorhinus townsendii ingens*) is a federally endangered subspecies restricted to north-central/western Arkansas and northeast Oklahoma. Although the population is estimated at less than 2,000 individuals, few previous studies evaluate nightly movements or habitat preferences. A two-year foraging study is in progress at a maternity complex in the Ozark St. Francis National Forest in Franklin County, Arkansas to assess the colony's foraging ecology in response to a gradient of prescribed fire and timber management activities. In 2021, 13 Ozark big-eared bats were radio-tagged, including 11 females and two males, during two trapping events. Each tagged cohort was tracked for seven nights using synchronized azimuths from at least five telemetry stations and generated a total of 431 locations. Using uniform-density kernel estimates on 11 bats and 404 locations, the generated mean home range (n = 431) was 804 ± 148 ha, and the mean core-foraging area was 121 ± 49 ha. Telemetry error was 316 ± 67 ha. The second year of study is anticipated in summer 2022. At completion, foraging areas will be described, and mixed-effects models will be used to evaluate preferences of forest-management types, stand composition, stand age, canopy height, elevation, slope magnitude, aspect, proximity to roost habitat, and proximity to water. Linking frequency of use with specific management activities can provide a better understanding of how active management affects the foraging behavior of Ozark big-eared bats. The results of the foraging analysis will be shared at the North American Society for Bat Research in August 2022.

Two Forms of Visual Surveys Indicate Population Trends for Rock Roosting Eastern Small-footed Bats
Paul R. Moosman, Jr.[1], Robert E. Adelstein[1] and Rick J. Reynolds[2]
1 Department of Biology, Virginia Military Institute, Lexington, USA; 2 Virginia Department of Wildlife Resources, Verona, USA

Winter cave and mine surveys are an important monitoring tool for some species of bats, but the method is not equally effective across species and regions. Many bat species that have poorly understood winter populations roost in rocky habitat features during the active season. In North America, > 40% of bat species roost in rock outcrops in some part of their range, and aggregations of bats at such sites represent underutilized opportunities to assess their populations. We used a dual survey approach to assess the status of the rock-roosting eastern small-footed bat (*Myotis leibii*) in Virginia, a species with uncertain population status. We estimated the abundance of bats roosting on 6 talus slopes using random plot surveys in June and July, from 2013–2021, and compared these data with surveys from 11 hibernacula, from 1969–2021. Negative binomial generalized linear models suggested abundance declined at some hibernacula but was stable or increased at others, and the trend in overall winter numbers was neutral (β ± se = -0.007 ± 0.024). Abundance in winter was slightly lower before white-nose syndrome (WNS) arrived in Virginia (β ± se = -0.46 ± 0.20; p = 0.024). Similarly, abundance on talus slopes varied between sites (p = 0.004) but the overall trend in summer populations appeared stable over time (β = -0.08 ± 0.06; p = 0.19). Talus surveys produced comparable results to hibernacula surveys and they have improved the sensitivity and reliability of monitoring for eastern small-footed bats in Virginia. We recommend a similar approach for monitoring talus-roosting bats in other regions, where hibernacula data may be sparse or potentially unreliable.

Natural Isolation: Egyptian Fruit Bats' Behavioral Response to an Immunological Challenge and Implications for Disease Transmission
Kelsey R. Moreno[1], Maya Weinberg[1], Lee Harten[1], Valeria B. Salinas Ramos[2,3], L. Gerardo Herrera M.[3], Gabor A. Czirjak[4] and Yossi Yovel[1,5]
1 Department of Zoology, Tel Aviv University, Tel Aviv, ISR; 2 Department of Agriculture, University of Naples Frederico II, Naples, ITA; 3 Estacion de Biologia Chamela, Universitdad Nacional Autonoma de Mexico, Mexico City, MEX; 4 Department of Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU; 5 Sagol School of Neuroscience, Tel Aviv University, Tel Aviv, ISR

While a highly effective behavioral strategy, social living carries many risks, such as increased pathogen and parasite transmission. How highly social, and especially free-ranging, mammals mitigate this risk is poorly understood. We used lipopolysaccharide (LPS) injection to imitate bacterial infection in both a captive and a free-ranging colony of an extremely social mammal – the Egyptian fruit bat (*Rousettus aegyptiacus*). We monitored behavioral and immunological responses using an arsenal of methods, including on-board trackers, video, weights, and blood immune markers. LPS-challenged bats exhibited an increased immune response, as well as classical illness symptoms including fever, weight loss, anorexia, and lethargy. Notably, in both colonies immune challenged individuals actively isolated themselves from the group for approximately two days by

leaving the social cluster. This is in stark contrast to the normal, high contact behavior of this species and differs from the manner in which social connections to sick individuals are reduced in other vertebrates. Concurrently, free-ranging individuals ceased exiting the colony room to forage, confirming that well-established findings of foraging cessation in laboratory and livestock settings extend to free-ranging animals as well. Such behaviors likely directly benefit infected individuals by conserving energy, supporting the immune response, and minimizing predation risk while reducing risk of contagion to group members and spill-over events. Further work following bacterial transmission patterns aims to provide more detail on the precise effects of these behaviors on contagion.

Bats and their Unique Immunity and Metabolic Adaptations

Diana Moreno-Santillan
University of California Berkeley, Berkley, USA

Comprising more than 1400 species, bats possess adaptations unique among mammals including powered flight, slow life history and unusual longevity despite small size. While positive selection has been found in molecular mechanisms of DNA repair and immune function genes, analyses to date have been limited to a few highly divergent lineages, reducing the scope of inference for gene family evolution. Here we compare whole-genome data for 42 phylogenetically divergent bat species, with a particular emphasis on multi-gene family evolution. In agreement with previous analyses, we find lineage-specific expansions of the APOBEC family, whose roles intersect metabolic and immune functions, and complete loss of the pro-inflammatory PYHIN gene family across the whole clade. Consistent with the evolution of unusual immune responses against intracellular pathogens such as viruses, we found evidence of positive selection and shifts in the duplication rate of interferons. Given the important metabolic role of members of the APOBEC family, we investigated links between expansions and unique dietary adaptations as well as hibernation, these links implicate shifts in ecological demands with the evolution of both novel sugar-based diets of frugivorous and nectarivorous species, and the emergence of hibernation as an energy-saving strategy. Taken together, our analyses support the hypothesis of a unique set of pleiotropic adaptations to flight shifting the metabolic profile of the clade as a whole, with subsequent changes in immune function in tandem with evolving metabolic demands driven by novel diets and extreme environments.

Use of Railway Underpass Tunnels on a Northern Landscape by Endangered Bats in Ontario, Canada

Derek Morningstar[1] and Steven Kell[2]
1 Myotistar, Cambridge, Ontario, CAN; 2 Shawanaga First Nation, Ontario, CAN

Endangered species in Canada are protected directly, as well as the habitat that they use. However, the protection of their habitat requires an understanding of the breadth of habitat types preferred by those species. Railway underpass tunnels are often disregarded as potential hibernation sites for bats because of their water and air flow and presumed lack of thermal protection. The regular disturbance from overhead rail traffic is also considered a deterrent. However, in the traditional territory of the Shawanaga First Nation, we have identified the first known use from bats of multiple species using these tunnels, both through acoustic survey and physical entry. The tunnels vary in length and depth and the range in over-winter temperature and humidity. Peaks in acoustic activity during both spring emergence and fall swarming indicate the use of this resource by bats, later confirmed with photo evidence of them in the winter. Moreover, they move between these tunnels throughout the winter, evidence shown as some tunnels had bats present in January but not in November. Future studies will use radio-telemetry to track the movements of bats among these tunnels during swarming and early hibernation and potentially on larger movements though the Motus system. We recommend that these types of tunnel structures along railways should be inspected for bat presence in other areas, especially where those bats are protected under Species-at-Risk legislation.

Epidemic Waves of Highly Diversified Henipa-related Viruses in Egyptian Rousette Bats, South Africa

Marinda Mortlock[1], Marike Geldenhuys[1], Muriel Dietrich[2], Jonathan H. Epstein[1,3], Jacqueline Weyer[1,4,5], Janusz T. Pawęska[1,4,5] and Wanda Markotter[1]
1 Department of Medical Virology, University of Pretoria, Pretoria, ZAF; 2 UMR Processus Infectieux en Milieu Insulaire Tropical, Reunion Island, FRA; 3 EcoHealth Alliance, New York, USA; 4 Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases of the National Health Laboratory Services, Johannesburg, ZAF; 5 Department of Microbiology and Infectious Diseases, University of Witwatersrand, Johannesburg, ZAF

The Egyptian rousette bat species (*Rousettus aegyptiacus*) has been identified as a host to a range of viral species such as paramyxoviruses related to the Henipavirus genus, which is associated with zoonotic diseases of high consequence in Asia and Australia. We expanded these findings by assessing the viral dynamics in a southern African Egyptian rousette population through a longitudinal biosurveillance study targeted towards henipavirus diversity and excretion. A total of 2567 samples collected between 2012–2019 either from individual bats (spleen, urine, and rectal swabs), or from the cave floor beneath roosting bats (urine and fecal), were tested for the presence of henipavirus RNA using a hemi-nested RT-PCR targeting the conserved polymerase gene of members in the Orthoparamyxoviridae sub-family. Phylogenetic analysis identified 18 putative Henipavirus and genus-related viral species, and through analysis of the temporal excretion dynamics, three viruses were shown to display different seasonal dynamics. The winter and spring periods for the local region were identified as high-risk for virus spillover and transmission. Additionally, annual peaks in viral excretion are likely driven by subadults and might be linked to the waning of maternal immunity and recolonization of the roost. Given that longitudinal excretion studies of bat-borne pathogens are limited, these findings provide insight into this bat-virus relationship which can be extrapolated to other countries across the geographical distribution of the Egyptian rousette bat. Furthermore, findings can be communicated to local communities to aid in prevention measures of exposure, spillover, and transmission of viral pathogens from bats.

Bats on the Move: Modeling Seasonal Changes in Species Distributions on a Global Scale

Shelby P. Moshier, Jamin Wieringa and Bryan Carstens
Evolution, Ecology and Organismal Biology Department, Ohio State University, Columbus, USA

Identifying how species interact with and move around their environment is a fundamental goal of ecological research. Patterns of species' movements are well understood in iconic groups of organisms such as insects, fish, and birds that often display large-scale and conspicuous seasonal migratory movements across the landscape. Chiropterans represent a group where we know seasonal movements occur in some species, but our understanding of the patterns and factors influencing these movements is lacking. One method of studying these patterns are species distribution models (SDMs), which combine ecological distribution data and environmental variables in a statistical framework to predict the range of a species

during a given period of time. Here we used SDMs to study spatiotemporal patterns and predictors of seasonality in bats. We built seasonal SDMs for almost 400 species worldwide, the most extensive model set for bats to date. Then, using these models, we assessed the importance of bioclimatic variables, trait data, and life history information as factors that influence when and why bats are moving around the landscape. We also calculated quantitative measures of the degree to which a species' tracks their niche through the seasons and centroid distance to approximate the distance of seasonal movement. These measures of niche overlap and centroid distance differed depending on family and bats known or suspected to be migratory had longer centroid distances. Climate, morphological traits associated with flight and diet, and dietary guilds were also important predictors of the spatiotemporal patterns of distribution change in bats.

The Past, Present, and Future of Bat Research in Mongolia

Dalannast Munkhnast[1,2], Joseph R Hoyt[3] and Jargalsaikhan Ariunbold[1,2]
1 Department of Biology, Mongolian National University of Education, Ulaanbaatar, MNG; 2 Bat Research Center of Mongolia, Ulaanbaatar, MNG; 3 Department of Biological Sciences, Virginia Polytechnic Institute, Blacksburg, USA

Bats in Mongolia have received considerably less attention from researchers and the general public compared to other charismatic mammalian species. There are currently 19 species of bats that have been recorded in Mongolia, most of which are listed as data deficient by the IUCN. This underscores the lack of attention on bats across Mongolia, and further research and collaborative work is needed. First, we will summarize over a hundred years of scientific observations collected on Mongolian bats and second, we will provide an overview of knowledge gaps where further research is needed. We performed a literature review, including expedition reports, books, and peer-reviewed papers published from 1863 to 2022. We then examined these studies to determine the research focus. We found that previous research (before 2000) focused on investigation of bat species diversity, morphology, and distributions. This work was mostly contributed by Russian explorers, scientists and Mongolian researchers. Over the last two decades (from 2000 to 2022), we find that research has expanded to cover bat ecology, as well as numerous aspects of phylogeny, genetic diversity, taxonomic revisions, and infectious disease (host-pathogen interactions and ectoparasites). This work was primarily conducted by joint teams between Mongolian researchers and international researchers in Canada, Germany, Korea, and the United States. Results from these past and ongoing research efforts will be particularly important to enhance conservation of bats in Mongolia. However, large knowledge gaps still remain, related to long-term population monitoring, and questions about the greatest conservation threats.

Automate Species Identification of Bat Echolocation Calls Using Artificial Intelligence

Kevin L. Murray, Thomas Prebyl, Jared Swenson and Kimberly J. Bay
Western EcoSystems Technology, Inc, Bloomington, USA

Acoustic detectors are commonly used to remotely monitor bat populations. The resulting acoustic recordings must be classified by a bat biologist with expertise in call classification in order to obtain reliable information. The rarity of this expertise and time constraints have prompted efforts to automatically classify bat species in acoustic recordings using a variety of learning methods. There are several software programs available for this purpose, but they are imperfect and the United States Fish and Wildlife Service often recommends that a qualified acoustic analyst review bat call identifications even if using these software programs. We built a model to classify bat species using modern computer vision techniques. We used innovative data management techniques to isolate echolocation pulses and produce images of echolocation calls. These echolocation images were used to train deep learning computer vision models that automatically classify bat calls to species. Our model classifies 10 bat species from eastern North America, several of which have protected status. We found that both our validation accuracy (93%) and testing accuracy (90%) were relatively high and that our software performed well when compared to other automated identification software. Our results indicate that our approach is effective at classifying bat species from acoustic recordings, and our trained model will be incorporated into new bat call identification software: WEST-EchoVision.

Retinal Ganglion Cell Topography and Spatial Resolution in Three Indian Pteropodid Bats

Baheerathan Murugavel[1], Mindaugas Mitkus[2,3], Hema Somanathan1 and Almut Kelber[2]
1 IISER TVM Centre for Research and Education in Ecology and Evolution (ICREEE), School of Biology, Indian Institute of Science Education and Research Thiruvananthapuram, Kerala, IND; 2 Lund Vision Group, Department of Biology, Lund University, Lund, SWE; 3 Institute of Biosciences, Life Sciences Center, Vilnius University, Vilnius, LTU

Pteropodidae is the only phytophagous bat family that predominantly depends on visual and olfactory cues for orientation and foraging. During the day, pteropodid bats of different species roost in sites with varying light exposure. Pteropodids have larger eyes relative to body size than insectivorous bats. Retinal topography has been studied in less than 10% of the approximately 200 pteropodid species, a behavioral estimation of spatial resolution is available only for *Pteropus giganteus* (currently *medius*), and little is known about the relationship between their roost site preference and visual ecology. Here, we present retinal ganglion cell topography topographic maps and theoretical estimates of spatial resolution in three southern Indian pteropodid species with different roosting preferences. The foliage-roosting *Cynopterus sphinx* and the cave-roosting *Rousettus leschenaultii* have a similar anatomical spatial resolution (2.7 and 2.8 cycles/degree, respectively). The anatomical estimate for the larger tree-roosting *P. giganteus* is higher (4.0 cycles/degree) than the spatial resolution that had been determined in behavioral tests. Like other pteropodids and unlike other vertebrates, all three studied species have choroidal papillae. Based on all 15 pteropodid species studied to date, roost type has no relationship to eye size or visual acuity. For a general understanding of the sensory ecology of pteropodid bats, that perform key ecosystem services in the tropics, it will be essential to study additional species in the future.

The Relationship Between Sensory-Mechanical Modularity and Disparity, and its Association with Dietary Diversity

Gregory L. Mutumi[1], Ronald P. Hall[2], Brandon P. Hedrick[3], Laurel R. Yohe[4,7], Alexa Sadier[5], Kalina T.J. Davies[6], Stephen J. Rossiter[6], Karen E. Sears[5], Liliana M. Dávalos[7,8] and Elizabeth R. Dumont[1]
1 Life and Environmental Sciences, University of California–Merced, Merced, USA; 2 Graduate Program in Quantitative Systems Biology, University of California–Merced, Merced, USA; 3 Department of Cell Biology and Anatomy, School of Medicine, Louisiana State University Health Sciences Center, New Orleans, USA; 4 Department of Earth and Planetary Science, Yale University, New Haven, USA; 5 Department of Ecology and Evolutionary Biology, University of California-Los Angeles, Los Angeles, USA; 6 School of Biological and Chemical Sciences, Queen Mary University of London, London, GBR; 7 Department of Ecology and Evolution, Stony Brook University, Stony Brook, USA; 8 Consortium for Inter-Disciplinary Environmental Research, School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, USA

Many studies find that fitness is linked to feeding morphology, behavior, and performance. Novel feeding structures open new niches and correlate with diet in vertebrate lineages. High disparity in sensory systems is also associated with increased dietary diversity in several clades. The skull supports feeding structures and sensory systems that allow animals to navigate their surroundings and effectively forage and feed. Although mechanical and sensory structures coexist in the head, their relationships and interactions remain unknown. The combination of divergent cranial morphologies and sensory system volumes in phyllostomids makes them an ideal system for testing hypotheses concerning degree of integration of sensory and feeding traits in relation to morphological disparity and taxonomic radiation. Within the bat superfamily Noctilionoidea, we analyzed hard and soft tissue scans of 35 ecologically diverse species. We evaluated the modularity of mechanical and sensory structures and tested their association with dietary niche and morphological disparity. According to our findings, mechanical and sensory modules form two distinct super-modules, and the degree of modularity of these two suites varies across taxa. The disparity of sensory and mechanical systems, whether considered separately or together, is correlated with the modularity of sensory systems rather than mechanical systems. The interaction between sensory and mechanical modules appears to moderate the degree to which each system occupies shape-space. Additionally, the predominant influence of sensory modularity on disparity shows that sensory ecology possibly plays a leading role in the radiation of taxa, supporting a sensory first hypothesis of movement into new dietary niches.

Range-wide Population Structure of Hoary Bats, Eastern Red Bats, and Silver-haired Bats

Juliet Nagel[1], Bryan C. Carstens[2], H. Lisle Gibbs[2], Jamin G. Wieringa[2] and David M. Nelson[1]
1 Appalachian Laboratory, University of Maryland Center for Environmental Science, Frostburg, USA; 2 Department of Evolution, Ecology, and Organismal Biology and Ohio Biodiversity Conservation Partnership, Ohio State University, Columbus, USA

Long-distance migratory bat species are killed in large numbers at industrial wind-energy facilities each year, especially hoary bats (*Lasiurus cinereus*), eastern red bats (*L. borealis*), and silver-haired bats (*Lasionycteris noctivagans*), yet many questions remain about basic population demographics such as size and structure. Previous genetic studies with these species used samples from a fraction of each species' range, sometimes just a single location. Here we address the following question: What is the population structure of hoary bats, eastern red bats, and silver-haired bats across North America? To accomplish this, we used Genotype-by-Sequencing (GBS) to analyze 375 genetic samples from dozens of locations spread across the species' ranges. Most (75 %) samples were from turbine-killed bats; smaller numbers came from live-captured bats, museums, or rabies labs. All samples were from bats caught or collected during their summering period, as defined by previously published stable hydrogen isotope data from their fur. Illumina reads were processed using the Stacks bioinformatics pipeline and analyzed for single-nucleotide polymorphisms (SNPs). Population structure for each species was assessed using principal component analysis (PCA). Hoary bats and eastern red bats showed no geographic pattern, supporting panmictic population structure for these species. The PCA for silver-haired bats revealed longitudinal population structure along component 1, which accounted for 2.06% of all variation. Geographically, this results in an apparent east-west separation near the Rocky Mountains, though with some spatial overlap.

Has White-nose Syndrome Changed the Behavior or Physiology of Little Brown Bats?

Lauren M. Nash[1], Haven S.J.S. Soto[1], Kristina A. Muise[1], Yvonne A. Dzal1, Quinn E. Fletcher[1], Liam P. McGuire[1], Kaleigh J.O. Norquay[1], Quinn M.R. Webber[1], Anuraag Shrivastav1 and *Craig K.R. Willis[1]
1 Department of Biology and Centre for Forest Interdisciplinary Research, University of Winnipeg, Winnipeg, CAN

Recent research has identified genotypic shifts in bats surviving white-nose syndrome (WNS) but phenotypic changes are not well understood. Pre-hibernation fat reserves could affect overwinter survival and remnant bats from some hibernacula now store more winter fat than bats did before WNS. Behavioral traits, like sociability and activity, could also shift because they can affect risk of infection and energy expenditure. We studied pre- and post-WNS Myotis lucifugus in Manitoba, Canada to test whether WNS has changed pre-hibernation body mass, plasma triglycerides (an index of food intake), sociability (tendencies of individuals to associate with others) and activity (rates of movement in the environment). We captured swarming bats before and after WNS invaded in 2017. In 2013 and 2019 we measured body mass and plasma triglycerides. In 2014 and 2018 we used a y-maze to quantify sociability and activity. We found no change in body mass or triglycerides but sociability scores shifted after WNS. The direction of this shift differed from our prediction, however, with post-WNS bats more sociable than pre-WNS bats ($p = 0.0006$). We cannot rule out within-individual plasticity as an explanation but sociability, as measured in the y-maze, is repeatable in bats and heritable in other taxa so these differences could reflect evolutionary change. Increased sociability could be selected for if it increases tendencies of individuals to seek out other bats for social thermoregulation during spring WNS recovery. Understanding phenotypic shifts following WNS could be important for management because these shifts could influence habitat requirements of remnant populations.

Tracking Silver-haired Bat Migrations in Western North America Using Multiple Stable Isotopes

Kyle R. Nelson[1], Geoff Koehler[2] and Brian M. Starzomski[1]
1 School of Environmental Studies, University of Victoria, Victoria, CAN; 2 NHRC Stable Isotope Laboratory, Environment and Climate Change Canada, Saskatoon, CAN

Wind energy development is a recognized and expanding threat to migratory bats, including North America's silver-haired bat (*Lasionycteris noctivagans*). Silver-haired bats are known to overwinter in the Georgia-Puget Lowland, an area of temperate coastal climate stretching from Vancouver, Canada to Portland, USA. However, the migratory origins of these overwintering individuals are unknown, although expanding wind energy development in adjacent regions could pose a threat along their migratory routes. Stable isotopes have been used to identify silver-haired bats' latitudinal movements east of the Continental Divide, but the mountainous geography of western North America has been prohibitive to migratory studies that often depend on only one stable isotope, commonly hydrogen. We modeled the spatial distributions of multiple stable isotopes, carbon, nitrogen, and hydrogen, using hair samples from museum specimens of silver-haired bats collected across the western portion of their range. We used these isotope distributions and the stable isotope values from individuals overwintering in the Georgia-Puget Lowland to determine areas of probable migratory origin. Our preliminary results show evidence of multiple migration strategies for silver-haired bats overwintering in the Georgia-Puget Lowland. Some individuals show little to no migratory movement, while others travel up to 1000 km across mountain ranges to overwinter in the temperate climate of the Pacific coast. These results demonstrate the applicability of using multiple stable isotopes to studying migratory movements in western North America, and that the longitudinal movements of silver-haired bats potentially put them into conflict with regions of expanding wind energy development between their summer and winter grounds.

An Unexpected Topology for Phyllostomidae and its Implications for the Evolution of Diet
Nicolas Nesi[1], Joshua Potter[2], Joseph Walker[3], Kalina Davies[2], Laurel Yohe[4], Liliana Dávalos[5] and *Stephen Rossiter[2]
1 Microbial Adaptation Research Group, Normandy University, Caen, FRA; 2 Department of Biological and Behavioural Sciences, Queen Mary University of London, London, GBR; 3 Department of Biological Sciences, University of Illinois at Chicago, Chicago, USA; 4 Department of Geology and Geophysics, Yale University, New Haven, USA; 5 Department of Ecology and Evolution, Stony Brook University, New York, USA

Leaf-nosed bats (family Phyllostomidae) are a model system for understanding the evolution of diet. From a putative insectivorous ancestor, members of this clade diverged to feed on fruit, nectar, blood and vertebrates. Here we describe a large-scale phylogenetic reconstruction of the Phyllostomidae based on coding sequences for 13,000 loci from 47 species from across the group. Our well-resolved tree indicates that the subfamily Phyllostominae—which mostly specialize on vertebrates or arthropods—evolved from plantivores. This unexpected topology is recovered by different methods and points to striking convergent evolution in diet. First, either plant-feeding evolved twice in phyllostomid bats, in the glossophagines and subsequently in the clade comprising the frugivores and lonchophyllines, or plant-feeding evolved once with a subsequent reversal to an animal-based diet in the phyllostomines. We consider the implications of these results for the evolution of diet and metabolism.

Estimation of Roost Fidelity of Kitti's Hog-nosed Bat Using Mark-Recapture Approach
Thongchai Ngamprasertwong[1], Monsicha Wangthongchaicharoen[1] and Paul A. Racey[2]
1 Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, THA; 2 Centre for Ecology and Conservation, University of Exeter, GBR

Karst landscapes are highly sensitive to human disturbance, especially in western Thailand where Kitti's hog-nosed bat, *Craseonycteris thonglongyai*, lives in limestone caves near rivers. Due to its small size, this cave-dwelling bat has little energy reserves and its foraging range is limited within less than a kilometer from its roost. However, there is little information on roost use of this bat species as well as its faithfulness to its roost. With the tiny size of p-Chip (500 x 500 x100 microns), this laser-light-activated microtransponder provided an opportunity for tagging the world's smallest bat species. From December 2018 to July 2020, Kitti's hog-nosed bats were caught monthly after returning from foraging after dusk or before dawn at a limestone cave in Sai Yok District, Kanchanaburi Province. A total of 277 bats were tagged with p-chips and 70 (25%) were recaptured during the study period. No sign of damage or inflammation caused by p-chip tagging was observed in all recaptured bats, both in the short term (few days) and the long term (<3 years). Higher recapture rates were observed during the breeding season (January to June) whereas those in the non-breeding season (July to December) were lower. The highest recapture rate (60–80%) was found during the lactation period (May and June). Lower roost fidelity in the non-breeding season suggests the possibility of a roost network structure and temporary movement between nearby roosts.

Water-works? Implications of Large-scale Everglades Restoration for Bats, Particularly the Endangered Florida Bonneted Bat
Laura P. Nicholson[1], Elizabeth C. Braun de Torrez[2] and Holly K. Ober[3]
1 Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, USA; 2 Florida Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, Gainesville, USA; 3 Department of Forest Ecosystems and Society, Oregon State University, Corvallis, USA

Wetlands provide critical foraging habitat for bats, but over half of wetlands worldwide are degraded or destroyed. Although wetland restoration efforts have increased, little is known about the impact on bats. Understanding these effects is important for endangered species like the Florida bonneted bat (*Eumops floridanus*). We investigated the impacts of a large-scale hydrologic restoration in the Florida Everglades to document habitat use by *E. floridanus* and the greater bat community. We conducted acoustic surveys at 194 sites across a restoration gradient (unrestored, partially restored, restored, and reference) in 2020 and 2021, and recorded 16 nights across 4 distinct sampling periods spanning the dry and wet seasons. We measured hydrologic and vegetation metrics to investigate drivers of bat activity within the context of restoration. Acoustic files were classified in Kaleidoscope Pro and all *E. floridanus* calls were manually verified. Generalized linear mixed models indicated that restoration status was significant for both response variables, but with greatest activity in the unrestored category for the greater bat community, and greatest activity in reference category for *E. floridanus*. Both activity of the greater bat community and *E. floridanus* were driven by temperature, vegetation community, and percent forest edge. In addition, *E. floridanus* activity increased with hydroperiod and distance to canals, whereas activity of the bat community was not driven by hydroperiod and decreased with distance to canals. Insights from this study will inform immediate management decisions for this endangered species and contribute to our understanding of how bats are influenced by hydrologic restoration.

Could Summer Roosting Habitat Enhancement Help Bats Recover from White-nose Syndrome?
Kaleigh J.O. Norquay[1], Quinn E. Fletcher[1], Nicole A.S.-Y. Dorville[1], Christina M. Davy[2], Gabriela Mastromonaco[2] and Craig K.R. Willis[1]
1 Department of Biology and Centre for Forest Interdisciplinary Research (C-FIR), University of Winnipeg, Winnipeg, CAN; 2 Department of Biology, Carleton University, Ottawa, CAN; 3 Toronto Zoo, Toronto, CAN

Many strategies proposed to address white-nose syndrome (WNS) involve actions during winter. For most species at risk, however, protection and enhancement of critical habitat is often most fundamental. For bats recovering from WNS, high quality summer habitat could reduce stress, improve condition and increase reproduction. We tested this habitat enhancement hypothesis for *Myotis lucifugus* in central Canada. Between 2016 and 2019 we installed one three-chamber roost box within 20 m of the entrance to one of 39 *M. lucifugus* maternity colonies. Boxes at 19 colonies were enhanced with black exterior insulation, an interior heating coil and a thermostat set to 30°C, just below thermoneutrality. Boxes at the remaining 20 control colonies were simply painted black. By 2019 all sites were WNS-positive and half of experimental boxes showed evidence of occupation. Compared to controls, enhanced boxes had warmer, more stable temperatures. Cortisol, which reflects chronic stress, was lower in guano collected beneath enhanced boxes ($p < 0.001$). During spring, pregnant females from colonies with enhanced boxes were heavier (12.1 ± 1.7 g) than those from colonies without enhanced boxes (10.7 ± 1.5 g, $p = 0.004$). Moreover, once pups were flying, the ratio of juveniles to adults at colonies with an enhanced box was also greater (0.43 ± 0.30 versus 0.22 ± 0.27 for controls, $p = 0.03$). Our results support the habitat enhancement hypothesis and highlight the importance of summer roosts for WNS-affected bats. Determining how we might enhance habitat for more forest-dependent species, less likely to use artificial structures (e.g., *M. septentrionalis*), should be a priority for WNS research.

Why Eat Bats? Attitudes, Norms and Access
Benneth Chigozie Obitte and Tigga Kingston

Department of Biological Sciences, Texas Tech University, Lubbock, USA.

Hunting for consumption is a leading cause of bat extinction. In Sub-Saharan Africa, 20% of all bat species are consumed for protein, highlighting an important conservation threat and risk of zoonotic disease spillover. The potential of interventions to promote positive behavioral change toward bat conservation is now well established, but the effectiveness of such plans hinges on their ability to identify and target the drivers of behavior. To understand why people consume bats as a foundation of effective intervention planning, we employed the Theory of Planned Behavior (TPB) framework. The Theory of Planned Behavior stipulates that the intention to perform a behavior is a function of three sociological constructs: attitude, subjective norm, and perceived behavioral control. To evaluate the relative contributions of these constructs, TPB operates in a structural equation modeling framework. We administered 812 questionnaires across three communities in southern Nigeria that frequently eat the cave-dwelling fruit bat, *Rousettus aegyptiacus*. Questionnaires were based on TPB. We also collected socio-economic data. Across the three communities, about 50% of respondents consumed bat meat. Positive attitudes towards bat meat consumption was largely driven by taste and affordability. In addition, most respondents were more likely to eat bat meat because their friends did so, highlighting the influence of the subjective norm as a driver of bat meat consumption. Findings from this study will provide a more comprehensive understanding of bat meat consumption behavior to strengthen the effectiveness of conservation interventions and reduce public health risks.

Survey On Hunters' Profiles, Practices, Motivations and Perceptions to Progress Towards Adaptive Management of Flying Foxes

M. Oedin[1,2,3,4], A. Millon[4], J. Brouillon[5], E. Vidal[6], VD. Dang[1], JJ. Cassan[1], S. Noury[1], M. Brinkert[1], C. Meresse[7] and F. Brescia[2]
1 Direction du Développement Economique et de l'Environnement, Koné, NCL; 2 Institut Agronomique néo-Calédonien, Equipe Agriculture Biidiversité et valorisation), Païta, NCL; 3 Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, Aix Marseille Université, CNRS, IRD, Avignon Université, Nouméa Cedex, NCL; 4 Aix Marseille Université, CNRS, IRD, Avignon Université, Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, Technopôle Arbois-Méditerranée, Aix-en-Provence, FRA; 5 Institut Agronomique néo-Calédonien, Equipe équipe Territoires, Acteurs et Usages), Centre de Recherches Nord Thierry Mennesson, Pouembout, NCL; 6 UMR Entropie, Université de La Réunion, CNRS, Labex-Corail, Institut de Recherche pour le Développement, Nouméa Cedex, NCL; 7 Direction du développement durable des territoires, Centre administratif de la province Sud, Nouméa Cedex, NCL

In New Caledonia, South Pacific, flying-foxes (*Pteropus ornatus and tonganus*) are hunted for food by all communities and by the indigenous Kanak community for cultural purposes as well. This hunting, both legal and illegal, represents a large and unsustainable annual harvest. In order to provide advisory services to managers, we conducted a survey to better understand hunters and their current practices. In 2020, we collected 680 anonymous hunter questionnaires from the Northern Province (NP) and the Southern Province (SP), 70% of which were flying-fox hunters. Among flying-fox hunters, we found significant differences between NP and SP regarding their type of residence, their hunting motivations and their number of hunting trips in 2019 ($p < 0.05$). Their age, number of flying-foxes hunted per hunter per trip in 2019, and their level of compliance with regulations were not significantly different between NP and SP ($p > 0.05$). Among flying fox-hunters, we found a significant difference between their type of residence regarding their hunting motivations, their level of reconciliation with regulations, their number of hunting trips, and their number of flying-foxes hunted per hunter and per trip in 2019 ($p < 0.05$). Thus, although the spatial ecology of these species would lead us towards management at the archipelago scale, socio-cultural specificities in terms of hunting practices and use of flying-foxes seem to differentiate the NP and the SP. This work highlights the need for parallel studies, in ecology on species and in social sciences on hunting, to implement adaptive management of hunted species.

Studying Community and Trophic Structure in Neotropical Bat Faunas

Phillip J. Oelbaum[1,2], Kenneth C. Welch Jr.[1,2], Hugh G. Broders[3], Melissa R. Ingala[4,5] and Nancy B. Simmons[5]
1 Department of Biological Sciences, University of Toronto Scarborough, Toronto, CAN; 2 Department of Cell and Systems Biology, University of Toronto, Toronto, CAN; 3 Department of Biology, University of Waterloo, Waterloo, CAN; 4 Department of Biological Sciences, Fairleigh Dickinson University, Madison, USA; 5 Department of Mammalogy, American Museum of Natural History, New York, USA

Neotropical bat faunas are among the most diverse mammalian communities in the world, with species that span at least six trophic guilds: frugivores, nectarivores, insectivores, carnivores, piscivores, sanguivores. In some areas there are dozens of sympatric bat species foraging and reproducing at the same time. Studying these assemblages may permit us to address central questions in ecology, such as "how can so many species coexist?" Using stable isotope analysis, we examined the ratios of carbon (δ13C) and nitrogen (δ15N) in hair to measure the two-dimensional trophic niches of 35 species of bats captured at Lamanai and Ka'kabish in Belize. We plotted species niche breadth to make inferences about the overall structure of the community in isotope space. Whereas ecologists have often grouped bat species into broadly organized trophic guilds, we found that many species did not fit into their predicted guild, and that there is significant overlap among perceived guilds. Additionally, we found numerous cases of overlapping isotopic niches for species within guilds, indicating potential for interspecific competition. Overlapping diets were also found in fecal metabarcoding data from our study area, suggesting that many species overlap in what prey species and plant items they are eating on a nightly basis. Intraspecific variation in diet should also be considered as a mechanism for interspecific coexistence, particularly supporting large populations of similar species at the same locality. Species with broader trophic niches (generalists) may help facilitate resource sharing with species that have narrow niches (specialists).

Bat Energetics and Modeled Implications on White-nose Syndrome Susceptibility

Sarah H. Olson[1], Dan Crowley[2], Brett Dickson[3], Yvonne A. Dzal[4,5], Nathan Fuller[6], Catherine Haase[7], David T. S. Hayman[8], Reed Hranac[8], Emily M. Johnson[6], Emma L. Kunkel[6], Cori L. Lausen[9], Meredith L. McClure[3], Liam P. McGuire[10], Raina K. Plowright[2], Kirk Silas[1] and Craig K. R. Willis[4]
1 Wildlife Conservation Society, Health Program, Bronx, USA; 2 Montana State University, Department of Microbiology and Immunology, Bozeman, USA; 3 Conservation Science Partners, Truckee, USA; 4 University of Winnipeg, Department of Biology, Winnipeg, CAN; 5 Bat Conservation International, Austin, USA; 6 Texas Tech University, Department of Biological Sciences, Lubbock, USA; 7 Austin Peay State University, Department of Biology, Clarkesville, USA; 8 Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, Palmerston North, NZL; 9 Wildlife Conservation Society Canada, Kaslo, CAN; 10 University of Waterloo, Department of Biology, Waterloo, CAN

White-nose syndrome (WNS) mortality varies considerably among species, populations, and individuals. We hypothesized that this differential mortality is related to species-level bioenergetic traits and environmental factors. We tested our hypothesis using empirical data and

bioenergetic models. At pre-WNS-arrival sites, located across large latitudinal (~2900 km) and longitudinal (~2100 km) gradients, we measured morphometric traits of 3073 bats, representing 14 species, and collected environmental data within hibernacula. We conducted respirometry (n = 506 bats) and quantitative magnetic resonance (n = 249 bats). We evaluated these new data to create inter- and intraspecific energetic profiles of hibernation physiology for 13 species. Analyses revealed interspecific variation in rates of evaporative water loss formed two species clusters, with high and low rates matching levels of WNS mortality. These hibernation energetic data allowed us to populate a refined mechanistic WNS survivorship model that now includes evaporative water loss, to make inferences about WNS susceptibility for different species. We incorporated the mechanistic survivorship estimate as a predictor of winter occurrence, along with landscape attributes, in an ecological niche model to estimate the pre-WNS occurrence probability of five species. We then updated these estimates under conditions of WNS exposure and future climate change predictions to project their combined impacts. These data, analyses, and modeling tools are presented to help inform bat management and mitigation activities, such as species listings, by identifying significant predictors of winter habitat, rate of evaporative water loss as a WNS risk factor, as well as likely susceptible and more resilient species and populations.

Who Migrates? Phylogenetic and Population Perspectives on Migration in Changing Climates

M. Teague O'Mara[1,2,3] and April M. Wright[1]

1 Department of Biological Sciences, Southeastern Louisiana University, Hammond, USA; 2 Department of Migration, Max Planck Institute of Animal Behavior, Radolfzell, DEU; 3 Smithsonian Tropical Research Institute, Gamboa, PAN

Migration is a seemingly simply resource-driven behavior where an individual moves between two locations. However, the distance traveled, timing, physiological preparation, and demographics of who migrates varies greatly among bat species. These migratory movements require large energetic investment and entail considerable risk as animals move from current habitats and foraging areas, to those that are less familiar. Despite this, migration has evolved dozens of times among bats, but recent work has highlighted on-going changes to migratory patterns across a number of species and populations. Can these changes be predicted based on current understanding of bat migration, ecology, and population dynamics? To understand more about changing migration patterns and the potential for the loss of migratory behaviors in bats, we take a phylogenetic approach to infer how populations will migrate, particularly as environments change. By combining the ecological, physiological, and functional traits of migratory and non-migratory species, we begin to identify the processes that guide transitions among complex migratory traits in bats, and predict how populations respond to changing environmental conditions.

Similar Size but Different Frequency: Comparing the Echolocation Behavior of *Hipposideros jonesi* and *Hipposideros* aff. *ruber*

Bismark Appiah Opoku[1,2], Daniel Aniewu[2], Annette Denzinger[3] and Marco Tschapka[1,4]

1 Institute of Evolutionary Ecology and Conservation Genomics, University of Ulm, Ulm, DEU; 2 Batlife Ghana, Kumasi, GHA; 3 Animal Physiology, Institute for Neurobiology, University of Tübingen, Tübingen, DEU; 4 Smithsonian Tropical Research Institute, Balboa, PAN

The echolocation behavior of bats is largely adapted to the preferred habitat type and foraging mode. The Old World families Rhinolophidae and Hipposideridae are narrow space flutter-detecting foragers that use constant frequency (CF) echolocation calls. In general, the frequency of the CF component declines as body size increases, and may exceed 100 kHz in smaller species. However, some species show distinctly lower and higher echolocation frequencies than expected by size. We studied a morphologically distinct species, the 10g *Hipposideros jonesi*, that shows an unusually complex nose leaf and giant ears, compared to similar-sized hipposiderids, such as species of the *H. caffer* complex. Such unusual morphology could indicate interesting behavioral deviations from the general patterns. We therefore recorded echolocation sequences of *H. jonesi* and *H. ruber* in a flight tent and during free flight in an agricultural habitat in central Ghana and compared echolocation parameters, such as call duration, CF and FM duration, duty cycle and pulse interval. In a resting position, *H. jonesi* used an extremely low CF with a peak frequency of 46.1 kHz, while *H. ruber* called at 135.4 kHz. The observed CF frequency of *H. jonesi* does not follow the usual relation to body size and is among the lowest recorded for small hipposiderids. Further, with a mean CF duration of 15.9 ms (max 19.6 ms), the calls of *H. jonesi* were three times as long as those of *H. ruber* (mean 4.9 ms, max 6.2 ms). These differences reflect adaptations to different foraging strategies.

Evaluating the Potential Spread of White-nose Syndrome in Central and Southern Chile

Gonzalo Ossa[1,2], Joseph S. Johnson[3] and Thomas Lilley[4]

1 ConserBat EIRL, San Fabian de Alico, Ñuble, CHL; 2 Asociación Murciélagos de Chile Pinüike, Santiago, CHL; 3 Ohio University, Athens, USA; 4 Finnish Museum of Natural History, Helsinki, FIN

The presence of the fungus causing WNS in South America has not been investigated nor is it known how it could spread and affect endemic bat populations. We conducted a two-year study in central and southern Chile to investigate the potential for the spread of WNS using three approaches: swabbing bats and hibernacula for the causative agent, *Pseudogymnoascus destructans*; evaluating the suitability of winter temperatures for fungal growth; and examining how geographic distance and topology affects the connectedness of bat populations. We did not detect *P. destructans* on bats or hibernacula. Known hibernation sites in Chile are uncommon but those studied showed a range of temperature that could facilitate the proliferation of the fungus. The population structure showed significant isolation-by-distance and therefore the potential spread of WNS through bat-to-bat contact may be slowed due to high degrees of isolation amongst populations. Human-assisted transport is the most likely route for the fungus to enter the distribution range of the southernmost bats, which utilize extended torpor facilitating disease. To conclude, the lack of hibernation sites attracting large congregations of hibernating bats at these southernmost latitudes would most likely drive a disease dynamic very dissimilar to what was seen in Eastern North America.

Frog-eating Bats and Prey Mating Calls: Efficient Eavesdroppers, Evasive Advertisers, and Multimodal Cocktails

Rachel A. Page

Smithsonian Tropical Research Institute, Balboa, PAN

Eavesdropping predators exert strong selection on sexually advertising prey, exploiting their signals for prey detection, assessment, and localization. Investigating the interaction between calling frogs and frog-eating bats, we assess costs and benefits associated with multimodal signaling in simple acoustic environments, in noise, and in echoacoustic clutter. We find that both female frogs (potential mates) and frog-eating bats (heterospecific eavesdroppers) prefer multimodal signals to unimodal ones, and that signal by-products, in the form of ripples on the water surface produced by the inflation and deflation of the male frog's vocal sac, significantly increase both rival male behavior and predator attacks. We investigate the effect of noise and echoacoustic clutter on bat preferences for uni- versus multimodal cues, and quantify bat localization behavior

amidst heterospecific chorus noise with and without the presence of a robotic frog with a dynamically inflating vocal sac. Our studies illustrate the role of environmental complexity in mediating costs and benefits associated with multimodal signaling.

Monitoring Biodiversity in Cotton Landscapes – An Automated System Using Bespoke Hardware with Embedded Machine Learning
Stuart Parsons[1], Paul Roe[2], Phillip Eichinski[2], Tim Chant[1], Lance Devine[1], Tara Capel[1], Roger Coles[1], Oisin Mac Aodha[3], Kate Jones[4] and Susan Fuller[1]
1 School of Biology and Environmental Science, Queensland University of Technology, Brisbane, AUS; 2 School of Computer Science, Queensland University of Technology, Brisbane, AUS; 3 School of Informatics, University of Edinburgh, Edinburgh, GBR; 4 Department of Genetics, Evolution & Environment, University College London, London, GBR

The Australian cotton industry is setting targets to improve its environmental footprint and produce sustainable cotton. This project aims to assist the industry meet these targets by developing and deploying innovative acoustic technologies to actively monitor, manage and report on biodiversity targets at multiple scales. The project has focused on bats and birds as key indicators of biodiversity, and monitors for their presence using unique hardware and software. We have developed the first autonomous sensor capable of recording and identifying bats and birds in near real-time using convolutional neural networks (CNNs). For bats, two CNNs are used to process calls. The first monitors the incoming data stream and classifies calls in real time as either "Bat" or "Not Bat". If classified as a bat, the sound is then passed to a larger CNN capable of identifying the 12 key species or species groups located in the Australian Cotton regions (average correct ID rate <90%). Results are then uploaded to an online system called "What's on my Farm" that will allow growers to monitor biodiversity on the farms. The sensor costs approximately $1200 per unit. The CNN algorithms and hardware plans will be made open source (not for commercial use) at the end of the project.

Chiropterans are a Hotspot for Horizontal Transfer of DNA Transposons in Mammalia
Nicole S. Paulat[1], Jessica M. Storer[2], Diana D. Moreno-Santillán[1], Austin B. Osmanski[1], Kevin A.M. Sullivan[1], Jenna R. Grimshaw1, Jennifer Korstian[1], Michaela Halsey[1], Carlos J. Garcia[1], Claudia Crookshanks[1], Jaquelyn Roberts[1], Arian F.A. Smit[2], Robert Hubley[2], Jeb Rosen[2], Emma C. Teeling[3], Sonja C. Vernes[4,5,6], Eugene Myers[7], Zoonomia Consortium, Danny Rojas[8], Liliana M Davalos[9,10] and David A Ray[1]
1 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 2 Institute for Systems Biology, Seattle, USA; 3 School of Biology and Environmental Science, University College Dublin, Dublin, IRL; 4 Neurogenetics of Vocal Communication Group, Max Planck Institute for Psycholinguistics, Nijmegen, NLD; 5 Donders Institute for Brain, Cognition and Behaviour, Nijmegen, NLD; 6 School of Biology, University of St Andrews, Fife, GBR; 7 Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, DEU; 8 Department of Natural Sciences and Mathematics, Pontificia Universidad Javeriana Cali, Valle del Cauca, COL; 9 Department of Ecology and Evolution, Stony Brook University, Stony Brook, USA; 10 Consortium for Inter-Disciplinary Environmental Research, Stony Brook University, Stony Brook, USA

Transposable elements are repetitive DNA sequences that can mobilize within and across genomes via copy-and-paste or cut-and-paste mechanisms. Such activity is an important mechanism contributing to genetic diversity and innovation. Bats (order Chiroptera) have repeatedly been shown to experience horizontal transfer of transposable elements at what appears to be a high rate compared to other mammals. We investigated the occurrence of horizontally transferred DNA transposons involving bats with the expectation of identifying more horizontally transferred transposons than previously known, as bats have far greater recent (< 50 million years) DNA transposon accumulation than other mammals. Transposable element annotation across 251 mammal genomes and subsequent nucleotide BLAST searches with a curated mammalian transposon consensus sequence library revealed patchy distribution patterns for hundreds of DNA transposons primarily present in bats. Additional BLAST searches across eukaryote genome databases, orthologous insertion searches, and sequence clustering yielded over 200 putative horizontally transferred elements within bats. Twelve elements were shared across distantly related mammalian clades, two other transposons were shared with a fish and two lizard species. Our results indicate bats are a hotspot for horizontal transfer of DNA transposons. The timing of these events are broadly consistent with the diversification of several bat clades, supporting the hypothesis that DNA transposon invasions have contributed to genetic diversification of bats.

Modeling Winter Bat Foraging Associations on Working Forests in the Southeastern US Coastal Plain
Santiago Perea[1], Steven B. Castleberry[1], Angela L. Larsen-Gray[2], Daniel U. Greene[3] and Guillermo Fandos[4]
1 Warnell School of Forestry and Natural Resources, University of Georgia, Athens, USA; 2 National Council for Air and Stream Improvement, Inc., Blacksburg, USA; 3 Weyerhaeuser Company, Environmental Research South, Columbus, USA; 4 Department of Biodiversity, Ecology and Evolution, Complutense University of Madrid, Madrid, ESP

Insectivorous bats in temperate zones evolved strategies such as migration or hibernation to face challenges of reduced resource availability and increased energy demand during winter. In the southeastern United States Coastal Plain, many bats are year-round residents and remain active during winter or migrate from colder areas seeking milder temperatures. In addition to being the winter destination for migratory species, southeastern Coastal Plain forests may represent important areas for remnant populations of species impacted by white-nose syndrome. Working forests represent a large proportion of southeastern Coastal Plain forests, yet winter bat habitat associations and how forest management practices affect use remains understudied. Therefore, our goal is to evaluate factors influencing winter bat activity and foraging habitat selection on working forests in the southeastern Coastal Plain. From January to March 2020−2022, we deployed Anabat Swift acoustic detectors and measured site- and landscape covariates in loblolly pine (Pinus taeda) stands in Georgia, Louisiana, South Carolina, Mississippi, Florida, and North Carolina. We recorded eight individual species and two species groups. Preliminary analyses suggested that temperature played an important role in winter bat activity and detectability, and that site- and landscape covariates influenced occupancy for some species. Our results will provide baseline information on winter bat communities and foraging habitat associations to inform managers of habitat features important to wintering bats, and thus increase conservation opportunities within working forests.

Living the City Life: Nectar-Feeding Bats in Mexico City
Samara Pérez-Harp, Fernando Gual-Suárez, Daniela Padrón-Alemán and Rodrigo A. Medellín
Laboratorio de Ecología y Conservación de Vertebrados Terrestres, Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de México, MEX

Accelerated urbanization has profoundly modified ecosystems and their biodiversity. It is known that several bat species are present in these urban environments. However, certain species can be negatively affected by vegetation loss, fragmentation, and human buildings, as well as light,

noise, and air pollution, depending on the taxonomic group. Studies have been mostly focused on insectivorous bats and information on nectar-feeding species is limited. In Mexico City, one of the largest cities in the world, information on this particular group is limited to species lists and some sporadic reports. Considering this knowledge gap, we monitored four urban parks of different areas of Mexico City, from February 2021 to February 2022, setting mist nets close to flowering chiropterophilous plants. Each park was visited 2 nights every month and mist nets remained open for 5 hours after sunset. All captured bats were marked with an 8 mm PIT tag, for individual identification, and released in situ. In total, we recorded 371 captures of 221 individuals. Four of the five species historically recorded in the city were captured. The composition of bat ensembles in each park displayed a temporal variation, probably related to seasonal changes on resource availability and the species' migratory movements. This study shows that urban parks with chiropterophilous plants can allow nectar-feeding bats to persist in highly urbanized cities such as Mexico City.

EchoPitch: Using Acoustics to Measure and Manage Risk to Bats at Commercial Wind Energy Facilities

Trevor S. Peterson[1] and Adam Rusk[2]
1 Stantec Consulting Services Inc., Topsham, USA; 2 Stantec Consulting Services Inc., Kansas City, USA

Widespread bat fatalities at wind projects across North America highlight the inability to avoid risk to bats through siting alone, necessitating measures to minimize bat fatalities once turbines are operational. Nighttime turbine curtailment during relatively low wind speeds is the most widely used measure to minimize bat fatality but remains unpopular due to the associated energy production loss. Curtailment is now a standard permit requirement in many regions, although scant quantitative information exists to guide setting parameters such as cut-in wind speeds. Acoustic bat detectors offer a solution for designing and evaluating curtailment strategies to balance energy loss and risk reduction. Quantitative feedback on variation in bat activity in the rotor zone sets the stage for tailoring curtailment strategies with measurable targets for risk reduction. Unlike carcass monitoring, which provides information on bat fatalities alone and is typically hampered by small sample sizes due to curtailment, acoustic detectors can directly measure the amount of bat activity occurring (and therefore successfully avoided) when turbines are curtailed. We will summarize results of extensive turbine-based acoustic monitoring conducted at commercial wind energy facilities across multiple states in 2012–2021 that demonstrate a positive relationship between the rate of bat passes exposed to turbine operation and bat fatality rates and highlight the ability to evaluate and adaptively manage curtailment strategies using acoustics. These data provide a window into behavior of bats near turbines, provide an ideal basis for adaptively managing risk to bats, and could lessen the need for costly carcass monitoring.

Host and Environmental Correlates of Coronavirus Prevalence in Bats of Western Asia

Kendra Phelps[1], Luke Hamel[1], Ketevan Sidamonidze[2], Lela Urushadze[2], Nisreen Alhmoud[3], Rasit Bilgin[4], Andrew Spalton[5], Zahran Ahmed Al-Abdulsalam[5], Astghik Ghazaryan[6], Nijat Hasanov[7], Shahzad Ali[8], John Neddermeyer[1,9], William Karesh[1] and Kevin J. Olival[1]
1 EcoHealth Alliance, New York, USA; 2 Department of Virology, Molecular Biology and Genome Research, R.G. Lugar Center for Public Health Research at National Center for Disease Control & Public Health, Tbilisi, GEO; 3 Bio-Safety & Bio-Security Centre, Royal Scientific Society, Amman, JOR; 4 Institute of Environmental Sciences, Boğaziçi University, Istanbul, TUR; 5 Office for Conservation of the Environment, Diwan of Royal Court, Muscat, OMN; 6 Faculty of Biology, Yerevan State University, Yerevan, ARM; 7 Institute of Zoology, Azerbaijan National Academy of Sciences, Baku, AZE; 8 Department of Wildlife & Ecology, University of Veterinary & Animal Sciences, Lahore, PAK; 9 Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, AZ, USA

Surveillance of bat-associated coronaviruses is geographically biased, with Western Asia understudied despite being a biogeographical 'mixing pot' of bat species from Europe, Africa, and Asia. To determine the prevalence of coronaviruses circulating in bat species of Western Asia, we conducted robust, regional field surveillance from 2018–2022 in 7 countries (Armenia, Azerbaijan, Georgia, Jordan, Oman, Pakistan, and Turkey). We non-lethally sampled 4,278 bats of 37 species from 50 sites, and as of April 2022, 60% of fecal samples have been screened for coronaviruses using RdRp-specific primers at two regional labs (Georgia, Jordan). Overall coronavirus prevalence across all bat species in Western Asia was high (18%) but varied widely by species. *Rhinolophus ferrumequinum*, the species with the largest distribution in the region, had the highest prevalence (33%). Furthermore, we assessed the influence of host traits and environmental conditions on coronavirus prevalence. Sex and age class were correlated with coronavirus prevalence but again varied amongst species, e.g., juvenile female *R. ferrumequinum* exhibited significantly higher prevalence than their counterparts. Coronavirus prevalence was influenced by community-level dynamics at sampled sites, with a positive correlation between species diversity and number of bat species and families with prevalence. Measures of bat-human interactions, specifically human population density and visitation frequency at sampled sites, interestingly were correlated with a lower coronavirus prevalence in bats captured at sites. Our preliminary results highlight the importance of considering host and environmental correlates in virus surveillance to better understand the underlying dynamics that may promote transmission risk.

Comparative Ecophysiology of the Bat Pathogenic Fungus *Pseudogymnoascus destructans*: Enzymatic Curtailment, Lipases Production and Strong Conidial Resilience

Jiří Pikula[1], Tereza Veselská[2,3], Karolína Homutová[2], Paula García Fraile[2], Alena Kubátová[3], Natália Martínková[4] and Miroslav Kolařík[2]
1 Department of Ecology and Diseases of Zoo Animals, Game, Fish and Bees, University of Veterinary Sciences Brno, Brno, CZE; 2 Laboratory of Fungal Genetics and Metabolism, Institute of Microbiology, Czech Academy of Sciences, Prague, CZE; 3 Department of Botany, Faculty of Science, Charles University, Prague, CZE; 4 Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, CZE

The genus *Pseudogymnoascus* encompasses soil psychrophilic fungi living also in caves. Some are opportunistic pathogens; nevertheless, they do not cause outbreaks. *Pseudogymnoascus destructans* is the causative agent of the white-nose syndrome, which decimates cave-hibernating insectivorous bats. We used comparative eco-physiology to contrast the enzymatic potential and conidial resilience of *P. destructans* with that of phylogenetically diverse cave fungi, including *Pseudogymnoascus* spp., dermatophytes and outdoor saprotrophs. Enzymatic potential was assessed by Biolog MicroArray and by growth on labelled substrates and conidial viability was detected by flow cytometry. *Pseudogymnoascus destructans* was specific by extensive losses of metabolic variability and by ability of lipid degradation. We suppose that lipases are important enzymes allowing fungal hyphae to digest and invade the skin. *Pseudogymnoascus destructans* prefers nitrogenous substrates occurring in bat skin and lipids. Additionally, *P. destructans* alkalizes growth medium, which points to another possible virulence mechanism. Temperature above 30 °C substantially decreases conidial viability of cave fungi including *P. destructans*. Nevertheless, survival of *P. destructans* conidia prolongs by the temperature regime simulating beginning of the active season, suggesting that conidia could persist on the body surface of bats and contribute to disease spread during bat seasonal movements.

Bats as Ecosystem Engineers in Iron Ore Caves in the Carajás National Forest, Brazilian Amazonia
Luis B. Piló[1], Allan Calux[2], Rafael Scherer[3] and Enrico Bernard[1]
1 Laboratório de Ciência Aplicada à Conservação da Biodiversidade, Departamento de Zoologia, Universidade Federal de Pernambuco, Recife, BRA; 2 Carstografica – Karst Applied Research Centre, Campinas, BRA; 3 Grupo Espeleológico de Marabá, Marabá, BRA

Ecosystem engineers are organisms that modify their environment by changing the distribution of materials and energy, with effects on biotic and abiotic ecosystem components. However, the mechanisms behind their influence are still poorly known. We detail the role of bats as ecosystem engineers in iron ore caves in the Carajás, Brazilian Amazonia. We analyzed and described the guano-related chemistry in bat caves, radiocarbon-dated those deposits, and explain the role bats had on structuring those caves. Composed by insects, guano was rich in organic matter, with high concentrations of carbon, nitrogen, phosphorus pentoxide and ferric oxide, plus potassium oxide, calcium and sulfur trioxide. Guano deposits were ~22,000 to 1,800 years old. Guano pH was acid (2.1 to 5.6), like the percolating waters (pH ≥1.5), with phosphate, iron, calcium, nitrate and sulfate. Acid solutions due to guano decomposition/microbial activity corroded the caves´ floor and walls, enlarging them: caves with colonies had horizontal projections 4.5 times larger, areas 4.4 times larger, and volumes 5.0 times bigger than the regional average, plus more abundant, diversified and bigger speleothems. As bioengineers, the presence of bats and their guano along millennia resulted in very unique ecological, evolutionary and geomorphological processes. However, mineral activities and the loosening of licensing and cave protection rules is a real threat to Carajás´ bat caves, whose destruction is an unacceptable loss of speleological and biological heritage. Whenever they occur, bat caves and their colonies must be fully protected and left off-limits of mineral extraction.

Foraging Sites of Greater Noctule Bats in Relation to the Landscape
Micaela T. Pineda[1], Dina K. N. Dechmann[2,3,4,5], Elena Tena[6], Carlos Ibáñez[6], Javier Juste[6,7] and M. Teague O'Mara[1,2,3]
1 Department of Biological Sciences, Southeastern Louisiana University, Hammond, USA; 2 Department of Migration, Max Planck Institute of Animal Behavior, Radolfzell, DEU; 3 Smithsonian Tropical Research Institute, Panama City, PAN; 4 Department of Biology, University of Konstanz, Konstanz, DEU; 5 Centre for the Advanced Study of Collective Behaviour, Konstanz, DEU; 6 Estación Biológica de Doñana, Sevilla, ESP; 7 CIBER of Epidemiology and Public Health, Madrid, ESP

The greater noctule bat (*Nyctalus lasiopterus*) is the largest bat species in Europe, and is a partially carnivorous aerial hawking hunter renowned for its capture of migrating birds. However, its biology and behavior have been poorly studied due to its elusive nature and low population densities. While previous studies suggested foraging typically occurs at altitudes up to 1659 m above ground level (AGL), greater noctules also forage <1 m off the ground. To test how greater noctules use three-dimensional space and the landscape below it, GPS locations, barometric pressure, and accelerometer data were collected from 21 individuals in Doñana, Spain, between spring 2018 and fall 2019, and their movements classified into four broad categories using a hidden Markov movement model. Although greater noctules reached a maximum flight altitude of 2132 m AGL, mean altitude was 166 m AGL for area restricted search, 68 m AGL for slow forage flight, 75 m AGL for move, and 105 m AGL for commute. In the spring, individuals foraged primarily over "marsh with vegetation" habitat, and in the fall over "herbaceous cultivation other than rice". Overall, 38% of foraging behaviors were over "marsh with vegetation". Greater noctules typically had 2 h flight durations with a maximum of 6.8 h, and mean flight distance of 37 km with a maximum of 152 km. Mean flight altitudes were lower than previously assumed and only 0.3% of their foraging time was spent in heights necessary for catching migrating birds, occurring more often in fall than spring.

Changes in Migratory Behavior of *Tadarida brasiliensis* in the South-Central United States
Shawn A. Pladas[1], Winifred F. Frick[2] and M. Teague O'Mara[1,2,4]
1 Department of Biological Sciences, Southeastern Louisiana University, Hammond, USA; 2 Bat Conservation International, Austin, USA; 3 Department of Migration, Max Planck Institute of Animal Behavior, Radolfzell, GER; 4 Smithsonian Tropical Research Institute, Gamboa, PAN

Effects of climate change on migration are apparent across a wide array of taxa. The Brazilian free-tailed bat (*Tadarida brasiliensis*) is a common and widely distributed bat of the Americas with long-distance (> 1,000 km), migratory populations in Mexico and the South-Central United States. Bracken Cave in Texas is a major maternity colony during the summer months and supports a population of over 2.5 million bats. Historically, this population would disperse after pups became volant in late summer and leave the roost entirely during winter months. Recently, however, research has shown increasing numbers of overwintering bats at Bracken Cave. It is unclear if these overwintering individuals consist of a growing non-migratory population or if there is an increasing number of northern migrants short-stopping at Bracken Cave during migration. Utilizing stable isotope analysis this research aims to reveal the population dynamics of overwintering bats at Bracken Cave. By developing a better understanding of these changes in migratory behavior at critical roosting locations conservation managers can better protect these sites year-round. Insights from this winter population can also guide future research across other temperate roosting locations, bolster evidence for range expansions, and elucidate changes in this species' reproductive phenology.

A Non-karst Overwintering Strategy for Rock-roosting Bats in the Appalachian Mountains of Virginia
Emily K. Pody[1], Paul R. Moosman Jr.[2] and Thomas G. Jones[1]
1 Department of Biological Science, Marshall University, Huntington, USA; 2 Department of Biology, Virginia Military Institute, Lexington, USA

White-Nose Syndrome (WNS), a disease caused by the fungus *Pseudogymnoascus destructans* (*Pd*), has been a major factor in the rapid decline of North American bat populations. This disease has had the greatest impacts on species that hibernate in caves and mines where microclimates are optimal for *Pd* growth. However, some cave hibernating species of bats also overwinter in aboveground rock outcrops. We investigated the use of vertical rock faces and outcroppings by bats during winter in west-central Virginia. We monitored the presence of roosting bats and roost microclimate at 4 sites in a riverine gorge by conducting 14 visual rappelling surveys weekly between late October and early March. We found 3 species roosting in the rock-faces: 22 Big Brown bats (*Eptesicus fuscus*), 2 Eastern Small-footed bats (*Myotis leibii*), and 1 Silver-haired bat (*Lasionycteris noctivagans*). Bats exhibited low roost fidelity and appeared to switch roosts within the rock faces throughout the monitoring period. Preliminary data suggest roosts climates were not consistent with optimal growth of *Pd*. We suspect this alternative overwintering strategy could reduce susceptibility and spread of WNS for some bat species.

Response of a North American Bat Species to Immunization with Ebola-Like Virus Particles
Lisa E. Powers, Luis Víquez-R, DeeAnn M. Reeder and Kenneth A. Field
Department of Biology, Bucknell University, Lewisburg, USA

As part of a comparative initiative examining the bat immune response to Ebola antigens, we conducted a pilot study in big brown bats (*Eptesicus fuscus*). We immunized bats with Ebola virus-like particles (eVLPs) at two dosages: a low dose (n = 6) that is typical of eVLP studies in other mammals, and a high dose (n = 5) that was 5x the typical dose. All bats were boosted 21 days after the first inoculation. As non-natural Ebola hosts, we predicted a modest response to primary inoculation and a robust response to the booster shot, with greater responses at the higher dose. We collected blood samples periodically for 56 days after primary immunization. Body temperature was recorded by data loggers affixed to the skin. We developed an ELISA to assay anti-Ebola glycoprotein (GP) titers in samples. As expected, ELISA results showed a greater response in the high dose group that was more robust after the booster. High dose bats also displayed a greater febrile response following the booster, delaying their normal daily drop into torpor by 4−5 hours for two days. There were no consistent trends in GP antibodies over time in the low dose group. Unexpectedly, 9 bats had positive titers prior to inoculation. The results of this pilot study have informed the design of our ongoing studies in Ugandan bats. They suggest that bats may require exposure to greater levels of Ebola proteins than other mammals in order to generate a response. The finding of positive titers in uninoculated bats should be explored further.

Evaluating the Conservation Status of Bats in Southern Africa

Mariette Pretorius[1,2], Ara Monadjem[3], Mark Keith[2] and Wanda Markotter[1]

1 Department of Health Sciences, University of Pretoria, Pretoria, ZAR; 2 Department of Agriculture, University of Pretoria, Pretoria, ZAR; 3 Department of Biological Sciences, University of Eswatini, Kwaluseni, ZAR

A common assumption in conservation is that species within protected areas (PAs) are buffered from extinction. This assumption is problematic for bat species with incompletely understood habitat requirements, leading to misclassification under the IUCN Red List and resulting in reduced conservation efforts, ultimately impacting extinction risk. We evaluated the current conservation status of southern Africa bat species by linking several bat life-history traits with current IUCN global classifications and threats and assessing the role of current PAs in protecting bats. Collection records of bat species and their IUCN Red List classifications were compared to ecological traits and reported threats to categorize risk for 130 bat species across 11 families. Occurrence records were compared to a protected area database using spatial analysis to determine the proportion of species represented. Most southern African bat species were Least Concern (71%). However, only a minority of bat species (16%) had stable population trends, and most were considered roost-limited (45%). Of the species for which threats were reported (59%), habitat loss (78%) and agricultural expansion and pesticide use (42%) were most often reported. Threatened bat species belonged to Rhinolophidae, Pteropodidae, Molossidae and Hipposideridae, with many threatened species being dispersive, roost limited and congregatory. Our study reported 27% more bat species located in PAs than the IUCN. Nonetheless, only 36% of species were reported from protected areas, indicating that the substantial bat richness of southern Africa is currently not well-represented in conservation actions. Targeted conservation actions for bat species in southern Africa should be made a priority.

Viral Maintenance in Small, Isolated Bat Populations: Using the Christmas Island Flying-fox as a Case Study

Laura A. Pulscher[1], Alison J. Peel[2], Karrie Rose[3], Justin A. Welbergen[4], Michelle L. Baker[5], Victoria Boyd[5], Samantha Low-Choy[2,6], Dan Edson[7], Chris Todd[4], Annabel Dorrestein[4], Jane Hall[3], Shawn Todd[5], Christopher C. Broder[8], Lianying Yan[8,9], Kai Xu[10], Grantley R. Peck[5] and David N. Phalen[1]

1 Sydney School of Veterinary Science, Faculty of Science, University of Sydney, Sydney, Australia; 2 Centre for Planetary Health and Food Security, Griffith University, Nathan, Australia; 3 Australian Registry of Wildlife Health, Taronga Conservation Society Australia, Mosman, Australia; 4 Hawkesbury Institute for the Environment, Western Sydney University, Richmond, Australia;5 Australian Centre for Disease Preparedness, Geelong, Australia; 6 Office of the Vice Chancellor, Arts/Education/Law, Griffith University, Brisbane, Australia; 7 Department of Agriculture, Water and the Environment, Canberra, Australia; 8 Department of Microbiology, Uniformed Services University, Bethesda, USA; 9 Henry M. Jackson Foundation for the Advancement of Military Medicine, Bethesda, USA; 10 Department of Veterinary Biosciences, College of Veterinary Medicine, Ohio State University, *Columbus, USA*

Small, geographically isolated bat populations may not be able to maintain acute immunizing viruses that rely on large populations for viral maintenance but instead may rely on viruses establishing persistent infections or inducing short-lived natural immunity. Therefore, studies of small, geographically isolated bat populations provide a unique opportunity to understand viral maintenance mechanisms in bat populations. The Christmas Island flying-fox (*Pteropus natalis*) is a small, geographically isolated bat population making it an ideal model species to understand viral maintenance. Using multiplex serological and molecular techniques, and attempts at viral isolation, this study sought to determine if multiple viral families including paramyxoviruses, betacoronaviruses, or Australian bat lyssavirus could be maintained in this small, geographically isolated population. From 2015 to 2018, serum or plasma (n = 190), oral swabs (n = 199), feces (n = 31), urine (n = 32) and urine swabs (n = 25) were collected from 228 Christmas Island flying-foxes. Analysis of serological data using a Bayesian Gompertz mixture model provided evidence that the Christmas Island flying-foxes are maintaining a pararubulavirus and a betacoronavirus but not other viruses tested. No viral nucleic acid was detected, and no viruses were isolated. Our study provides support that small, isolated bat populations can maintain various coronaviruses and paramyxoviruses. However, the absence of some pathogens could have implications for the conservation of the Christmas Island flying-fox if a novel disease were introduced into the population through human carriage or invasive species.

Bat Flies of Frugivorous Bats: A Source of Supplemental Nutrients or Just Pathogen Vectors?

Riana V. Ramanantsalama[1], Jörg U. Ganzhorn[2], Judith Vololona[3], Muriel Dietrich[1], Steven M. Goodman[4,5] and Camille Lebarbenchon[1]

1 UMR Processus Infectieux en Milieu Insulaire Tropical, Université de La Réunion, La Réunion, FRA; 2 Universität Hamburg, Hamburg, DEU; 3 Université d'Antsiranana, Antsiranana, MDG; 4 Field Museum of Natural History, Chicago, USA; 5 Association Vahatra, Antananarivo, Madagascar, MDG

On Madagascar, using infrared videos taken in a cave day roost, individual *Rousettus madagascariensis* (Pteropodidae) was estimated on average to consume 37 hematophagous bat flies (Streblidae and Nycteribiidae) per day. A range of pathogens have been isolated from these ectoparasites. It is unknown if ectoparasite ingestion by bats provides a nutritional benefit. Hence, we examine if consuming bat flies by *R. madagascariensis* offsets nutrients absent in locally available native and introduced fruits, and if such behavior acts to supplement this species' diet. Bat flies were collected on captured *R. madagascariensis* in a natural dry deciduous forest in northern Madagascar. Ficus spp. (Moraceae) and varieties of *Mangifera indica* (Anacardiaceae) were sampled. Nitrogen levels in ectoparasites and fruits was evaluated with an elemental analyzer following pyrolysis. Lipids were extracted with ether using a fat analyser. Soluble sugar was assessed using the phenolic-sulfuric acid assay. The dietary contribution of these ectoparasites for *R. madagascariensis* is 49% of the daily protein requirements. This is an important proportion for a

species considered to be exclusively frugivorous. Bacteria such as Bartonella and Rickettsia, and viruses of the Peribunyaviridae family have been detected in bat flies; but currently, it is not known if transmission of these pathogens via bat ectoparasites can occur. Our results represent an interesting predator-prey interaction where nutritional aspects, prey abundances and pathogen dynamics interact.

A Long-forgotten Topic: Hibernating Bats in Mexico, Five Years of Work after a Fifty Year-gap

Daniel Ramos-H[1], Aarón Romero-Ruiz[1], Cárol Sierra-Durán[1], Daniela Cafaggi[1], Ganesh Marín[1,2] and Rodrigo A. Medellín[1]
1 Laboratorio de Ecología y Conservación de Vertebrados Terrestres, Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de México, MEX; 2 School of Natural Resources and the Environment, University of Arizona, Tucson, USA

Bat hibernation has been extensively studied in the temperate areas of the world, primarily in the U.S., Canada, and Europe. Mexico lies at the crossroads of the Nearctic and the Neotropical Regions, with its northern half falling clearly within the temperate Nearctic realm. Less than 15 reports of hibernating bats in Mexico, mostly from over 50 years ago with a few in the last 20 years, contain 25 hibernacula of five species. Surveys of *Pseudogymnoascus destructans* (*Pd*) and its ability to cause white-nose syndrome in higher latitudes but only rarely in the south of the U.S., prompted us to reinitiate the study of hibernating bats in Mexico. We searched for hibernacula from 2018 to 2022, and sampled for *Pd* surveillance. We explored over 150 below-ground sites in 11 Mexican states along three mountain ranges. Our records doubled the number of hibernating bat species and quadrupled the number of hibernacula for Mexico. We progressively increased the collection of bat swab samples. Samples of 2018 and 2019 were negative by PCR for Pd. Those of the other three winter periods have not yet been analyzed. Hibernacula were most commonly found at higher elevations where oak and conifer forests occur. The mountains and temperate ecosystems of central and northern Mexico encompass appropriate climatic conditions for bat hibernation, providing winter roosts with relatively stable, above-freezing temperatures. Continued hibernation exploration and constant surveillance for the presence of the *Pd* fungus is very important for the conservation of bats in Mexican temperate ecosystems in the winter.

Transposable Elements, the Basis of Bats' Evolutionary Plasticity

David Ray
Department of Biological Sciences, Texas Tech University, Lubbock, USA

Bats are unique among mammals, exhibiting powered flight, powerful immunity, extreme longevity, and substantial dietary variety, among other traits. These phenotypes find their ultimate foundations in the genome. Thus, it is no surprise that bat genomes are also unique, with many bats harboring genomic parasites that are not found in other eutherians. These parasites, transposable elements (TEs), can induce substantial structural and functional genomic change over short evolutionary time frames. Indeed, TEs have been described as 'drivers of genome evolution'. Our laboratory has recently examined TE repertoires among over 250 mammal genome assemblies and characterized the exceptional diversity present in bats. I will discuss how TEs induce phenotypic changes in relation to the singular TE landscapes that characterize many bat genomes. I will also discuss how bat genomic defenses may impact their ability to tolerate unusual (among mammals) TE repertoires and the potential sources of the genomic invaders via horizontal transfer.

Conservation Science in Action: An Update on the Collaborative Response to White-nose Syndrome

Jonathan D. Reichard[1], Vratika Chaudhary[2,3], Evan H. Campbell Grant[2], Jordi Segers[4] and Jeremy T. H. Coleman[1]
1 Ecological Services, United States Fish and Wildlife Service, Hadley, USA; 2 Eastern Ecological Science Center, United States Geological Survey, Turners Falls, USA; 3 Department of Ecosystem Science and Management, Pennsylvania State University, University Park, USA; 4 Canadian Wildlife Health Cooperative, Charlottetown, CAN

Since discovery in 2007 at a handful of sites in New York, white-nose syndrome (WNS) has rapidly expanded into bat populations across the US and Canada. Pioneering research and strong partnerships have propelled our understanding of this once mysterious and novel threat to North American bats. Over a relatively short time, the WNS response community has developed knowledge and a variety of targeted management strategies to benefit bats that are most vulnerable to the disease. The WNS National Plan is a multi-species recovery plan for hibernating bats that establishes the framework through which government agencies coordinate research and management to combat the disease and advance bat conservation. Under this framework, multiple management options have been developed to improve survival of susceptible bats and programs established to enhance our understanding of the status of bat populations. With partners we mapped WNS management strategies onto a conceptual model to illustrate where and how different actions affect the WNS system. The resulting tool is a resource to guide action and support management for achieving desired outcomes for hibernating bats. The coordinated response to WNS has resulted in hundreds of publications and presentations advancing our understanding of bat and disease ecology, and includes contributions by several hundred partners across North America and beyond, collaborating to study, monitor, and conserve bats.

Broad Scale, Collaborative Acoustic Monitoring Improves Available Science Informing Conservation of North American Bats

Brian E. Reichert[1], Winifred F. Frick[2,3], Bethany R. Straw[1], Brad Udell[1], Kathryn M. Irvine[4], Jonathan Reichard[5], and Jeremy Coleman[5]
1 U.S. Geological Survey, Fort Collins Science Center, Fort Collins, USA; 2 Bat Conservation International, Austin, USA; 3 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA; 4 U.S. Geological Survey Northern Rocky Mountain Science Center, Bozeman, MT, USA; 5 U.S. Fish and Wildlife Service, Hadley, USA

Collaborative acoustic monitoring over broad scales offers a cost effective, efficient means of informing bat conservation. An important challenge to collaborative monitoring is motivating local engagement with enough buy-in from stakeholders while providing adequate top-down direction for scientific rigor, quality control, and coordination. Collaborative monitoring programs, such as the North American Bat Monitoring Program (NABat) must reconcile this inherent tension between top-down control and bottom-up engagement. NABat reconciles this tension with a hierarchical master sample survey design, integrated analyses, dynamic data curation, regional monitoring hubs, and knowledge delivery through web-based infrastructure. The aim of the program is to provide pro-active and strategic science to support decision-making for the conservation of 46 species of bats occurring within the U.S. and shared by Canada and Mexico. NABat now has grown to include more than 160 partnering organizations, contributing over 65 million acoustic records on 39 bat species. NABat safely stores these data with an approved and actively maintained data management plan and web-based technologies that support opportunities for growth, data-sharing, and analysis. Acoustic data contributed to NABat have now been used to inform U.S. Fish and Wildlife Service's Species Status Assessments for three species under consideration for listing under the U.S. Endangered Species Act. In 2022, summer acoustic monitoring data were used in the development of the

first-of-its-kind Status and Trend report for nine species of bats. These recent advancements demonstrate the power of collaborative acoustic monitoring, top-down coordination, and bottom-up enthusiasm, yet continued local engagement is critical for long-term success.

Out of the Darkness: The Willingness for Diurnal Flight by *Myotis lucifugus* Across Alaska

Jesika P. Reimer[1,2], Karen M. Blejwas[3] and Laura A. Kaupas[2]
1 Department of Wildlife, Fish and Conservation Biology, University of California Davis, Davis, USA; 2 Alaska Center for Conservation Science, University of Alaska Anchorage, Anchorage, USA; 3 Alaska Department of Fish and Game, Juneau, USA

In theory, nocturnal bats at northern latitudes are limited by time as a resource with short summer seasons and short summer nights. While insectivorous bats exhibit primarily nocturnal behavior, bats that live at northern latitudes must deal with long periods of little to no solar night. While this behavior has been well documented above the Arctic Circle, we were interested in the intersection between spatial and temporal variation in night length across latitude, and whether there is a distinct geographic or temporal point where the willingness to forage in daylight becomes more pronounced. We analyzed acoustic activity recorded over a three-year period at 22 *Myotis lucifugus* maternity colonies ranging in latitude from 58°N to 64°N across Alaska. Diurnal flight was observed at 82% of our sites, during an average of 14% (range: 0–40%) of nights and was more common prior to sunset rather than post-sunrise. We observed a positive relationship between diurnal flight and increasing latitude, with diurnal flight becoming more pronounced above 62°N. We observed a negative relationship between the proportion of diurnal bat passes and increasing night length, with the greatest diurnal activity occurring around solstice. These results suggest that there is a minimum amount of time required by *M. lucifugus* to gather sufficient resources at northern latitudes such that the benefit and their willingness to fly during periods of high illumination outweighs the potential risk of predation or other factors that influence the nocturnal preference of bats.

Impacts of Agricultural Development on Stress and Immunity in the Carollia Bats of Northwest Ecuador

Phoebe L. Reuben and Hannah K. Frank
Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, USA

Bats are widespread in altered areas and vary in their tolerance for disturbance, making them an ideal system in which to evaluate the impact of human activity on wildlife, particularly on health and immunity. The consequences of human development are especially relevant in the highly biodiverse ecosystems of the Neotropics, where an agricultural economy has led to decades of deforestation and increased contact between humans and wildlife. Stress is a critical metric for recognizing and predicting responses to changing environmental conditions and for understanding the associated fitness costs, but is often reduced to cortisol alone. Research that examines a wider range of physiological responses is needed to better understand the biological significance of stress. Here, we sampled three species of *Carollia* bats in the Chocó biogeographic region of Ecuador in agricultural, current reforestation, and forested land-use plots that were monitored for a range of environmental and climatic parameters. We collected samples from all bats to quantify body condition index and reproductive state, fecal cortisol levels, neutrophil to lymphocyte ratios, white blood cell differentials, and current viral infections. This suite of physiological responses allows us to establish specific relationships between varying environmental conditions and changes in organismal fitness. Understanding which specific factors negatively impact physiological fitness will help direct focus to the most effective interventions, which could include developing stress- minimizing farming practices and identifying impactful areas for future reforestation. Preliminary results and methods are presented here for feedback.

Wind Energy Production Leads to Habitat Loss for common noctule bats in Europe

Christine Reusch[1], Stephanie Kramer-Schadt[1,2] and *Christian C. Voigt[1]
1 Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU; 2 Institute of Ecology, Technische Universität Berlin, Berlin, DEU

In Germany, wind energy production is expanding largely along coastal areas and in forests. Coastal sites are used by migratory bats as migratory corridors and forests for roosting. Therefore, expansion of wind energy production along the coast and at forested sites may be in conflict with the conservation of bats. We used miniaturized global positioning system (GPS) tracking of more than 70 common noctule bats (*Nyctalus noctula*) to shed light on the spatial interactions of a high collision risk bat species in coastal landscape and at inland sites dominated by forests. At our coastal site in northern Germany, we analyzed the movement tracks of 11 common noctules based on >6,000 locations and at our inland forest those of 60 common noctule bats based on >8,000 spatial positions. We used three spatial approaches to infer on the preferred and avoided landscape features in interaction with wind turbines. At both study sites, we observed that the majority of bats avoided wind turbines over distances of several km. Avoidance behavior of bats toward wind turbines has not been considered largely during past impact assessments. Although avoidance of bats toward turbines may come at the benefit of reducing the individual vulnerability at wind turbines, avoidance may nonetheless lead to habitat loss by the operation of wind turbines. Turbine-related habitat losses may become critical for affected bats when wind turbine densities are high.

Integrating Multiple Survey Techniques to Document Shifting Bat Communities in the Wake of White-nose Syndrome

D. Scott Reynolds[1,7], Kevin Shoemaker[2], Susi von Oettingen[3], Stephen Najjar[4], Jacques P. Veilleux[5] and Paul R. Moosman[6]
1 Department of Science, St. Paul's School, Concord, USA; 2 Department of Natural Resources & Environmental Science, University of Nevada, Reno, USA; 3 United States Fish and Wildlife Service, Concord, USA; 4 New Boston Space Force Station, New Boston, USA; 5 Department of Biology, Franklin Pierce University, Rindge, USA; 6 Department of Biology, Virginia Military Institute, Lexington, USA; 7 North East Ecological Services, Concord, USA

The long-term study of bat communities often reflects a diverse set of sampling methodologies that are difficult to integrate into a single measure of relative abundance. We developed a Bayesian state-space model to integrate such data into a common currency, captures per unit effort. We used acoustic monitoring and mist-net capture data over an eight-year period (2006–2014) from a bat community in central New England to test the model. Integrating these data is critical to characterize changes in community structure or composition over time, such as one would expect following an emergent infectious disease such as white-nose syndrome (WNS). The integrated data model shows a significant decline in the abundance of little brown myotis (*Myotis lucifugus*) since 2006, and an increase in abundance of the eastern small-footed myotis (*M. leibii*), the eastern red bat (*Lasiurus borealis*), and the big brown bat (*Eptesicus fuscus*). These results are consistent with our understanding of the impact of WNS on these species. The success of this model provides opportunities to quantify shifts in other communities where multiple sampling methodologies were employed with inconsistent sampling effort, and therefore provides natural resource managers quantitative data to inform conservation and management recommendations.

Physical Factors Impacted Bat Activity More Than Vegetation factors in an Urban Cemetery Ecosystem
Christopher S. Richardson[1], Alexis Rizzuto[2], Mina Burton[2] and Laura Borrelli[3]
1 Natural Science and Mathematics, Lesley University, Cambridge, USA; 2 Mount Auburn Cemetery, Cambridge, USA; 3 Cambridge Rindge and Latin School, Cambridge, USA

Research on the impact of urbanization on bats in Cambridge, Massachusetts has involved citizen scientists, including Lesley undergraduate students, collecting acoustic data and using mist nets to assess bat species diversity, abundance, and activity. Mount Auburn Cemetery (MAC) in Cambridge is a historic green space in the heavily urbanizing landscape of metropolitan Boston. Citizen scientists have been active with researchers since 2016 to help carry out continuing urban biodiversity research in MAC, including studies on arthropods, including insect pollinators, amphibians, birds, and mammals, including bats. Our research on bats has focused on factors influencing bat activity in this urban wildlife habitat. We worked with an integrative GIS mapping project to incorporate data into a collective resource for analyzing diversity, abundance, and activity patterns of bats. We asked what are the 34 most important physical and vegetation structure variables or factors that influence bat activity in an urban ecosystem. We hypothesized that vegetation structure variables are more influential. We examined how several GIS variables (elevation, slope, vegetation density, and vegetation height) affected bat activity as measured by calls recorded or heard per visit at a site in a night. We used Anabat detectors to record bat calls. Over two different years, we found slope and elevation (physical factors) had stronger correlations with bat calls per visit than vegetation density or vegetation height did. Additionally, in one year, no correlation was found between bat calls per visit and vegetation density while in the other year only a weak correlation existed.

Monitoring the Bat Community at a Wind Park in a Nordic Boreal Forest
April Irene Riderbo McKay[1], Sarah Elizabeth Johns[1], Richard Bischof[1], Jeroen van der Kooij[2], Fiona Mathews[3] and Katrine Eldegard[1]
1 Norwegian University of Life Sciences, Ås, NOR; 2 Natuformidling van der Kooij, Slattum, NOR; 3 University of Sussex, Brighton, GBR

All Nordic bat species rely on forest for critical phenological events but there lacks sufficient evidence to inform best practices for conserving bat communities in boreal forests in Fennoscandia. Nordic wind parks are increasingly developed inside of forests, against the advice of international bat conservation guidelines. We monitored a Norwegian wind park located in a boreal forest. Dog-handler led searches were conducted at all turbines (n = 15) approximately biweekly July−October, combined with searcher efficiency and carcass removal trials. Bat acoustic activity was monitored across the park continuously from ground level at natural sites, on turbine pads, and from a met tower at 45 and 90 m heights (16 detector locations, 60 detector nights per site on average). Insect camera traps paired with acoustic detectors captured flying nocturnal insect abundance. We describe bat acoustic activity using foraging guilds (long, medium, and short range echolocators; LRE, MRE, SRE) and behavior (commuting, feeding, social), verified manually. Two bats (*Vespertilio murinus*) and 10 avian carcasses were found. Bat acoustic monitoring revealed that feeding activity across all guilds, and overall SRE activity, was highest at natural habitats. We observed peaks in feeding activity at dawn and dusk, with LRE and SRE bats more active at dusk and dawn, respectively. Trends in activity across all bat guilds and behavior are explored in relation to biotic (insect abundance, habitat types) and abiotic (wind, temperature, photoperiod) conditions. Our results can inform future management practices of bats in Nordic boreal forests.

Evolutionary History of Bats: An Overview of Important Fossils and Recent Discoveries
Tim B. Rietbergen
Naturalis Biodiversity Center, Leiden, NLD

Bat fossils are often considered rare and are mostly represented by small bone fragments or isolated teeth. However, bat fossils are found almost worldwide and represent both extinct as extant species. What do we know about them? How do fossils help us understand their present-day geographic distribution and diversity? What are the major gaps in our knowledge of early bat evolution and how should we approach them? Presented here is an overview of important bat fossils and recent discoveries from inside and outside the United States. The importance of fossil bat research is discussed with a major focus on two important localities: Green River Formation in Wyoming & Messel quarry in Germany. This avenue of research will inform us about the taxonomic classification of bats and the evolution of their morphology, distribution, and behavior.

The Insectivorous Microbats of Adelaide, South Australia
Harry Peter Rigby Rust
Green Adelaide, South Australian Department of Environment and Water, Adelaide, AUS; School of Biological Sciences, University of Adelaide, Adelaide, AUS

For the first time ever, an intensive, city-wide survey is being undertaken to determine insectivorous microbat diversity in the City of Adelaide. Bats are an integral part of urban biodiversity, with roles in pollination, insect pest control, and bolstering food chains, however, relatively little is known about the microbat populations residing throughout Adelaide City and its surrounding urbanized, parkland and light industrial areas. With urbanization increasing, it is important to understand which species are present, and how they might need to adapt to a continually changing landscape, or alternatively, how we may help them adapt. Funded by a South Australian initiative - Green Adelaide, this survey ranges from Gawler to Aldinga, covering 60 sites across a variety of defined 'habitat types' surveyed over two seasons in 2021 and 2022. Early findings suggest there is a great diversity of forest-dwelling microbat species throughout Adelaide city, with the greatest average level of diversity being found within peri-urban backyards. Furthermore, it has been observed that microbat species are abundant surrounding inland wetlands in Adelaide, and relatively absent surrounding coastal wetlands. I will present the methods used to record and classify bat echolocation calls, several findings for notable bat species and their usage of the defined habitat types, and discuss possible future uses of the survey data for determining the requirements and potential for adaptability of different microbat species to urbanization.

Regional Migration of Three Bat Species in the Eastern United States
Piper L. Roby, Steve S. Samoray and Mark W. Gumbert
Copperhead Environmental Consulting, Inc., Paint Lick, USA

Life history information for most federally listed bat species is known for summer and winter habitat impacts. However, migration information between these habitats is less well known. We tracked spring migrating Indiana bats via aerial radio-telemetry from 2009–2022, tricolored bats in 2018, and gray bats in 2019 and 2021. Migration timing occurs earlier in the south due to warmer weather, and spring emergence duration is longer

for hibernacula with more bats. Tricolored bat migration speed was the fastest (22.5 ± 3.8 kph) followed by gray bats (17.4 ± 2.1 kph) and Indiana bats (11.2 ± 0.7 kph). Tricolored bats rarely foraged during migration (14.9% of total flight time), Indiana bats foraged 32.4% of flight time, and gray bats foraged the most (41.8% of flight time). These three species primarily migrated in a direct manner regardless of landscape type, including gray bats that are typically associated with waterways. Indiana bats used tree roosts typical for the species. Gray bats typically used cave roosts, but we documented two individuals roosting in trees during spring migration. Tricolored bats used dead leaf bundles as typical roosts, but the locations of these roosts were interesting: one tricolored bat roosted in three different live Bradford pear trees, one roosted in an abandoned squirrel nest, and another roosted in pine trees in a neighborhood. Indiana bat spring migration data has provided valuable information for regulatory decisions, but the limited data collected on other regional migrants indicates their behavior and habitat requirements differ from Indiana bats.

The Effects and Feasibility of Vaccinating Bats against White-nose Syndrome

Tonie E. Rocke[1], Ariel E. Leon[1], Bruce Klein[2], Jorge E. Osorio[3] and J. Paul White[4]
1 U.S. Geological Survey National Wildlife Health Center, Madison, USA; 2 School of Public Health and Medicine, University of Wisconsin, Madison, USA; 3 School of Veterinary Medicine, University of Wisconsin, Madison, USA; 4 Wisconsin Department of Natural Resources, Madison

To test whether vaccination against the fungal pathogen, *Pseudogymnoascus destructans* (*Pd*), that causes white nose syndrome (WNS) in bats could be effective in reducing the impacts of the disease, we conducted field trials in *Myotis lucifigus* (Mylu) in Wisconsin from 2019–2022. The vaccine constructs tested are recombinant, virally vectored vaccines that express *Pd* antigens developed by us and approved for field use by USDA's Center for Veterinary Biologics. Approximately 1,300 Mylu were orally administered one of two vaccine constructs or a placebo during fall swarm, inside or outside hibernacula, or at maternity colonies, in late summer over the 3-year period. The bats were individually identified with forearm bands and passive integrated transponder (PIT) tags. Wing swabs were collected and tested by qPCR to measure *Pd* loads, and survival rates were determined using radio frequency identification detectors (RFID) and manual surveys of sites. Our results demonstrated that vaccination was safe for bats and resulted in positive outcomes, including lowered *Pd* loads and improved survival for some cohorts. The effectiveness of vaccinating bats against *Pd* to prevent WNS will depend on locating suitable locations and populations for vaccine application, as well as timing of application in relation to disease emergence and the ease and seasonal timing of application.

Insights Into Forestry Management Practices to Influence Bat Communities in Illinois

Brittany A. Rogness, Tara Hohoff, Sarah Gaulke, Jordyn Chace and Mark Davis
Illinois Natural History Survey, Champaign, USA

Bats rely heavily on forested areas for roosting and foraging, but in Illinois, only approximately 14% of the state is forested. Of the 13 bat species in the state, six are listed as Illinois Species in Greatest Conservation Need, three are federally listed as threatened or endangered, and two additional species are candidates for listing under the Endangered Species Act. With such limited habitat for forest-dwelling bats, we seek to understand what decision-making processes land managers are implementing to influence bat communities and habitat across the state. We created a database of forestry professionals and land managers in Illinois through public information online and sent an email asking to participate in a survey to gain insights into broad forestry management practices. After the survey completion, we conducted follow-up semi-structured phone interviews with survey participants to gain further insights into their perceptions of bat habitat and management in Illinois. Specifically, we sought to understand more about roost habitat, foraging, and water management practices with the consideration of bats across the state. This research will act as an initial analysis to gauge knowledge on the influence of management practices on bats and understand priorities for Illinois foresters and land managers.

Heritability of Body Size in *Rhinolophus ferrumequinum*

Luke Romaine[1], Megan L. Power[2], Roger D. Ransome[1], Stephen Rossiter[3], Emma C. Teeling[2] and Gareth Jones[1]
1 School of Biological Sciences, University of Bristol, Bristol, GBR; 2 School of Biology and Environmental Science, University College Dublin, Dublin, IRL; 3 School of Biological and Behavioural Sciences, Queen Mary University of London, London, GBR

Determining the proportion of phenotypic variation explained by 'nature' or 'nurture' is a fundamental aim of evolutionary biology. The variance in a trait attributable to genetic factors (i.e., nature) within a population is known as heritability (h^2) and is key to understanding how traits respond to selection. The application of quantitative genetic analysis to long-term field studies of wild animal populations has revolutionized our understanding of how various traits evolve under ecological conditions. Such studies are rare in bats. The greater horseshoe bats (*Rhinolophus ferrumequinum*) at Woodchester Mansion, UK have been continuously monitored for 62 years. Juvenile development is characterized by rapid growth of the forearm (a reliable indicator of body size) during lactation, whereas the fingers reach their adult size post-weaning, as feeding becomes independent. Hence, the final skeletal size may reflect both maternal quality and early foraging efficiency. It is unknown whether forearm and finger length are heritable. Here, we combine a 27-year pedigree, comprising ~1800 individual bats, with data on forearm and fifth finger length. We apply the 'animal model' to decompose phenotypic variance into its genetic and environmental components. Both forearm ($h^2 = 0.66$) and finger length ($h^2 = 0.64$) were strongly heritable – suggesting, in this population, temporal changes in body size largely signify evolutionary responses. Nevertheless, the considerable residual and birth year effects reflect the important role the local environment plays in shaping phenotypic variance in early life. Our results give insight into how bat populations respond to selection in the context of environmental change.

Tricolored Bat Foraging Site Use and Selection During the Spring and Fall in Northwestern South Carolina

Eduardo Rosales[1], Susan C. Loeb[2] and David S. Jachowski[1]
1 Department of Forestry and Environmental Conservation, Clemson University, Clemson, USA; 2 U.S. Forest Service, Southern Research Station, Clemson, USA

Recent studies focusing on factors affecting bat survival and population recovery from WNS suggest the importance of fat reserves pre- and post-winter hibernation (i.e., spring and fall). Tricolored bats (Perimyotis subflavus) have experienced some of the largest population declines due to WNS. Our goal was to determine suitable foraging habitat for tricolored bats in northwestern South Carolina during spring (March–May) and fall (September–November). We determined occupancy at 68 sites during spring and fall of 2021 using acoustic detectors, and related tricolored bat occupancy to forest management, forest structure, and forest composition. We stratified stands on the Andrew Pickens Ranger District (APD) of the Sumter National Forest using forest type and past forest management, and selected sites using the spatially balanced Generalized Random Tessellation Stratified sampling design. We placed acoustic detectors at selected sites for three nights and recorded vegetation structure and

landscape data for each site. We identified bat calls using Kaleidoscope Pro software, and calls identified as tricolored bats were manually vetted. We ran single season occupancy models to assess habitat use. During spring, occupancy was greater at sites with less canopy cover. During fall, occupancy was greater at sites with less basal area. Our results suggest the importance of open habitat for suitable foraging sites pre- and post-hibernation in northwestern South Carolina. Because access to open habitat likely minimizes energy expenditure and therefore enhances fat acquisition, forest management that increases open habitat may provide tricolored bats greater chances of survival and recovery from WNS.

Investigating the Effects of Anthropogenic Noise Pollution on Echolocating Bats in Upstate New York, USA
Nicole D. Rose and Maria Sagot
Department of Biological Sciences, State University of New York at Oswego, Oswego, USA

Natural background noises are common in the environment. Thus, bat communication systems are inherently equipped to overcome those noises. Anthropogenic noises, on the other hand, are an emerging global pollutant, and they pose new challenges, as they can interfere with vocal communication and navigation. Furthermore, many bat species have adapted to live and forage in and around human made structures such as houses, buildings and streetlights, enhancing their exposure to artificial noises. Previous studies have shown that bats can alter echolocation pulse parameters and activity patterns in response to loud anthropogenic sounds such as road networks and energy extraction infrastructure. Although artificial noises produced in or around houses and buildings are not typically considered disruptive, little is known on how weaker artificial noises affect bat echolocation parameters and activity. We hypothesized that bats will alter their echolocation and activity patterns in response to urbanized noise pollution to facilitate vocal exchanges within noisy environments. To test our hypothesis, we recorded echolocation activity using passive and active acoustic monitoring in both pristine and urbanized areas in Upstate New York. We found a reduced number of species foraging in urbanized areas compared to pristine environments. Moreover, bats occupying urbanized habitats altered their echolocation pulse parameters, as well as their activity patterns. Anthropogenic noise is a significant threat to animals that have adapted to live in human-altered environments. This study demonstrates that echolocating bats, which actively depend on sound for navigation and communication, can serve as bioindicators to quantify the ecological effects of artificial sound pollution.

Landscape of Energy, Collective Behavior, and Spillover Risk of Hendra Virus in Eastern Australia
Manuel Ruiz-Aravena[1], Andrew Hoegh[2] and Raina K. Plowright[1]
1 Department of Microbiology and Cell Biology, Montana State University, Bozeman, USA; 2 Department of Mathematical Sciences, Montana State University, Bozeman, USA

Land use change is recognized as a primary driver of zoonotic pathogen spillover from wildlife to human populations. A crucial component of transmission of pathogens from wildlife to humans is the nature and intensity of contacts between wild reservoirs and humans or bridge hosts. Hendra virus is a zoonotic pathogen that circulates in flying foxes in Eastern Australia. Black flying foxes are the main reservoir species of importance for transmission to horses, and through horses to humans. This spillover events, present higher likelihood during winter months, periods of low availability of foraging resources for flying foxes. These periods of food shortage influence both physiology and behavior of black flying foxes, increasing viral shedding and reducing their foraging movements, which results in potentially higher contacts with horses, and therefore spillover risk. In this work, we present and discuss the evidence on how food availability affects movement and roost behavior of flying foxes, how it affects their foraging decisions that may influence the nature and intensity of contacts with horses. We discuss the use of computational methods and active radar technology to inform ecological interventions to mitigate and reduce the risk of viral transmission from bats to humans.

Habitat Use Acoustics for Pre-construction Turbine Micro-siting
Adam R. Rusk
Stantec Consulting Services, Oklahoma City, USA

A commonly accepted setback from bat habitat when micro-siting wind turbines is 1,000 feet. However, not all protected bat species respond to their habitat the same way. A lack of site-specific and species-specific turbine setback constraints can lead to unnecessary restrictions in micro-siting. To account for these nuances in species and local population habitat use, Stantec performed stratified acoustic sampling at two pre-construction wind facilities in southwest Missouri. The purpose of these two surveys was to evaluate if a 1,000-foot setback from streams is sufficient for minimizing turbine interaction with gray bats (*Myotis grisescens*). Fifty acoustic bat detectors were set out at each project for up to seven nights. Using gray bat passes per detector night as a response variable predicted gray bat activity throughout each project as a function of land cover. Stantec found that distance to maternity cave roosts is a major factor in predicting activity levels but also depends on the primary direction the bats travel from the colony. Area of forested cover and distance to trees and streams were also important variables in one of the models. The highest activity sites were immediately adjacent to streams and increasing distance resulted in decreases in recorded activity. Initial pre-construction results suggest limiting construction near quality habitat near cave roosts. However, setbacks may be overly conservative and site-specific data could allow for turbine siting closer to riparian corridors without increasing risk to gray bats. Additional surveys performed post-construction, accounting for potential attraction to turbines, could substantiate these results.

Bat Meat: Preference or Necessity? The Role of Protein Limitation in Driving Bat-Hunting
Abigail L. Rutrough and Tigga Kingston
Department of Biological Sciences, Texas Tech University, Lubbock, Texas, USA

Overhunting is one of the leading threats to biodiversity and has driven bat population declines in parts of Africa, Asia, and Oceania. Protein limitation is one proposed mechanism that drives people to hunt wild meat. This hypothesis posits that areas with decreased access to conventional protein sources, such as livestock and fish, will have the highest incidence of bushmeat hunting. However, the role protein limitation has in driving bat hunting is unclear, especially at large spatial scales. Here we test whether areas with decreased access to conventional protein sources will have higher rates of bat hunting. We built a suite of models using the machine learning program Maxent. Models were trained with over 500 records of hunting behavior from over 70 countries collected from existing literature and social media. These models use latent variables hypothesized to drive protein limitation, including access to aquatic protein, access to livestock, access to larger game mammals, and ability to purchase conventional proteins. We selected the top model using AICc model selection and withheld a subset of the training data to test predictive ability. We found protein limitation was not a major driver of bat hunting at a continental scale but may drive hunting on islands. Protein limitation is often assumed

to drive game meat hunting, yet our work shows this is not the case in many bat hunting hotspots. Future work will explore influences of bat ecology, cultural norms, and food insecurity on bat hunting.

Individual Social Roles in the Organization of *Myotis lucifugus* Maternity Societies
Caleb Ryan and Hugh Broders
1 Department of Biology, University of Waterloo, Waterloo, CAN

Myotis lucifugus are a widespread North American temperate bat species whose females form summer maternity groups to give birth to and raise their young. In these groups individuals establish preferential associations with other bats resulting in the formation of associating sub-groups within the larger maternity society. Despite these apparent preferences, there is significant mixing between groups as bats frequently switch roosts. This leads us to question how individuals may be uniquely associating in their society. Beginning in 2012 at Salmonier Nature Park, Newfoundland, Canada we have tagged bats with PIT tags and monitored a system of 11 roost boxes across a 1.1 km^2 area using PIT tag antennas. We have recorded 975 unique bats using these monitored roost boxes and using this have created yearly social networks of bats in their day roosts based on the assumption that bats roosting together during the day are associating. Bats in each network were ranked based on their betweenness centrality, a measure of how often the shortest path between two individuals in a network is bridged by a certain individual often used to describe knowledge brokers. We found that while all bats frequently switch roosts, a subset of bats are frequently switching between subgroups and appear responsible for connecting the maternity society and that these roles are consistent across years. This research suggests that individual differences in social roles may be responsible for the organization of maternity societies and further highlights the importance of individual details in understanding population dynamics.

Bat Selfies: Photographic Surveys of Flying Bats
Jens Rydell[1], Danilo Russo[2], *Price Sewell[3], Ernest C. J. Seamark[4], Charles M. Francis[5], Sherri L. Fenton[6] and M. Brock Fenton[6]
1 Department of Biology, Lund University, Lund, SWE; 2 Wildlife Research Unit, Dipartimento di Agraria, Universita degli Studi di Napolio Federico II, Naples, ITA; 3 Copperhead Environmental Consulting, Paint Lick, USA; 4 AfricanBats NPC, Kloofsig, ZAF; 5 Canadian Wildlife Service, Environment and Climate Change Canada, Ottawa, CAN; 6 Department of Biology, University of Western Ontario, London, CAN

The recent pandemic and other environmental concerns have resulted in restrictions on research and surveys involving capture and handling bats. While acoustic surveys have been widely used as an alternative survey method, in this study, we show how photographic surveys can offer an important contribution to study and survey bats. We outline approaches, using high speed flash and automated trip beams to obtain photos of flying bats of sufficient quality for reliable identification of species. We show, through a series of examples of setups and photographs, that photography is effective for surveying bats at a variety of sites, where bats roost, drink, and forage. We note, however, that photographic surveys cannot replace capture in all situations. In addition, although photographing bats is less invasive than capturing them, it can involve disturbance, so we stress the importance of minimizing the impact of such operations on bats.

The Importance of Vocal Roles in Spix's Disk-winged Bats During Roost Finding
Maria Sagot[1], and Gloriana Chaverri[2,3]
1 Department of Biological Sciences, State University of New York at Oswego, Oswego, USA; 2 Sede Sur, Universidad de Costa Rica, Golfito, CRI; 3 Smithsonian Tropical Research Institute, Balboa, PAN

In group living, social roles are beneficial because they can reduce social conflicts and energetic expenditures. For instance, Spix's disk-winged bats (*Thyroptera tricolor*), a species that uses highly ephemeral roosts, are known to have distinct social roles in acoustic signaling to coordinate roost finding. Their groups are composed of one or few vocal bats, while the rest of the group members produce no or few calls during roost finding. Having a mix of acoustic roles can promote better decision-making and reduce energetic expenditures. However, if the number of vocal bats is large, it might decrease coordination, create confusion, and affect coordination. In this study, we manipulated the number of vocal bats within social groups to determine the effects on group coordination and roost finding efficiency. We found that having many vocal bats increases roost finding time and the chances of groups splitting into multiple roosts. However, if more than one vocal bat is present, group members tend to follow the individual that produces more vocalizations. This demonstrates that having more than one vocal bat within groups is beneficial; however, a large number of them can affect group coordination. Our results highlight the importance of group vocal composition in roost finding, as well as the ecological mechanisms determining group formation.

BattyCoda: Novel Software for Bat Social Call Annotation and Automated Classification
Angeles Salles and Gabriela Nuñez-Mir
Department of Biological Sciences, University of Illinois at Chicago, Chicago, USA

Bats are social animals that have a wide repertoire of communication calls that may vary across individuals and across populations within a species. Most automated programs for the annotation of bat calls focus on classifying calls by species based on the acoustic features of their echolocation calls. For lab and field experiments where bats can be monitored and the species identified morphologically, species identification through acoustics is not necessary. Yet, for experiments in which we evaluate intra-species interactions, social call identification and categorization becomes a necessity. Open-source neural networks for classification of social calls for dolphins and birds generally require hundreds to thousands of annotated exemplars to train the network for each category. In bats, compared to echolocation calls, communication calls occur infrequently, thus, gathering a high number of exemplars to train a network becomes a challenge. Here, we present the current state of a preliminary project where we aim to produce a customizable software package - BattyCoda - that can be used to simultaneously annotate bat communication calls and train a supervised classifier with as little as 20 exemplars per call category.

Filling Data Gaps to Improve Estimates of Bat Virus Spillover
Cecilia A. Sánchez[1], Hongying Li[1], Kendra L. Phelps[1], Carlos Zambrana-Torrelio[1,2], Lin-Fa Wang[3], Peng Zhou[4], Zheng-Li Shi[4], Kevin J. Olival[1] and Peter Daszak[1]
1 EcoHealth Alliance, New York, USA; 2 Department of Environmental Science and Policy, George Mason University, Fairfax, USA; 3 Duke-NUS Medical School, Singapore, SGP; 4 Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, CHN

Emerging diseases caused by coronaviruses of likely bat origin have disrupted global health and economies for two decades. Evidence suggests that some bat Severe Acute Respiratory Syndrome-related coronaviruses (SARSr-CoVs) could infect people directly, and that their spillover is more frequent than previously recognized. Each zoonotic spillover of a virus represents an opportunity for evolutionary adaptation and further spread among humans; therefore, quantifying the extent of this spillover may help target prevention programs. We derived biologically realistic range distributions for known bat SARSr-CoV hosts in Southeast Asia and quantified their overlap with human populations. We then performed a probabilistic risk assessment that incorporated this spatial overlap data with literature-informed estimates of human-bat contact, viral seroprevalence among humans with bat contact, and human SARS antibody duration. We estimated that a median of ~66,000 people are infected with SARSr-CoVs annually in Southeast Asia. These data on the geography and scale of spillover can be used to target surveillance and prevention programs for potential future bat-CoV emergence. Further, this exercise highlighted areas where additional knowledge could refine estimates of SARSr-CoV spillover rates, including the potential role of intermediate hosts, the influence of bat biology and ecology, and socio-ecological factors involved in human-bat contact.

High Bat Fatality Rates Estimated at Wind Farms in Southern Spain

Sonia Sánchez-Navarro[1], Jens Rydell[2], David Gálvez-Ruiz[3] and Carlos Ibáñez[1]
1 Department of Evolutionary Ecology, Estación Biológica de Doñana, Sevilla, ESP; 2 Department of Biology, Lund University, Lund, SWE; 3 Department of Statistics & Operational Research, University of Sevilla, Sevilla, ESP

An astonishing number of bat fatalities (2,371 belonging to 15 species) were recovered at wind farms in Cádiz, the south of Spain, in the period 2005–2016. We carefully analyzed a subset of this sample with the aim of estimating the fatality rate in the year 2011, the year for which we had the most complete data set (582 fatalities at 38 wind farms). In order to estimate the true fatality rate, we conducted search-efficiency and scavenger-removal trials in nine of the wind farms, involving 122 turbines and 284 observed fatalities and calculated the searchable surface of the study area and the whole province. An annual fatality rate of 13.0 dead bats per turbine (9.4 per MW) was estimated. According to our own estimator, 11,914 (IC 11 450−12,381) bats were killed by wind turbines in Cádiz in 2011. This is among the highest fatality rate ever recorded for bats at wind turbines anywhere in the world, even when we have been conservative. There is an urgent need for efficient mitigation measures at windfarms with high-rate bat's fatalities but also it is needed to run trials to know how well the post-operational monitoring is done and how far are from the reality. Clearly, current official post-construction surveillance programs are not efficient for searching bats and therefore mask a high bat fatality rate, thereby probably preventing the implementation of needed suitable mitigation or preventive measures.

Gut Microbiome Variation Explains a Large Amount of Variation in Digestive Efficiency in Mexican free-tailed Bats

Oscar Sandate[1], Craig Tipton[1], Matthew Fox[1], Marilyn Mathew[1], Gregory Knox[1], Liam McGuire[2], Tigga Kingston[1], Todd Little[1] and *Caleb Phillips[1]
1 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 2 Department of Biology, University of Waterloo, Waterloo, Canada

Gut microbiomes are thought to be fundamental to macro-organism health, and factors influencing composition of microbiomes are being elucidated. Contribution to host energy acquisition from diet is hypothesized to be one of the major roles gut microbiomes play relevant to host function. Although a large part of compositional variation in gut microbiomes is often explained by dietary variation, the relationship between gut microbiomes and digestive efficiency, that is the ability of an organism to extract calories from food, is poorly known. Given the high energetic demands of bats in combination with their short food retention times, they are a good system to jointly study gut microbiomes and digestive efficiency. Mexican free-tailed bats, *Tadarida brasiliensis*, were studied at Frio Cave, Texas spanning a period of migratory arrival, pregnancy, lactation, weaning, and departure. Information about fecal microbiome composition, dietary composition, bacterial load, and caloric content was measured for individuals. The key finding from analysis was that inter-individual variation in gut microbiomes explained a significant and large (~50%) amount of inter-individual variation in digestive efficiency. This relationship could not be recovered using commonly implemented statistical approaches but was revealed through a structural equation model that incorporated a new and generally applicable pre-modeling parcel optimization strategy developed during this study. The implication of this work is that gut microbiomes are consequential to meeting bat energetic demands.

Effects of Pesticides in Neotropical Bats - An Integrative Approach

Natalia Sandoval-Herrera[1,2], and Kenneth C. Welch Jr.[1,2]
1 Department of Ecology and Evolutionary Biology, University of Toronto, Ontario, CAN; 2 Department of Biological Sciences, University of Toronto Scarborough, Ontario, CAN

Bats provide valuable ecosystem services by eating large amounts of insects, helping to control many agricultural pests. Foraging in croplands, however, can represent a threat for bats that can be exposed to pesticides by eating contaminated prey. Although toxicant exposure has been identified as a major threat for bat populations in temperate countries, little research on this topic has been conducted in neotropical systems, where the use of pesticides is extensive, and which harbor the highest bat diversity. Here we studied the vulnerability of insectivorous bats foraging in or near crops to pesticides and the effects of these chemicals on their physiology and behavior. We assessed the risk of exposure by quantifying foraging activity of bats in crop fields and screening pesticide residues in their diet in Lamanai, Belize, and Colima, Mexico; regions with accelerated habitat loss driven by agricultural expansion. To study the effects of such exposure, we used an integrative approach evaluating responses at different levels of biological organization: cells (enzyme activity), physiology (immune response), and behavior (spatial memory). We present evidence of the suitability of some of these biomarkers to monitor pesticide exposure in free-ranging bats. We also discuss how working with well-studied bat communities, like Lamanai in Belize, provides the opportunity to understand how ecological traits affect the ability of different bat species to cope with environmental stressors at different scales. This information will enable better predictions regarding the implications of the Anthropocene on bat populations and identify current threats for their conservation.

Malaria Parasites of Bats Feature Different Patterns in a Diverse Host Group

Juliane Schaer
Institute of Biology, Humboldt University, Berlin, DEU

Mammals are hosts to malaria parasites of ten different genera, with nine of them being present in bats out of which seven exclusively infect bats, emphasizing that bats feature the highest diversity of malaria parasites. Further, phylogenetic studies suggest that bats have played an important

role in the evolutionary history of the whole group of malaria parasites. To date, malaria parasites have been described from eight of the 21 bat families. Thereby, the parasite genera seem to be specific to certain bat families, e.g., *Plasmodium* and *Hepatocystis* have been recorded from species of Hipposideridae and Pteropodidae only, whereas *Nycteria* parasites infect bats of multiple families across both chiropteran suborders. Considering the high diversity of *Plasmodium* species, it is quite striking that only three species have been described from bats and that these *Plasmodium* species are specific to only one African bat species respectively. In contrast, *Hepatocystis* parasites are highly abundant in bat species in Africa, Asia, and Australia; feature low host species specificity and rather represent species complexes. Only five species of *Polychromophilus* parasites have been described, but with two predominant species *P. murinus* and P. melanipherus infecting numerous vespertilionid and miniopterid bats worldwide. Moreover, *Polychromophilus* is the only genus that has been reported from bats in temperate and tropical regions, whereas the distribution of all other parasite genera is limited to bats in the Old-World tropics. I will present an overview of different patterns of haemosporidian parasites in bats.

Roosting Bats Across an Urban Gradient in Central Coastal California

Bethany C. Schulze[1], Fred G. Watson[1], Jennifer M. Duggan[1] and Winifred F. Frick[2]
1 Department of Applied Environmental Science, California State University, Monterey Bay, Seaside, USA; 2 Bat Conservation International, Austin, Texas, USA and Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, Santa Cruz, USA

Ecosystem health and function in habitats around the world are threatened by a variety of stressors, one of which is urbanization. Foliage roosting bats such as hoary bats (*Lasiurus cinereus*) and western red bats (*Lasiurus blossevillii*) may be used as bioindicators of an ecosystem's response to the stressor of urbanization because of their habitat selection for roosting and foraging. We investigated these species' foraging activity along urban-natural habitat gradients in central coastal California during migration (fall/spring) and winter seasons. Both live captures and acoustics were used to determine foraging associations and male/female capture ratios. We modeled foraging activity and habitat use by conducting analyses including landscape, distance, and abiotic factors and compared models using Akaike's Information Criterion scores. Both hoary bats and western red bats were captured during the fall and winter seasons and were 11.4 times more likely to be captured at natural habitat sites than urban. Male hoary bats were 2.9 times more likely to be captured than females, and all western red bats captured were males except for one female. Both species were found to be active throughout the winter with the lowest levels of activity during January and were detected more frequently at sites surrounded by substantial natural habitat. These results aid in our understanding of habitat thresholds for cryptic foliage roosting bats which may reflect ecosystem sensitivities to urbanization. Conservation efforts involving habitat restoration in the future may be able to use the activity of these species as an indicator of success.

Using Wild Bats to Investigate the Cellular Basis of Longevity

Karen Sears
Ecology and Evolutionary Biology and Molecular, Cell and Developmental Biology Departments, University of California Los Angeles, Los Angeles USA

Identifying cellular processes that drive longevity in long-lived mammals, including humans, is a critical goal of biomedical research. However, progress toward this goal has been hamstrung because most lab mammals are short-lived and therefore make less than ideal models for aging in long-lived mammals. Bats, in contrast, are among the longest-lived mammals for their size and many do not exhibit changes in mortality or fertility until high ages. With collaborators, we recently developed genome-wide, methylation-based methods that accurately estimate chronological age across mammalian species and tissues. With these new genomic tools, we can explore relationships between chronological and cellular-level aging in wild bats. We first focused on three species from Cameroon: *Hipposideros ruber*, *Rhinolophus alcyone*, and *Rousettus aegyptiacus*. IHC results demonstrate that tissues from all species exhibit consistently low levels of DNA damage and cellular senescence with increasing age, relative to mouse. However, they also suggest that species reach this endpoint through two paths. *Hipposideros ruber* and *R. alcyone* exhibit reduced ROS, possibly through increased mitochondrial efficiency, while *R. aegyptiacus* exhibits higher ROS at levels comparable to mouse. We also found a negative ($p < 0.05$) association between telomere length and age for all species. We are currently expanding our studies to diverse New World bats (>20 species). Given the significant differences we have already observed among only three species, we expect this broader sampling of wild bats will yield varied and informative data on the cellular basis of aging in long-lived mammals.

A Phantom Ultrasonic Insect Chorus Repels Low-flying Bats, but Most are Undeterred

Jodi L. Sedlock[1], Dylan G.E. Gomes[2,3], Juliette J. Rubin[2,4], Sarah Woody[1], Buyung A.R. Hadi[5] and Jesse R. Barber[2]
1 Biology Department, Lawrence University, Appleton, USA; 2 Department of Biological Sciences, Boise State University, Boise, USA; 3 Cooperative Institute for Marine Resources Studies, Hatfield Marine Science Center, Oregon State University, Newport, USA; 4 Department of Biology, University of Florida, Gainesville, USA; 5 Sustainable Impact Platform, International Rice Research Institute, Los Baños, PHL

The acoustic environment can serve as a niche axis, structuring animal behavior by providing or obscuring salient information. Meadow katydid choruses occupy the ultrasonic, less studied, realm of this acoustic milieu, form dense populations in some habitats, and present a potential sensory challenge to co-occurring ultrasonic-hearing animals. Aerial-hawking insectivorous bats foraging immediately over vegetation must listen for echoes of their prey and other cues amidst the chorus din. We experimentally created the cacophony of a katydid chorus in a katydid-free rice paddy using an aggregation of 100 ultrasonic speakers in a 25x25 m grid to test the hypothesis that aerially hawking bats are averse to this noise source. We alternated between chorus-on and chorus-off hourly, and acoustically monitored bat activity and arthropod prey abundance. We found that our phantom katydid chorus reduced bat activity nearest the sound source by 39.3% (95% CI: 7.8−60.0%) for species whose call spectrum fully overlapped with the chorus, and elicited marginal reductions in activity in species with only partial spectral overlap. Our study suggests that ultrasonic insect choruses degrade foraging habitat, potentially suppressing bats' ecosystem services as consumers of pests; and, given the global distribution of meadow katydids, may provide an underappreciated force modifying animal behavior in other grassland habitats.

Efficacy of p-Chip Tag Implementation in the Wing and Leg of Big Brown Bats

Shane D.I Seheult[1], Raj Panchal[1], Alex V. Borisenko[2], Patrick J. Bennett[1] and Paul A. Faure[1]
1 Department of Psychology, Neuroscience and Behavior, McMaster University, Hamilton, CAN; 2 Department of Integrative Biology, University of Guelph, Guelph, CAN

Mark-recapture techniques are critical for studying the ecology of wild animals. Current marking methods in bats have practical limitations and may cause morbidity. We tested a new, miniaturized (500x500 µm), light-activated microtransponder called the p-Chip (PharmaSeq, Inc.) as a prospective marking technique in a captive colony of big brown bats (*Eptesicus fuscus*). We assessed post-implantation effects and long-term reliability of p-Chips injected subcutaneously above the second metacarpal on the wing (n = 30) and above the tibia (n = 13). Following implantation, p-Chips were scanned with a hand-held laser wand on post implantation days (PIDs) 1, 8, 15, 22, 32, 60, 74, 81, 88, 95, and 1 year later on PID 464. We recorded: (1) total animal handling time, (2) scan time, (3) number of laser wand flashes, (4) p-Chip visibility, and (5) bat health. Average scan times increased over the duration of the study; however, the number of wand flashes decreased, suggesting p-Chip recording efficacy increases with user experience. The visibility and readability of p-Chips implanted in the wing was higher, suggesting the 2nd metacarpal was a better implantation site compared to the tibia. Morbidity in tagged bats was similar to baseline values for the colony. Scan efficiency on PID 464 was comparable to earlier days, indicating p-Chips may be applicable for long-term studies. Our results suggest that p-Chips may be viable for extended field testing in a standardized location on bats and may become an effective alternative to traditional mark-recapture methods used to study bat ecology.

The Distribution and Conservation of Island Bats in Langkawi Archipelago of Malaysia

Juliana Senawi[1], Stephen Rossiter[2] and Tigga Kingston[3]
1 Universiti Kebangsaan Malaysia, Selangor, MYS; 2 Queen Mary University of London, London, GBR; 3 Texas Tech University, Lubbock, USA

The island ecosystem contains some of the most vulnerable habitats, which have been heavily affected by both historic and current anthropogenic threats, including land-use intensification and climate change. Comprising over 1,400 described species, bats are a major component of mammalian diversity. Enabled by their flight capability, a large component of bat diversity can be found on islands (ca. 60% of species) and ca. 25% of bat species are insular endemics. Yet, studies of island bats, especially regarding their distribution and conservation in Malaysia, are still lacking. Langkawi archipelago comprises 104 islands of diverse sizes. To model the distribution of threatened island bats of Langkawi, the latest IUCN Red List Categories were used to define relative risk of extinction of each species. Differences in the proportion of threatened (NT, VU, EN, or CR), non-threatened (LC), and Data Deficient (DD, Not Evaluate and undescribed) species between single-island endemics as compared to those occurring on multiple islands was tested using the Pearson's chi-squared test of independence (χ^2). There were 7 threatened, 38 non-threatened and 5 data deficient species recorded across 12 islands of Langkawi archipelago. This fundamental understanding of Langkawi archipelago distributions will provide novel insight into conservation value of bats in isolated habitats.

Redefining 'Umbrella Species': When Protecting Bats Means Protecting Biodiversity

Sheherazade
PROGRES (Prakarsa Konservasi Ekologi Regional Sulawesi), Jl. Hos Cokroaminoto No. 7, Luwuk, Banggai, Central Sulawesi, 94711, Indonesia

Amid the biodiversity crisis in Southeast Asia, conservation prioritization is critical yet flying foxes remain one of the most overlooked yet threatened species. Our initiatives in Sulawesi, Indonesia have identified impediments to fostering flying fox conservation and devised solutions to address them. The first challenge is the lack of scientific information, particularly on flying fox trade and ecosystem services. These two critical topics allow us to address specific major threats along with raise awareness and urgency among the local community, government agencies, and other scientists. The second challenge is the lack of legal tools to protect bats. The lack of formal protection opens up the opportunity for us to empower and work with the local community to become champions for bats while supporting their priorities in other development projects outside of conservation. Flying foxes are no longer hunted and are well-protected by the local community, resulting in an increase of the maximum number of roosting bats (2018: 8,376 to 2021: 35,707 ind.). The bats became an icon that the community is proud of, and the increasing number of bats secure their services for maintaining the forest and their guano for nourishing the sea. Equipped with lessons learned, we expanded our work to other bat colonies and other threatened species that face similar challenges. They may not be what is traditionally considered an umbrella species, but they inspire us to find creative solutions that benefit other wildlife and equip us with strong narratives that biodiversity is worth protecting.

What Do We Not Know? Quantifying Data Gaps and Biases in Knowledge of Bat Co-Roosting

Aja C. Sherman[1], Cullen Geiselman[1], Nancy B. Simmons[2], Nathan S. Upham[3], Jorrit H. Poelen[4,5], DeeAnn M. Reeder[6], Sandro Bertolino[7], Quentin Groom[8], Kendra Phelps[9], Donat Agosti[10] and Anna R. Willoughby[11,12]
1 Bat Eco-Interactions Project, Houston, USA; 2 Department of Mammalogy, American Museum of Natural History, New York, USA; 3 School of Life Science, Arizona State University, Tempe, USA; 4 Ronin Institute of Independent Scholarship, Montclair, USA; 5 Cheadle Center Biodiversity and Ecological Restoration, UC Santa Barbara, Santa Barbara, USA; 6 Department of Biology, Bucknell University, Lewisburg, USA; 7 Department of Life Sciences and Systems Biology, University of Turin, Torino, ITA; 8 Meise Botanic Garden, Meise, BEL; 9 EcoHealth Alliance, New York, USA; 10 Plazi, Berne, SWZ; 11 Odum School of Ecology, University of Georgia, Athens, USA; 12 Center for the Ecology of Infectious Diseases, University of Georgia, Athens, USA

Improved understanding of co-habitation of roosts by multiple species of bats is essential for estimating the risks of zoonotic disease transmission. However, ecological data on roosting environments, species richness, bat-bat interactions, viral infections, and other species interactions are scattered throughout the literature, making them difficult to study on a global scale. The research scope for most roost studies has been narrow, focusing on roost type, bat abundance, and locality data while failing to investigate interspecific roosting interactions. To meet this need, we have collaboratively built an open-access dataset of ecological interactions (including co-roosting, trophic, anthropogenic, and parasitic) extracted from the literature to improve our understanding of roost dynamics on a global scale, and to elucidate the role of shared roosts in disease transmission. As of April 2022, >11,500 interaction records involving >360 bat species from >137 countries encompassing a variety of habitats have been extracted from >175 publications spanning from 1860−2020, all accessible via the Coronavirus-Host community at Zenodo. With this benchmark dataset of open-access digitized interaction data, tools, and workflows, we provide evidence of co-roosting events that we aligned with multiple ontologies (interaction terms, taxonomies, administrative regions) and phylogenies suitable for high-throughput analysis We followed open access and FAIR (Findable, Accessible, Interoperable, and Reusable) data principles for extracting data and choosing methodologies. We identify biases in the coverage of bat interaction records, suggest new tools for biodiversity informatics, and explore obstacles and opportunities in the mining of eco-interactions previously lost in the annals of scientific literature.

Biases in Acoustic Surveying Results between the North American Bat Monitoring Program and Alternative Surveying Methods

Timothy A. Shier and Bradford Westrich

Division of Fish & Wildlife, Indiana Department of Natural Resources, Bloomington, USA

Many bat researchers are transitioning to collecting acoustic data using methods from the North American Bat Monitoring Program (NABat). Standardizing data collection efforts across the continent expands the breadth and utility of potential research and the possibilities of comparing results between studies. However, this does not preclude biases when using NABat data. In 2020 and 2021, acoustic data were collected from south-central Indiana using both NABat methods and alternative methods previously developed by the Indiana Department of Natural Resources. Data were collected from multiple comparable transects using identical hardware and then analyzed using an identical process. Results from matched transects indicate that substantial variations in results can exist between the two methods. It is therefore important to consider how NABat methods may introduce common biases into data collection efforts and analysis results. Perhaps of greater significance is how biases inherent to NABat methods may pervade the entirety of the continental dataset, thus introducing similar biases to any study using NABat data.

Large-team Multidisciplinary Collaborative Research on Bats in Belize

Nancy B. Simmons[1], M. Brock Fenton[2], Melissa Ingala[1,3], Neil Duncan[1] and Venetia Briggs-Gonzalez[4,5]
1 Department of Mammalogy, American Museum of Natural History, New York, USA; 2 Department of Biology, University of Western Ontario, London, CAN; 3 Department of Biological Sciences, Fairleigh Dickenson University, Madison, USA; 4 Lamanai Field Research Center, Indian Church, BLZ; 5 Fort Lauderdale Research and Education Center, University of Florida, Fort Lauderdale, USA

For the last 15 years, a unique field program has brought together researchers from over a dozen countries to study bats in and around the Lamanai Archaeological Reserve in northern Belize. Working at the Lamanai Field Research Center based at Lamanai Outpost Lodge, our loosely-organized team annually consists of 4570 people including a combination of senior researchers, postdocs, students, and others interested in bats and the biology of the area. Working together, this group has recorded thousands of bat captures and engaged in dozens of different research projects, many of which are cross-disciplinary and born from the unusual field environment that mixes scientists with very different levels of experience and areas of expertise. The Lamanai bat group has published over 70 papers including data on bats from the area, and the team – which varies in composition from year to year – continues to add new people, develop new projects, and build on past results. Diverse habitats (ranging from tropical deciduous forest to savanna including freshwater streams, ponds, and a wide lagoon), ongoing habitat fragmentation in the region (a result of agricultural expansion), and recent changes in team field methods (e.g., use of a centralized field numbering system for tracking bats and samples; PIT tagging all captured bats) are opening new opportunities for even more broad and integrative research in future years. The collaborative field environment fosters creative science, testing of new methods, sharing of ideas and data, and training of students and early career researchers in an inclusive and supportive environment.

Capture Rates of *Eptesicus fuscus* Increase Following *Pseudogymnoascus destructans* Invasion

Molly C. Simonis[1], Lynn K. Hartzler[2], Greg G. Turner[3], Michael R. Scafini[3], Joseph S. Johnson[4] and Megan A. Rúa[2]
1 Wright State University Environmental Sciences PhD Program, Dayton, USA; 2 Wright State University Department of Biological Sciences, Dayton, USA; 3 Pennsylvania Game Commission Bureau of Wildlife Management, Harrisburg, USA; 4 Ohio University Department of Biological Sciences, Athens, USA

Pseudogymnoascus destructans (*Pd*), the fungal pathogen causing white-nose syndrome, has devastated highly susceptible North American bat populations since its introduction in 2006. *Eptesicus fuscus* are less susceptible and resistant to *Pd* infections, thereby causing their populations to persist in greater numbers than highly susceptible species despite annual infections. However, to understand the full extent of *Pd* impacts on North American bat populations, research investigating how less susceptible, resistant bat populations change is critical. We hypothesized *E. fuscus* capture rates would increase over *Pd* invasion time due to a release from interspecific competition from highly susceptible species. We also hypothesized capture rate increases would be greater in northern compared to southern latitudes, mirroring spatial gradients for highly susceptible species mortalities. Using 30 years of capture records, we created Bayesian generalized linear models to determine how capture rates of adult *E. fuscus* or reproductive female *E. fuscus* changed across the eastern US from pre-*Pd* invasion through *Pd*-establishment. *Eptesicus fuscus* capture rates increased from pre-invasion to establishment years, and lactating and post-lactating bat capture rates increased with latitude by establishment years. This suggests *E. fuscus* may experience intraspecific competitive pressures with pathogen pressures following *Pd* introduction, and increased capture rates of lactating and post-lactating *E. fuscus* with latitude may create spatial gradients for those combined pressures. If *E. fuscus* reach their carrying capacity, pathogen pressures could contribute to steeper population declines to regulate their population. Continued monitoring of species less susceptible to infections is crucial for the future of North American bat populations.

Differences in Form and Function of the Stylohyal – Tympanic Bone Articulation in Laryngeally Echolocating Bats

Chelsie C.G. Snipes[1], Peter A. Newman[1], Scott C. Pedersen[2] and Richard T. Carter[1]
1 Department of Biological Sciences, East Tennessee State University, Johnson City, USA; 2 Department of Biology and Microbiology, North Dakota State University, Brookings, USA

To avoid masking incoming echoes with outgoing calls, bats use a low duty cycle (LDC) or high duty cycle (HDC) echolocation strategy. Generally, LDC echolocators separate the outgoing signal and returning echo temporally, while HDC echolocators separate the outgoing signal and returning echo in the frequency domain. Despite these differences, all echolocators must hear their outgoing call and subsequent echo within a short neural time window. It has been hypothesized that a stylohyal – tympanic bone articulation, which forms a bony connection between the larynx and auditory bullae in laryngeally echolocators, could serve to transfer the initial echolocation signal directly to the ear via bone conduction. We examined the hyoid and hearing apparatus from a variety of HDC and LDC echolocators and found unique stylohyal – tympanic articulations that correlate with echolocation strategy. This suggests that differences in morphology that correlate with echolocation strategy could be due to functional differences. We tested this by constructing 3D digital models from µCT scans of a *Rhinolophus ferremequinum* (HDC) and *Artibeus jamaicensus* (LDC) which were used to run acoustic analyses via finite element modeling. We found that bone conducted sound via the hyoid apparatus in both the LDC and HDC echolocators stimulates the eardrum within the threshold of hearing in both species, and the stylohyal – tympanic bone articulation in *A. jamaicensis* did so more efficiently. Further research will involve testing alternative pathways of bone conducted sound to the cochleae and comparisons between efficacy.

Comparison of Bat Acoustic Data Collected by AudioMoth and Song Meter Detectors in Southeast Alaska

Donald I. Solick[1], Karen M. Blejwas[2], Nicholas D. Solick[1] and Jesika P. Reimer[3]

1 Vesper Bat Detection Services, Fort Collins USA; 2 Alaska Department of Fish and Game, Juneau USA; 3 Department of Wildlife, Fish and Conservation Biology, University of California Davis, Davis USA

Acoustic monitoring has become a popular survey tool for bats. The recently developed AudioMoth detector (Open Acoustic Devices) has generated a lot of interest for large-scale and long-term monitoring of bats due to its small size and low cost (~$100 USD). However, concerns have arisen about the sensitivity of the microphone and recorded call quality compared to commercially available bat detectors. As part of surveys for the North American Bat Monitoring program, we deployed paired AudioMoth and Song Meter SM2BAT+ detectors (~$1000 USD; Wildlife Acoustics) at 22 locations in southeast Alaska. Acoustic files were then classified using Kaleidoscope Pro 5.4.1 software and manually vetted to species or species group. Analysis time was the same for AudioMoth and Song Meter data, though conversion of AudioMoth WAVT to WAV files was time consuming. Over four nights of monitoring, Song Meters recorded nearly five times as many bat files as AudioMoths and nearly seven times fewer noise files. These results suggest that, on average, AudioMoths are less sensitive to bat echolocation and more sensitive to non-bat ambient noise than Song Meters. Species diversity was similar across locations, though Song Meters recorded ~1 additional species per location. It appears the cost savings of AudioMoths may compromise assessments of species diversity for a location. However, the ability to sample more locations with low-cost AudioMoths, especially if the number of survey nights are increased, could compensate for its apparent deficiencies in bat detection.

Development of The Outer Ear in The Big Brown Bat (*Eptesicus fuscus*)

Renata Soljmosi, Carl E. Lyons and Paul A. Faure
Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN

The mammalian head, pinna and tragus filter airborne sounds, giving rise to the binaural acoustical cues for sound localization. In echolocating big brown bats (*Eptesicus fuscus*), the pinna and tragus filter reflections of the bat's vocalizations, allowing them to localize targets. Thus, it is important to understand the anatomical changes of the outer ear during development. Using a cellphone camera, we photographed the left ear of *E. fuscus* pups (n = 9) from postnatal day 1 (P1) to P30, and of adult bats of known age (n=4), to document outer ear development. We measured pinna length, pinna width at mid-length, and tragus length with ImageJ. We also traced the pinna outer margin to measure surface area and compared this to the calculated effective area. The data had high variance due to pups moving their ears and pictures being taken at different angles. Future work should further standardize data collection. Pinna surface area of *E. fuscus* pups increased with age and approached adult values, decelerating exponentially. Calculated effective area slightly, but consistently, underestimated measured pinna surface area in both pups and adults, regardless of pinna size or bat age. Tragus length also increased as a function of age and approached adult *E. fuscus* tragus length, decelerating exponentially. Pinna surface area and tragus length continued to develop while pups were still nursing from their mothers and before they became volant (near P30), suggesting accurate sound localization develops during the transition to powered flight and echolocation.

State Dependence of Arousal from Torpor in Brown Long-eared Bats (*Plecotus auritus*)

Rune Søråas[1], Mari Aas Fjelldal[1], Claus Bech[1], Jeroen van der Kooij[2], Karoline H. Skåra[1,3], Katrine Eldegard[4] and Clare Stawski[1,5]
1 Department of Biology, Norwegian University of Science and Technology, Trondheim, NOR; 2 Nature Education, Research and Consultancy van der Kooij, Slattum, NOR; 3 Centre of Fertility and Health, Norwegian Institute of Public Health, Oslo, NOR; 4 Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, Ås, NOR; 5 School of Science, Technology and Engineering, University of the Sunshine Coast, Queensland, AUS

To cope with periods of low food availability, and unsuitable environmental conditions (e.g., short photoperiod or challenging weather), many heterothermic mammals can readily enter torpor to save energy. However, torpor also entails costs, and quantitative energetics can therefore be influenced by individual state, such as available energy reserves. We studied the thermal energetics of brown long-eared bats (*Plecotus auritus*) in the northern part of their distributional range, including torpor entry, thermoregulatory ability during torpor, and how they responded metabolically to an increasing ambient temperature (Ta) during arousal from torpor. We found that torpor entry occurred later in bats with higher body mass. During exposure to an increasing Ta, all bats increased metabolic rate exponentially, but bats with higher body mass aroused at a lower Ta than those with lower body mass. In bats with low body mass, arousal was postponed to a Ta above the lower critical temperature of the thermoneutral zone. Our results demonstrate that physiological traits, which are often considered fixed, can be more flexible than previously assumed and vary with individual state. Thus, future studies of thermal physiology should to a greater extent take individual state dependent effects into account.

Time-scaled Interisland Demographics of a Caribbean Nectarivorous Bat

J. Angel Soto-Centeno[1,2]
1 Department of Earth and Environmental Sciences, Rutgers University, Newark, USA; 2 Department of Mammalogy, American Museum of Natural History, New York, USA

Dispersal and migration are at the core of biogeographic and ecological community theories. The movement of individuals into or out of a population helps determine its structure, patterns of ecological drift, and community assembly and persistence across time. Because of their ability to fly, bats are considered highly vagile among mammals and are often used as examples of extreme dispersibility holding records of colonization of remote archipelagoes (i.e., Hawaiian Hoary Bat, > 3500 km) and long-distance migration (i.e., Nathusius' Pipistrelle, >2200 km). In archipelagoes like the Caribbean, the ability of bats to overcome oceanic straits among islands is variable and reveal complex patterns of migration or structure even in species typically known to be quite dispersive in the mainland. Stemming from hypotheses of interisland connectivity in Caribbean bats, I assessed genetic data from the Greater Antillean Long-tongued Bat under phylogeographic and coalescent simulation approaches implementing a supervised machine learning framework to examine 1) the divergence and population limits across the entire distribution, and 2) the likelihood that the observed population patterns derive from constant, past, or present migration. Results showed population relationships incongruent to the currently known subdivisions and deep divergences present in most islands following a pattern of west to east colonization. Coalescent simulations supported a model past migration generating the current structure without movement in the present. This time-scaled demographic approach provided a new opportunity to uncover the process ruling complex interisland population connectivity and can aid in refining our understanding of bat community structure in the Caribbean.

Bats and Transportation: A Transportation Perspective

Dale W. Sparks, Virgil Brack, Jr., and Natasha Brown

Environmental Solutions & Innovations, Inc., Cincinnati, Ohio, USA

Most other presentations within this group will focus on the impacts of transportation infrastructure on bats. This has also been a focus of our research efforts over time. However, as consultants working for the transportation industry, we are also provided an opportunity to help biologists understand how bats impact transportation agencies. When bats are found in or adjacent to transportation infrastructure, transportation agencies often default to three interrelated questions: 1) are the bats a health hazard? 2) does this create a regulatory problem for my project? and 3) what can be done to minimize impacts to the bats? Honest, open communication between biologists and transportations professionals is essential for the successful development of transportation projects to minimize harm and maximize benefit to bats. We illustrate a series of projects where the needs of bats and transportation became intertwined and provide suggestions for how lessons learned on these projects can be broadly applied.

Bats, Ectoparasites, and Bacteria: Understanding the Hierarchical System

Kelly A. Speer[1,2] and Alexis M. Brown[3]
1 Center for Conservation Genomics, Smithsonian's National Zoological Park & Conservation Biology Institute, Washington, USA; 2 Department of Invertebrate Zoology, National Museum of Natural History, Washington, USA; 3 Department of Ecology and Evolution, Stony Brook University, Stony Brook, USA

Interactions between hosts and parasites are often viewed solely within the context of the evolution and ecology of these two organisms. However, microorganisms associated with each the host and parasite may mediate these interactions, making the microbiome integral to our understanding of host-parasite associations. In addition, parasites are a powerful but underutilized tool in studying their hosts. Here, we give examples of how a systems approach to bat research that includes parasites and microorganisms can improve inferences about evolution, infectious disease dynamics, and response to environmental change in bats. First, we discuss an example where bat ectoparasites reveal fine-scale patterns in bat dispersal. Parasites, through their reliance on a host, offer independent sources of information about the movement of a host and parasites typically have much more rapid generation times than their hosts. This allows parasites to function as a high-resolution marker of host dispersal. Secondly, we illustrate how bat ectoparasites carry arthropod-vectored pathogens of bats (i.e., *Bartonella*, *Polychromophilus*) and how these dynamics are influenced by habitat loss. Ectoparasites are often blood-feeding arthropods and function as vectors of disease to their host. Lastly, we examine the consequences of habitat loss on bat-ectoparasite-microbiome communities and find that this environmental change has cascading consequences through hierarchical communities. Taken together, these vignettes provide evidence of the value of parasites and microbiomes to bat research. It is our aim to encourage more bat biologists to collect parasite and microbiome data and collaboratively integrate a systems approach into their own research projects.

Fat Bats at the Bug Buffet

Sarah Stankavich, Amanda Adams, Tina Cheng and Winifred Frick
Bat Conservation International, Austin, USA

Previous studies have shown that some colonies of *Myotis lucifugus* are persisting after white-nose syndrome (WNS) infection due in part to increased fat stores. Increasing foraging efficiency of bats in fall and spring could allow bats to accumulate more fat before hibernation and improve recovery from WNS in spring, thereby increasing annual survival and aiding population recovery. In fall 2021, we set up UV-light lures near seven known hibernacula in four states and in spring 2022, we expanded to 17 sites in seven states. We monitored overall bat activity and foraging using acoustics and collected insects to calculate biomass and species richness. Compared to control sites, treatment sites had higher bat activity and higher insect biomass. Managing habitat to support insect prey for bats could be an important conservation priority and a scalable solution to ameliorate the survival of bats in the established area of WNS.

Reflections of Grinnellian and Eltonian Niches on Distribution of Phyllostomid Bats in Atlantic Forest

Richard D. Stevens
Department of Natural Resources Management, Texas Tech University, Lubbock, USA

Ecological niches are complex and result from interactions with both biotic and abiotic components of the environment. One recent distinction is between Grinnellian niche characteristics that reflect influences at large spatial scales such as climate and Eltonian niche characteristics that reflect influences at the local level such as distribution of resources and their allocation among species. I estimated Grinnellian and Eltonian niche characteristics of phyllostomid bats distributed throughout the Atlantic Forest, examined degree of phylogenetic non-independence of distribution and niche characteristics, and estimated relative contributions of niche characteristics to distribution across this large Neotropical region. Phylogenetic signal was weak for Grinnellian and strong for Eltonian niche characteristics. Both suites accounted for significant unique variation in distribution of phyllostomid bats in Atlantic Forest. Grinnellian niche characteristics accounted for more than five times the variation in distribution than Eltonian characteristics. Distinct Grinnellian and Eltonian perspectives on the niche provide valuable insights into the distribution of species. Indeed, diets and environmental tolerances are important constituents of ecological niches and have significant effects on distribution of species. For bats in Atlantic Forest, how species respond to the relatively long environmental gradients experienced there may be more important to distribution than does their responses to spatial variation in dietary resources.

Sickness Behavior and Social Networks in Vampire Bats

Sebastian Stockmaier[1,2], Simon P. Ripperger[1,3] and Gerald G. Carter[1,4]
1 Department of Ecology, Evolution, and Organismal Biology, Ohio State University, Columbus, USA; 2 Department of Integrative Biology, University of Texas at Austin, Austin, USA; 3 Museum für Naturkunde, Leibniz-Institute for Evolution and Biodiversity Science, Berlin, DEU; 4 Smithsonian Tropical Research Institute, Gamboa, PAN

Pathogens can trigger diverse changes in host social behaviors. Sickness behaviors often include lethargy and passive self-isolation (reduced contact between healthy and infected conspecifics). Here, we summarize our work on passive self-isolation in immune-challenged vampire bats, measured on multiple levels from individuals to networks. On an individual level, immune-challenged vampire bats reduce their grooming and social vocalizations towards conspecifics, but the magnitude of this effect depends on kinship between the interacting dyads. Healthy vampire bats do not avoid sharing food with recipients that are immune-challenged, and, so far, we have not observed any evidence of avoidance behaviors in our experiments. At the network level, we used a field experiment with next-generation proximity sensors in Lamanai, Belize, to test how sickness

behavior reduces individual connectedness. Immune-challenged bats associated with fewer bats, spent less time near others, and were less socially connected. Overall, our work illustrates how this passive self-isolation can slow the spread of pathogens and connects mechanistic observations from individuals in captivity to network-wide field observations relevant for models of disease spread.

Extra, Extra, Read all a-bat it! Analysis of Media Coverage of Bats in the United States
Victoria M. Stout
Environmental Studies Department, University of Colorado, Boulder, USA

It is essential to understand how bats are portrayed in the United States news media to effectively conduct outreach about bats. I retrieved 7664 news articles about bats from local and national publications within the United States from 1970–2021 and coded them for topic associations with bats, message framing, emotional valence, and outreach strategies used such as anthropomorphism, storytelling, or ecosystem services. The most frequent article topic (23%) made a link between bats and zoonotic diseases, primarily rabies, closely followed by conservation concern for bats (22%), primarily white-nose syndrome. Specific bat outreach opportunities (14%) and the science of bats (14%) were common topics while less common topics included explicit discussions of the ecosystem services provided by bats (8%), descriptions of bats inhabiting homes or buildings (7%), frustrations about bats delaying construction, logging, or wind farms (7%), and storytelling about individuals or individual bats (3%). Articles featuring positive language towards bats increased over time in stories featuring science, conservation concern, or outreach, but language remained extremely negative in articles about disease risk and bats in homes or buildings. Positive articles towards bats were found more frequently in nationally distributed newspapers, while local newspapers printed stories about "rabid bats" more commonly. Interestingly, nearly all articles that portrayed positive sentiment towards bats began by acknowledging the cultural stigmatization of bats, even in recent years. This suggests that negative attitudes towards bats are still persistent in the United States and are most likely perpetuated through frequent articles featuring sensationalist language connecting bats and rabies.

The Role of Emotions, Beliefs and Trust Among Stakeholders Involved in the Green–green-dilemma in Germany
Tanja M. Straka[1,3], Marcus Fritze[2,3] and Christian C. Voigt[3]
1 Institute of Ecology, Technische Universität Berlin, Berlin, DEU; 2 German Bat Observatory, Berlin, DEU; 3 Evolutionary Ecology, Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU

Green–green dilemmas are challenging. They involve two desirable environmental goals, yet with detrimental counter-effects. This is reflected in the wind energy sector in which the aim is to produce renewable energy for reducing global CO^2 emission but it is conflicting with conservation goals given the detrimental effect on airborne wildlife such as bats. Stakeholders involved in wind turbine projects discuss these conservation issues not only based on their knowledge and interests, but other cognitive and affective drivers can impact these discussions. We undertook as self-administered survey (n = 537 respondents) with six stakeholder groups from the wind energy and conservation sector in Germany to shed light on fundamental reasons for disagreements and lack of compromise. In detail, we assessed their i) beliefs and emotions related to the green-green dilemma, ii) their trust in stakeholders involved in decision making processes and lastly, iii) how beliefs and emotions influence this trust. We observed that beliefs about the importance of wind turbines and emotions towards wind turbines differed across stakeholders while emotions towards bats were generally positive. Overall, stakeholders had low trust in each other. Representatives from the wind energy sector had more trust in decisions made by politicians in this conflict compared to conservationists. Trust was most strongly influenced by beliefs about the importance of wind turbines that were in turn mediated by emotions. We argue that awareness of different beliefs and emotions among stakeholders should be acknowledged in this apparent conflict, particularly to foster collaboration processes that build on trust among stakeholders.

Seasonal and Inter-roost Variations in the Diet of Chrotopterus auritus in Calakmul, Campeche, Mexico
Fernando Gual Suárez, Luis A. Trujillo Sosa and Rodrigo A. Medellín
Laboratorio de Ecología y Conservación de Vertebrados Terrestres, Instituto de Ecología, National Autonomous University of Mexico, Mexico City, MEX

The woolly false vampire bat is a carnivorous bat that inhabits rainforest ecosystems across most of Central and South America, feeding on rodents, birds, and other bats. Most evidence of their diet is incidental. In Calakmul, we monitored three separate roosts of this bat from January 2019 to March 2020, with additional data from July and September 2021, to detect variations in their diet's composition through time and between roosts. All discarded prey remains were collected at each site on three-month intervals and identified through direct comparison to museum specimens from the study region, the use of keys, and expert assessments. To date, we have identified a minimum of 220 individual prey items of 53 species of birds, 226 individuals of 8 species of rodents, 56 individuals of 7 species of bats, 43 individuals of a shrew, 7 individuals of 2 marsupials, and 7 individuals of 2 frogs, as well as 66 individuals of 6 species of butterflies, 21 cockroaches, 64 beetles, 58 orthopterans, 16 cicadas, 4 dragonflies, and a few arachnids and plants. The bats' diets follow a seasonal pattern in response to changes in their prey's abundances and their own dietary needs. During the dry season, migratory birds and endemic rodents are abundant, while booming populations of orthopterans and lepidopterans during the rainy season are closely followed by their appearance in the bats' diets. Differences were observed in the makeup of the diets of bats between the roosts we studied, potentially related to differences in the surrounding matrix.

Hibernation Slows Epigenetic Aging in Big Brown Bats
Isabel R. Sullivan[1], Danielle M. Adams[1,2], Lucas J.S. Greville[3], Paul A. Faure[3] and *Gerald S. Wilkinson[1]
1 Department of Biology, University of Maryland, College Park, USA; 2 Department of Biological Sciences, Towson University, Towson, USA; 3 Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, CAN

Comparative analyses of bats have shown that hibernation is associated with increased longevity among species. However, it is not yet known how hibernation affects biological aging of individuals. Here we use DNA methylation (DNAm) as an epigenetic biomarker of aging to determine the effect of hibernation on the big brown bat, *Eptesicus fuscus*. First, we compare epigenetic age, as predicted by a multi-species epigenetic clock, between hibernating and non-hibernating animals and find that hibernation reduces epigenetic age. Second, we identify genomic sites that exhibit hibernation-associated change in DNAm, independent of age, by comparing samples taken from the same individual in hibernating and active seasons. This paired comparison identified over 3,000 differentially methylated positions (DMPs) in the big brown bat genome. Comparison to epigenomic databases reveals that DMPs with elevated DNAm during winter occur where chromatin states are enriched for transcription repression; DMPs with reduced DNAm during winter occur where chromatin states are enriched for transcription enhancers. Furthermore, genes near DMPs

are involved in regulation of metabolic processes and innate immunity. Finally, significant overlap exists between genes near hibernation DMPs and genes near previously identified longevity DMPs. Taken together, these results are consistent with hibernation influencing aging and increasing longevity in bats.

Evolution of Inner Ear Neuroanatomy of Bats and Implications for Echolocation

R. Benjamin Sulser[1], Bruce D. Patterson[2], Daniel J. Urban[3,4], April I. Neander[5] and Zhe-Xi Luo[5]
1 Richard Gilder Graduate School, American Museum of Natural History, New York, USA; 2 Negaunee Integrative Research Center, Field Museum of Natural History, Chicago, USA; 3 Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, USA; 4 The Sears Lab, Department of Ecology and Evolution, University of California Los Angeles, Los Angeles, USA; 5 Department of Organismal Biology and Anatomy, University Chicago, Chicago, USA

Phylogenomics of bats suggests that their echolocation either evolved separately in the bat suborders Yinpterochiroptera and Yangochiroptera or had a single origin in bat ancestors and was later lost in some yinpterochiropterans. Hearing for echolocation behavior depends on the inner ear, of which the spiral ganglion is an essential structure. For this study, we utilize computed tomography (CT) and histological investigations of the inner ear across 39 species of 19 families of bats. We report the observation of highly derived structures of the spiral ganglion in yangochiropteran bats: a trans-otic ganglion with a wall-less Rosenthal's canal. This neuroanatomical arrangement permits a larger ganglion with more neurons, higher innervation density of neurons and denser clustering of cochlear nerve fascicles. This differs from the plesiomorphic neuroanatomy of Yinpterochiroptera and non-chiropteran mammals. The osteological correlates of these derived ganglion features can now be traced into bat phylogeny, providing direct evidence of how Yangochiroptera differentiated from Yinpterochiroptera in spiral ganglion neuroanatomy. These features are highly variable across major clades and between species of Yangochiroptera and, in morphospace, exhibit much greater disparity in Yangochiroptera than Yinpterochiroptera. These highly variable ganglion features may be a neuroanatomical evolutionary driver for diverse echolocating strategies and are associated with the explosive diversification of yangochiropterans, which include most bat families, genera, and species.

Re-Envisioning Bat Wings as Multifunctional Propulsive, Sensory, and Thermoregulatory Structures

Sharon M Swartz[1,2]
1 Department of Ecology, Evolution, and Organismal Biology, Brown University, Providence, USA; 2 School of Engineering, Brown University, Providence, USA

The wings of bats are extraordinary structures that support a landmark trait of the Chiroptera: powered, flapping flight. Accordingly, much research has been devoted to uncovering specializations of the bat forelimb that enable flight capabilities, particularly generating aerodynamic forces. Less attention has focused on other ways that wings contribute performance and fitness. More integrative, synthetic appreciation of wing structure and function could enhance understanding of the origin and diversification of bat flight. I discuss three factors could potentially contribute to a more holistic appreciation of bat wings as key innovations. First, the capacity of bat wings to robustly reject substantial perturbations and to enact some low-speed maneuvers depends on their function as inertial appendages, distinct from their aerodynamics. Second, along with the typical sensory apparatus of the mammalian musculoskeletal system, bat wings possess a highly developed and remarkable sensory hair network, which together provide bats with an exceptional degree of sensorimotor integration. Third, wing surfaces are large, poorly insulated, well-vascularized appendages, cooler than core body temperature flight. High levels of performance in cold muscles requires adaptations at the tissue, cell, and/or molecular levels. The traits that improve inertial dynamics differ from those that heighten aerodynamic performance; architecture of sensory hair networks and their function and intraspecific variation have barely been quantified; and wing muscle physiological specializations are only beginning to be explored. Research programs that integrate these factors will improve our ability to uncover how bats came to possess the impressive, diverse flight abilities that we see today.

Longer Call Durations Increase Correct Classification of *Myotis sodalis* and *M. lucifugus*

Joseph M. Szewczak
Department of Biological Sciences, Cal Poly Humboldt, Arcata, USA

The congener species *Myotis sodalis* and *M. lucifugus* present ambiguous acoustic characteristics across their respective call repertoires. I used a set of 10,053 species-known distortion-free call samples recorded from tracked individuals in twelve states across their range to assess the effect of call duration on correct classification using SonoBat full spectrum-based call classification. The percentage of calls correctly classified increased as call duration increased. *M. sodalis* was correctly classified 0.0, 62.4, 87.6, 89.6, 94.8, and 100 % for call durations of <3, 3–4, 4–5, 5–6, 6–7, and >7 milliseconds, respectively. M. lucifugus was correctly classified 0.0, 79.4, 86.6, 89.0, 94.7, and 97.8 % for call durations of <3, 3–4, 4–5, 5–6, 6–7, and >7 milliseconds, respectively. The ambiguity inherent in shorter duration calls suggests that efforts to identify these species correctly should focus on recorded sequences having longer duration calls and exclude shorter duration call samples (e.g., <4 milliseconds). Some typical recording situations such as bats taking flight from hand-release or during roost emergence often make short duration calls that will likely result in spurious identifications. In addition, automated classification systems should not rely on reference libraries of predominantly short duration calls and should have a robust sampling of longer duration call types to properly represent these species' call repertoires for building reliable acoustic identification systems.

Global Medicinal Use of Bats: A sSystematic Literature and Social Media Review

Elaine S. Tackett, Tigga Kingston, Narges Sadeghmoghaddam and Abigail L. Rutrough
Department of Biological Science, Texas Tech University, Lubbock, USA

The hunting of bats for food and medicine is one of the greatest threats to bat conservation. While hunting for consumption is the focus of increased attention, the specific medicinal uses of bats are poorly documented, limiting mitigation efforts. Here, we determine the distribution of bat hunting for food and medicinal use and characterize medicinal use practices. We systematically surveyed English-language scientific literature and social media platforms utilizing keywords and hashtags in 27 languages. We found 198 papers and 1063 social media posts from 83 countries and territories. Although use for food was more common, with 1284 unique reports from 71 countries, bats were used to treat 42 ailments of 11 human body systems across 37 countries (453 reports). Asthma was the most common ailment, distantly followed by kidney conditions. Ten organs or body parts of bats were used medicinally, with bat meat (flesh) and fluids (blood, bile, and oil) the most common. Understanding the effects and

drivers of specific bat hunting practices will help guide conservation and public health efforts in the communities where bats are hunted. By pinpointing the ailments bats are being used for, outreach and alternative treatments can be introduced to replace the use of bats.

Transcriptomic Responses to Coronavirus Infections in African and North American Bats

Sara Talmage[1], Ken Field[1], Mingzixu Gao[1], Isabel Steinberg[1], Go Ogata[1], Ethan Field[2], Brent Sewall[3], Greg Turner[4], Jordan Simpson[1], Imran Ejotre[5], Laura Kurchez[1], Cali Wilson[6], Anguyo Dennis Foe[6], Juliane Schaer[5] and DeeAnn Reeder[1]

1 Biology Department, Bucknell University, Lewisburg, USA; 2 Materials Science and Engineering, University of California, Davis, USA; 3 Biology Department, Temple University, Philadelphia, USA; 4 Pennsylvania Game Commission, Harrisburg, USA; 5 Biology Department, Humboldt University, Berlin, DEU; 6 Odum School of Ecology, University of Georgia, Athens, USA; 7 Immunology and Molecular Biology Department, Makerere University, Kampala, UGA

Bats are the likely ancestral hosts of nearly all coronavirus lineages but, like most reservoir hosts, do not appear to experience significant illness. Using archived gastrointestinal (GI) tissue samples from two different species of bats, one from North America (*Myotis lucifugus*) and one from Africa (*Epomophorus labiatus*), we have characterized the presence of coronaviruses using viromic and PCR-based approaches. To determine how these hosts do (or do not) respond to infection, we are examining the whole-transcriptome changes in host gene expression that accompany coronavirus infection in the GI tract. RNA was isolated from the GI tracts of 26 North American bats and 150 African fruit bats and RNASeq was performed to a read depth of 4080 million read pairs per sample. Coronaviruses were detected either by using Kraken2 or STAR to map reads to viral transcripts or by PCR using nested degenerate primers for coronaviruses. The levels of alpha-coronavirus BtCoV-CDPHE15 detected in the *M. lucifugus* RNASeq reads correlated with their white-nose syndrome status, as expected, and was significantly higher in juveniles than adults. However, no coronaviruses were detected in the RNASeq reads from 150 *E. labiatus* GI samples using this viromic approach. Using consensus PCR, we have identified 10 of these same African fruit bats as positive for coronaviruses in RNA isolated from blood or fecal swabs. We will next look for changes in host gene expression that correlate with infection.

Harnessing Local Capacity to Uncover and Protect Hidden Afrotropical Bat Diversity

Iroro Tanshi

Department of Animal and Environmental Biology, University of Benin, Benin City, NGA; Department of Biology, University of Washington, Seattle, USA; Small Mammal Conservation Organization, Benin City, NGA; Department of Biological Sciences, Texas Tech University, Lubbock, USA

Gaps in local capacity impede study of Afrotropical bats, and limited historical data promote the view of a depauperate African fauna relative to Southeast Asia. Notwithstanding, a recent investigation of multiple dimensions of bat diversity established a species-rich site in Nigeria along a continuum of sites in Indonesia and Malaysia, highlighting the value of hotspots. Hotspots of Afrotropical bat diversity are mountainous, and the largest hyper-diverse area occurs between southeastern Nigeria-southwestern Cameroon. Bat species richness patterns along elevational gradients in the Nigeria-Cameroon transboundary area are poorly understood. To investigate drivers of species richness along elevational gradients, bats were surveyed in hitherto unsampled protected areas in southeastern Nigeria using complementary techniques (harp traps and mist nets); insects trapped using light traps; vegetation assessed in 2 x 2 m plots; and climatic variables acquired from Bioclim. Bat species richness was modeled against vegetation structure, climate, and insect abundance. Temperature was the main predictor of species richness – fewer bats in cold highland areas. This survey and the decade-plus Bats of Nigeria project prioritized local capacity strengthening, discovering 12 (eight caught exclusively in harp traps) new country records including *Hipposideros curtus*, a rare range-restricted Endangered species – now the focus of a community-based conservation program to protect forest and cave habitat from wildfires and disturbance. Clearly, uncovering hidden Afrotropical diversity relies on local capacity and deployment of complementary sampling techniques in under-sampled areas, driving intensive field-based programs. To scale-up local capacity for regional research and conservation, a training program for West African students was launched.

Bat Diversity Discontinuities Across Amazonian Biogeographic Provinces and Subregions

Valeria da C. Tavares[1,2], Leonardo C. Trevelin[1], William D. Carvalho[3,4] and Paulo E. D. Bobrowiec[5]

1 Biodiversity and Ecosystem Services Group, Instituto Tecnológico Vale, Belém, BRA; 2 Departament of Systematics and Ecology, Universidade Federal da Paraíba, João Pessoa, BRA; 3 Programa de Pós-Graduação em Biodiversidade e Meio Ambiente, Universidade Federal da Grande Dourados, Dourados, BRA; 4 Programa de Pós-Graduação em Biodiversidade Tropical, Universidade Federal do Amapá, Macapá, BRA; 5 Programa de Pós-Graduação em Ecologia, Instituto Nacional de Pesquisas da Amazônia, Manaus, BRA

Bats are taxonomically and functionally diverse in the Neotropics and worldwide, and particularly megadiverse in the Amazon, where their radiation is still poorly understood. We systematically reviewed bibliographic databases, summarized and analyzed information to understand the state-of-art of the general knowledge about Amazonian bats, and tested for distributional patterns building a matrix of bat occurrences along the biome. For the review we used literature databases such as Scopus and the Web of Science and followed a Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA). We grouped our compiled and matrix of Amazonian bat records by Endemism areas and tested for species composition variation considering different biogeographic scenarios using non-metric, multidimensional scaling ordinations based on Jaccard and modified Raup-Crick dissimilarity indices and performing permutational analyzes of variance. We retrieved approximately 200 studies, organizing data in the categories Diversity, Distribution, Taxonomy, Communities, Bioacustics, Diet and reproduction, Predation, Parasites, Zoonosis, Impacts. For the dissimilarity testing we used 3771 records from 104 localities. Compositional patterns were dissimilar considering the Guiana shield, Western and Eastern Amazon faunal division (Jaccard Permanova: $F = 2.73$, $df = 2$, $p = 0.001$; Raup-Crick Permanova: $F = 15.22$, $df = 2$, $p = 0.001$) discarding other Biogeographic provinces and grouping hypotheses. Research about Amazonian bats had substantially increased on several disciplines over the last decade, but the concentration and refinement of studies is still largely heterogeneous. We delimitate key questions in need of further research and critical information that is lacking to enhance the chances for their conservation.

Live forever? Genomes Reveal Bats' Abilities to Fight Disease and Ageing

Emma Teeling

School of Biology and Environmental Science, University College Dublin, Dublin, IRL

Of all mammals, bat possess the most unique and peculiar adaptations that render them as excellent models to investigate the mechanisms of extended longevity and potentially halted senescence. Indeed, they are the longest-lived mammals relative to their body size, with the oldest bat

caught being >41 years old, living approximately 810 times longer than expected. Bats also appear to have resistance to many viral diseases suggesting that their innate immunity is different to other mammals, perhaps playing a role in their unexpected longevity. Here the potential genomic basis for their rare immunity and exceptional longevity is explored across multiple bat genomes and divergent ageing and immune related markers (e.g., microbiome, telomeres, mitochondria, cellular dynamics, cytokine response) studied in wild bat populations of both the longest lived and shortest-lived genera of bats. Further, the next steps required to validate these field based and genomic based predictions are explored. These findings provide a deeper understanding of the causal mechanisms of ageing and tolerant immunity, potentially uncovering the key molecular pathways that could be utilized to benefit society.

Characterization of Indonesian *Pteropus alecto* Immunoglobulin Genes

Thongthai Thavornwatanayong[1], Sigit Wiantoro[2], Susan Tsang[3,4] and Bao Q. Vuong[1]
1 Department of Biology, The City College of New York and The Graduate Center, The City University of New York, New York, USA; 2 Museum Zoologicum Bogoriense, Research Center for Biology, Indonesian Institute of Science, Cibinong, IDN; 3 Department of Mammalogy, American Museum of Natural History, New York, USA; 4 Zoology Division, National Museum of Natural History, Manila, PHL

Bats are natural reservoirs for emerging and spillover viruses. Phylogenetic comparisons show that the closest known relative to SARS-CoV2 is a coronavirus isolated from a horseshoe bat. Similarly, paramyxoviruses (Hendra and Nipah viruses) have been isolated from Pteropus flying foxes; however, the bats show no symptoms of disease. The immunological mechanisms that permit viral persistence in bats remain largely uncharacterized. In particular, bat immunoglobulin (Ig) germline and coding sequences are poorly described. In this study, the constant regions of IgM and IgA genomic DNA and IgG RNA of Indonesian *Pteropus alecto alecto* were amplified, sequenced, and compared to the Australian *Pteropus alecto gouldi* IgM, IgA, and IgG mRNA sequences. *P. a. alecto* IgM showed (E541D), IgA (M428V), IgG (S 377D and S391P) as compared to *P. a. gouldi*. We speculate that the amino acid differences in IgG may contribute to structural changes in the Ig constant region or altered Ig affinity for Fc receptors, which could affect Ig function during pathogenic infections. Given the absence of admixture between these geographically separated Pteropus subspecies, these data suggest environmental selection for unique IgG constant coding sequence. Further characterization of *P. a. alecto* Ig coding sequences will expand our knowledge of bat Ig structure and function, which could be used to generate therapeutic Ig for spillover viral infections.

Can Insectivorous Bats Be Used as an Indicator for Monitoring Urban Bushland Restoration?

Kristen Thompson, Stuart Parsons and Susan Fuller
School of Biology and Environmental Science, Queensland University of Technology, Brisbane, AUS

Urban bushland patches are becoming increasingly fragmented due to land clearing and environmental degradation. In Brisbane, Australia, community volunteer groups are actively restoring vegetation through methods such as weeding and planting. The success of this restoration is measured using vegetation condition surveys, however these methods are time and resource intensive with little information on faunal restoration outcomes. A solution to this problem may lie in monitoring faunal indicators such as insectivorous bats as they rely on vegetation structural, functional, and compositional attributes for foraging and roosting. In the current study, SM3Bat detectors were deployed at 20 sites within the Brisbane region in paired remnant and restored habitats. Calls were manually identified and bat species compositional, functional groups and activity were investigated. A total of 21,027 bat passes were recorded with 7447 (35.42%) identified to 13 species. Overall, there were no significant differences in species, functional group composition, or activity between remnant and restored habitats. Insectivorous bat assemblages in urban restoration are diverse and often more active than in urban remnants, indicating that local site differences had an important effect. There was no relationship between bat activity and vegetation condition score or the activity of different functional groups and landscape attributes. However, there was a strong positive relationship between clutter-dependent bats and high cover of forbs and native shrubs, large trees and low weed cover. We conclude that this functional group of insectivorous bats can be used as an indicator for monitoring urban bushland restoration.

Importance of Mangroves for Bat Research and Conservation with Notes on Echolocation of *Myotis hasselti*

Vu Dinh Thong[1,2], Annette Denzinger[3] and Hans-Ulrich Schnitzler[3]
1 Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, VNM; 2 Graduate University of Science and Technology, Vietnam Academy of Science and Technology, Hanoi, VNM; 3 Animal Physiology, Institute for Neurobiology, Faculty of Science, University of Tübingen, Tübingen, DEU

Mangrove ecosystems play important ecological roles, including the mitigation of global climate change and biodiversity conservation. However, they have received little attention from scientists for the research and conservation of bats and general biodiversity. In Vietnam, bat species inhabiting mangroves have been relatively unstudied, while these ecosystems are located along the country's coastal zones and have declined dramatically due to the development of agriculture, wind energy and other threats. To initially fill this gap, we conducted a series of bat surveys in mangrove areas of northern and southern regions of Vietnam. Bats were captured using mist nets, mobile nets and hand nets. Their echolocation calls were recorded and analyzed using the PCTape system and Selena software, respectively. Five species were captured and recorded: *Cynopterus brachyotis*, *Macroglossus minimus*, *Myotis hasselti*, *Myotis pilosus* and *Taphozous melanopogon*. Four species (*C. brachyotis*, *M. minimus*, *M. hasselti* and *M. pilosus*) have been rarely documented from other ecosystems in Vietnam but have commonly been recorded and captured in mangrove areas. Of these species, *M. pilosus* is a globally "Vulnerable" species. While searching for prey, *Myotis hasselti* emitted high energy echolocation calls sweeping from about 96 to about 24 kHz with a signal duration of about 5 ms. This species sometimes uses social calls of a horseshoe-shaped structure, which last about 15 ms and are emitted about 26 ms in front of a search call. Results from our surveys indicated the importance and potential of mangroves for bat research and conservation.

Bats Roosting in Dead Norway Spruce Trees as a Result of the Bark Beetle Outbreak

Katarzyna Thor[1], Grzegorz Apoznański[2], Aneta Zapart[3], Mirosław Więcek[4] and Alek Rachwald[5]
1 Department of Animal Genetics and Conservation, Warsaw University of Life Sciences, Warszawa, POL; 2 Department of Vertebrate Ecology and Paleontology, Wrocław University of Environmental and Life Sciences, Wrocław, POL; 3 BUFOR, Dębica, POL; 4 NIETOPEREK, Gdynia, POL; 5 Forest Ecology Department, Forest Research Institute, Sękocin Stary, POL

Białowieża Primeval Forest (about 1,700 km^2, located in Poland and Belarus), covered with old mixed stands of mostly natural origin, is an important forest area in Europe from the point of view of protection of natural diversity. Norway spruce is a tree species which covers approx. 27%

of its area. Between 2012−2017 a large outbreak of the bark beetle *Ips typographus* took place in the forest, which left many dead standing trees. As a result of the research conducted using the radiotelemetry method in Białowieża Forest in 2020, we found that the Western barbastelle bat, *Barbastella barbastellus,* chooses nursery roosts in dead Norway spruce trees, colonizing a newly available source of shelters. Based on this, we found that the Western barbastelle has a preference for a type of roost rather than a tree species. Bark beetle outbreaks can cause a phenomenon that ultimately affects the vertebrate population, which makes the bark beetle a keystone species for a given habitat. Insect outbreaks in forests of primary, natural or semi-natural origin are one of the natural factors that shape the habitat. Removal of dead standing trees ("salvage logging") disrupts these processes, and in this particular case, also poses a direct threat to the protected bat species.

Values, Hunting and Management of Flying Foxes in New-Caledonia: Contribution of Social Science to Better Regulation

Laure Tindao[1], Lorena Bur[1], Kayel Meandu[1], Jonas Brouillon[1], *Malik Oedin[2,3], Catherine Sabinot[4], Fabrice Brescia[2], Séverine Bouard[1]
1 Institut Agronomique néo-Calédonien, Equipe équipe Territoires, Acteurs et Usage, Centre de Recherches Nord Thierry Mennesson, Pouembout, NCL; 2 Institut Agronomique néo-Calédonien, Equipe Agriculture Biodiversité et valorisation, Païta, NCL; 3 Direction du Développement Economique et de l'Environnement, Province Nord, Hôtel de la province Nord, Koné, NCL; 4 UMR ART-DEV, IRD, Université de Montpellier, Université des Antilles, Université de Guyane, Université de la Réunion, Centre IRD de Nouméa, Nouméa Cedex, NCL

In the northern province of New-Caledonia, management on the hunting of flying foxes (*Pteropus* species) is being revised. Since 2021, a social science study has been conducted to improve the understanding of the place of flying foxes in the symbolic and cultural apparatus of the province's inhabitants, indigenous or non-indigenous people. What are the associated values? What are the hunting practices, the norms and rules associated with their local management? To explore practices in a comprehensive way, we choose a qualitative approach based on more than 150 semi-structured interviews and ethnographic observations. Results show that flying foxes have a strong symbolic value; it refers to custom, totems, ancestors, but also to family meals, sharing, childhood memories, and the intergenerational transmission of hunting practices, all of which are part of a certain way of living the territories. Some informal hunting regulation systems are emerging locally, but it seems difficult to maintain them in the long run. If the official regulation system is relatively well known, it does not seem to be adapted to hunting and consumption practices. At the heart of cultural practices and coupled with biological and ecological issues, flying fox hunting sometimes generates conflicts: inserted in a complex system of values, places and practices, flying fox management and protection represent a real challenge. Taking into account this diversity is all the more important as the operational aim of this study is to contribute to a process of concertation to adapt the official regulation system and improve the preservation of these species.

A Taxonomic Review of Equatorial Guinea Bat Species to Base an Urgent Bat Conservation Policy

Laura Torrent[1,2,3], Diogo F. Ferreira[2,3], Joxerra Aihartza[4], Inazio Garin[4], Esther Abeme Nguema Alene[5], Luke L. Powell[2,3] and Javier Juste[6,7]
1 Biodiversity and Bioindicators Research Group, Natural Sciences Museum of Granollers, Granollers, ESP; 2 Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, PRT; 3 Biodiversity Initiative, Houghton, USA; 4 University of the Basque Country, Leioa, ESP; 5 National Institute for Forest Development and Management of the Protected Areas, Bata, GNQ; 6 Department of Evolutionary Ecology, Estación Biológica de Doñana, Sevilla, ESP; 7 Epidemiology and Public Health, CIBERESP, Madrid, ESP

Equatorial Guinea (EG), Central Africa, is one of Africa's most important hotspots of bat diversity. However, the most recent bat research published dates from the 1990s and focused only on insular species. The continental region has received no attention in scientific publications since the 1970s, which described 22 species. Furthermore, EG bats are already threatened by habitat loss. Thus, we have undertaken three expeditions since 2018 to survey the bat fauna. Furthermore, we reviewed an extensive museum collection from the region, compiled before the twenty-first century and stored at Doñana Biological Station (EBD-CSIC) in Spain. We combined traditional taxonomy, based on morphological characters, with molecular analysis to provide the updated checklist of bat species from the continental region of EG. During fieldwork we mostly used ground and canopy mist-nets to capture the bats. From each individual we collected external measurements as well as wing biopsy samples, guano and echolocation recordings. For the identification of museum specimens, we measured 15 external and 16 craniodental traits and extracted the bacula. From the biopsies, we extracted and amplified the mitochondrial gene Cytb, and the sequences were compared with homologous sequences available in GenBank. In total, we have confirmed so far the presence of 54 bat species in the region. Out of them, 31 are new records for the country. By improving the knowledge of bats species and their distribution in EG, we can lay the foundations for local authorities to direct their efforts toward protecting its fauna and reinforcing forest conservation.

Night Activity and Out of the Roost Social Interactions of the Woolly False Vampire Bat

Luis A. Trujillo, Fernando Gual-Súarez and Rodrigo A. Medellín
Laboratorio de Ecología y Conservación de Vertebrados Terrestres, Instituto de Ecología, Universidad Nacional Autónoma de México, Mexico City, MEX

The woolly false vampire bat (*Chrotopterus auritus*) is a carnivorous species that highly depends on forest remnants to survive. In this context, studying the movement ecology of this species is vital to understand habitat requirements or the response to habitat loss and fragmentation. As well, it is also relevant to provide context to these movements by recording interactions between individuals. Using miniature GPS devices, we monitored the nightly activity patterns and outside of the roost social interactions of *C. auritus* in southern Mexico. We obtained 180 activity nights from 15 bats of three different social groups. Individuals averaged 5 h outside the roost, a traveled distance of 12.14 km and a home range of 238.3 ha. Time spent outside of the roost was dedicated mainly to foraging activities. Most nights individuals remained on their own but for some occasions we report infrequent encounters between pairs of group members. The minimum distance reported in a dynamic interaction was 3 m between an adult female and a sub-adult male. For static interactions, we observed an overlap between home ranges from 0 to 100% depending on the pair of individuals. Additionally, we found that *C. auritus* performs movement patterns which avoid agricultural fields and other modified patches, carrying out more than 97% of their night activities in forest remnants. In southern Mexico, it seems that the woolly false vampire bat endures habitat modifications but relies on well-preserved semi-deciduous forest and secondary forest remnants to move throughout the landscape.

Bats and Rice: Assessing the Role of Bats as Insect Pest Suppressors in Rice Paddies

Carme Tuneu-Corral[1,2,3], Xavier Puig-Montserrat[1], Vanessa Mata[2], Mar Cabeza[3], Hugo Rebelo[2] and Adrià López-Baucells[1]
1 Biodiversity and Bioindicators Research Group, Natural Sciences Museum of Granollers, Granollers, ESP; 2 Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, PRT; 3 Global Change and Conservation Lab, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, FIN

Bats are important insect consumers and their role as natural pest controllers in agriculture has been increasingly studied. Rice is the main staple food of more than half of the world's population, playing an essential role in food security and economic growth, especially in developing countries. One of the major pests affecting this crop is the rice borer moth (*Chilo suppressalis*), a widespread species found in Australasia, Asia, and southern Europe. In this study, we assessed the ecosystem services provided by bats consuming the rice borer moth by using experimental exclosures combined with diet analyses in rice fields of Spain. We also evaluated whether the presence of bat ultrasounds altered the behaviour of this insect when mating and laying eggs in captivity. *Chilo suppressalis* is a tympanate moth, and we hypothesized it could be able to detect bat ultrasounds altering their normal reproductive behavior. The damage levels caused by *C. supressalis* in rice plants were >90% greater in areas where bats were excluded. We also observed that *C. suppressalis* females kept in captivity laid lower numbers of eggs (in average, 50% fewer) per laying in presence of ultrasounds. Our results quantify for the first time the potential of bats as pest suppressors in one of the most important crops for food security worldwide and evidence their benefits for rural communities. Further, our findings also suggest that bats may be protecting rice plantations with their mere presence by just emitting hunting ultrasound sequences during the summer nights.

Investigating the Vulnerability of Southern Hemisphere Bats to White-nose Syndrome

Christopher Turbill[1], Fritz Geiser[2], Jasmin Hufschmid[3], Lindy F. Lumsden[4], John M. Martin[5], Craig K.R. Willis[6], Nicholas C. Wu[1] and Justin A. Welbergen[1]

1 Hawkesbury Institute for the Environment, Western Sydney University, Richmond, AUS; 2 School of Environmental and Rural Science, University of New England, Armidale, AUS; 3 Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, AUS; 4 Department of Environment, Land, Water and Planning, Arthur Rylah Institute for Environmental Research, Heidelberg, AUS; 5 Taronga Institute of Science and Learning, Taronga Conservation Society Australia, Mosman, AUS; 6 Department of Biology, University of Winnipeg, CAN

The devastating impact of white-nose syndrome (WNS) in North America demonstrates the risk posed to naïve bat populations encountering *Pseudogymnoascus destructans* (*Pd*) as a novel pathogen. It is likely that *Pd* will be accidentally transferred to caves in Australia and elsewhere in the Southern Hemisphere, and there is an urgent need to assess the vulnerability of bats on southern continents to a WNS epidemic. This task is challenging, however, because of uncertainties about the potential for exposure to *Pd* and the sensitivity of these bat faunas to mortality from WNS. Our initial work provides evidence that the risk of WNS to Southern Hemisphere bats should be taken seriously. In Australia, favourable cave roost conditions for *Pd* growth exist across 30 to 100% of the ranges of eight bat species. Phylogenetic distance has little effect on the probability of *Pd* infection, suggesting Australian bats, like their North American counterparts, could also be sensitive to WNS. However, although winter torpor use has been studied in tree-roosting Australian bats, data on torpor-arousal patterns for cave-roosting species are very limited, hampering attempts to predict their sensitivity. In a Southern Hemisphere first, we have commenced a multi-institutional research program to collect missing data on cave roost conditions, hibernation patterns and overwinter energy budgets needed to build quantitative spatial models of vulnerability for Australian bats. We welcome input from the experience and substantial knowledge gained from North American studies to help us meet these objectives and better understand the risk of WNS to bats Down Under.

Cooling of Bat Hibernacula to Mitigate White-nose Syndrome

Gregory G. Turner[1], Brent J. Sewall[2], Michael R. Scafini[1], Thomas M. Lilley[3], Daniel Bitz[4] and *Joseph S. Johnson[5]

1 Pennsylvania Game Commission, Harrisburg, USA; 2 Department of Biology, Temple University, Philadelphia, USA; 3 Finnish Museum of Natural History, University of Helsinki, Helsinki, FIN; 4 CNX Gas Company LLC, Canonsburg, USA; 5 Department of Biological Sciences, Ohio University, Athens, USA

White-nose syndrome (WNS) is a fungal disease that has caused precipitous declines in several North American bat species, creating an urgent need for conservation. We sought to determine how microclimates and other characteristics of hibernacula have affected bat populations following WNS-associated declines. We also evaluated whether cooling of warm, little-used hibernacula could benefit bats. We found that winter counts of *Myotis lucifugus* were higher and increased over time in hibernacula with mid-winter temperatures of 3–6 °C. Counts of *Eptesicus fuscus*, *M. leibii*, and *M. septentrionalis* were likewise higher in colder hibernacula. Populations of *M. lucifugus* and *M. septentrionalis* increased most over time where there were more nearby sites, while *E. fuscus* counts remained high where they had been high before WNS onset. Winter counts were also higher in *M. leibii* in hibernacula with higher vapor pressure deficit (VPD) (particularly where >~0.1 kPa), and we found some evidence that *M. lucifugus* increased and *E. fuscus* counts were higher with higher VPD. In contrast, *Perimyotis subflavus* counts increased over time in warmer hibernacula and were unaffected by VPD. Within manipulated hibernacula, counts of *M. lucifugus* and *P. subflavus* increased with time since manipulation. Further, there were more *E. fuscus* where cooling was greatest, with some evidence for more P. subflavus in hibernacula sections that remained warm after manipulation. These data show bats are responding effectively to WNS through habitat selection and suggest that cooling warm sites receiving little use by bats is a viable strategy for combating WNS.

Bat Conservation Then and Now

Merlin D. Tuttle[1,2]

1 Merlin Tuttle's Bat Conservation; 2 Department of Integrative Biology, University of Texas, Austin, USA

At the time of NASBR's founding in the 1970s, media headlines were filled with disease exaggerations that were lucrative in gaining media readership, pest control business, and public health funding. By 1971, researchers at an American Association of Science meeting concluded that bats were in alarming decline and required immediate help. However, progress only became possible after bat biologists documented extreme human health risks from poisoning bats and put fear in perspective. In the 1980s and 90s, we made outstanding progress. Bats were documented to be safe neighbors. And those in Austin, Texas became an internationally famous tourist attraction. However, with the SARS outbreak of 2002, disease speculation again became a tempting source of funding. Unfortunately, this has led to a resurgence of public intolerance and killing. It's time to seriously question strategies for the future. How long can researchers afford to prioritize studies that result in self-fulfilling prophecies of bats carrying more diseases than other animals? Should we still be focused on stopping the spread or finding a cure for white-nose syndrome? Can restrictions on bat biologists solve WNS problems or prevent transmission of SARS-CoV-2 to bats? Finally, should restrictions that severely limit research on bat values, needs, and status trends be continued? Fifty years ago, when we founded NASBR, researchers were already alarmed by the precipitous decline of bats. Are decades of progress now at risk?

Long Term Capture Surveys in Southeastern Arizona Show Declining Numbers of Bats: Should we be Concerned?

Janet D. Tyburec[1] and Tim K. Snow[2]

1 Bat Survey Solutions, LLC, Tucson, USA; 2 Arizona Game and Fish Department, Tucson, USA

Since 1992, the authors have performed annual bat surveys in Cave Creek Canyon, Arizona. We noted concerning declines in captures of many species at this site, including *Pipistrellus* (now designated as *Parastrellus*) *hesperus*. This species was captured at an average rate of over six individuals per net-night in the early 1990s then declined to less than one individual per net-night throughout 2010s. We postulate that: (1) the local population has declined significantly; or (2) we are "teaching" resident bats capture methods, and the population now consists of fewer naïve individuals; or (3) populations for this species exhibit generational variability that can only be determined by exceptionally long-term monitoring. Because *P. hesperus* is one of the louder and easier to identify bats, analysis of acoustic data from the previous decade allows us to equate bat activity with population status. Since 2012, we performed simultaneous acoustic monitoring at capture sites. If bats are declining, we expect a decline in the number of recorded bat-passes from P. hesperus. But, if bats are merely learning to avoid capture, we expect no commensurate decline. From 2012−2020, bat activity was variable, with between zero and 20 bat-passes recorded from *P. hesperus* per-hour at capture sites where just zero to one individual was caught. However, analysis of data from 2021 and 2022 show between 20−30 bat-passes per-hour from *P. hesperus* in the acoustic data and capture rates increased to nearly five bats per net-night. Therefore, our data support that local populations of *P. hesperus* fluctuate at longer timescales.

Using Acoustics and Imaging to Assess Bat Behavior and Activity at Towers: Implications for Wind Energy

Robert Tyler[1], Sara Weaver[2], Brogan Morton[3], Nevin Durish4 and Sarah Fritts[1]
1 Texas State University, San Marcos, USA; 2 Bowman Consulting, San Marcos, USA; 3 Wildlife Imaging Systems LLC, Hinesburg, USA; 4 ESE Partners, Austin, USA

Wind energy production has dramatically increased but not without unintended environmental impacts, such as high bat mortality rates. Current pre-construction mitigation strategies acoustically monitor bat activity at planned wind energy facilities to predict mortality and improve siting. However, there is high variation between pre-construction models and post-construction fatalities, which could suggest either attraction of bats to wind turbines or high variability in acoustic monitoring methods. Thus, we supplemented acoustics with thermal cameras to monitor bats at three sites being surveyed for wind energy development at meteorological evaluation towers (MET) within the South Texas Plains. Using AXIS Q1942-E cameras, we recorded nightly bat activity in parallel with Song Meter 4 BAT-FS detectors. We used Kaleidoscope Pro 5 to identify bats in acoustic recordings and machine learning in Python 3.8.5 to distinguish bats from other thermal sources in thermal recordings. We analyzed detection counts produced from both methods using a linear-mixed effect model with a negative binomial distribution. We used atmospheric conditions as covariates and MET as random effects. Results suggest bat detections are greater overall with thermal cameras; however, each method has greater detections under various environmental conditions. Additionally, we observed behavioral patterns including changes in focal flight activity during consecutive nights and when more than one bat was in a frame that may suggest olfactory interactions with the MET, suggesting new hypotheses explaining bat attraction to wind turbines. We recommend implementing thermal imaging into future acoustic surveys to further examine bat activity and behavior in different ecosystems.

Novel Methods for Modeling Bat Abundance from Mobile Transect Data at Landscape Scales

Bradley J. Udell, Bethany R. Straw and Brian E. Reichert
U.S. Geological Survey, Fort Collins Science Center, Fort Collins, USA

Collaborative acoustic monitoring over broad scales offers a cost effective, efficient means of informing bat conservation. However, observation biases such as detectability, misclassification, animal movement (temporary emigration), and double counting present major challenges for inferring abundance and trends over time. Acoustic monitoring via mobile transects were specifically designed to eliminate the issue of double counting and provide an index of relative abundance. However, analyses of raw indexes do not account for observation biases, and inferences have been largely confined to the populations that occur along transects. The North American Bat Program (NABat) is a partner driver, multi-agency, international monitoring program that employs a spatially balanced sampling approach across North America (100 km2 grid cells, with subsampling within each) that supports inference across entire regions of interest. Recent advancements in abundance estimators allow for modeling abundance from acoustic monitoring data (auto IDs, and a subset of manually reviewed records) while accounting for both detectability/activity rates and misclassification rates. We extended these methods for modeling bat abundance from NABat mobile transect data by including an availability process of each transect within grid cell (given the transect length), and by accounting for heterogeneity in observation parameters. We investigated the use of these methods for mobile acoustic monitoring by applying these models to data in the NABat database. We found that these methods can reliably estimate trends in relative abundance over time at multiple spatial scales (transect, 100km^2 grid cells, states/provinces, range-wide), in addition to abundance-habitat relationships for each species.

Investigation of Cave Emergence Flight of Wild Echolocating Bats Using Nonlinear Granger Causality Analysis

Kazusa Ushio[1], Emyo Fujioka[1,2], Keisuke Fuji[3], Hitoshi Habe[4,5], Hiroaki Kawashima[6] and Shizuko Hiryu[1]
1 Faculty of Life and Medical Sciences, Doshisha University, Kyotanabe, JPN; 2 Graduate school of Agriculture and Life Sciences, Tokyo University, Tokyo, JPN; 3 Graduate School of Informatics, Nagoya University, Nagoya, JPN; 4 Faculty of Informatics, Kindai University, Higashiosaka, JPN; 5 Cyber Informatics Research Institute, Kindai University, Higashiosaka, JPN; 6 Graduate School of Information Science, University of Hyogo, Kobe, JPN

Many species of bats live in groups. In Japan, bats have been observed to leave their roosts in groups for several species, and the behavioral classification and estimation of roosting populations are important indicators of behavioral ecology. In this study, we used high-sensitivity stereo video cameras to measure the flight trajectories of bats (*Miniopterus fuliginosus*) emerging from the cave in three dimensions. We found that there were two main patterns of behavior at emergence: "leaving the cave" and "returning to the cave". The behavior of bats returning immediately after exiting the cave is thought to be light sampling behavior to check the illumination level outside the roost. Based on the results of the behavioral classification, the total population in the cave was estimated to be approximately 18,000 individuals. In addition, the bats exited caves efficiently in groups while avoiding collisions with other individuals. Then, we applied a nonlinear Granger causality method (Fujii et al., NeurIPS'21) to analyze the interactions among individuals during emerging from the cave. As a result, the forward individuals tended to "be repulsed" from the rear individuals, while the rear individuals tended to "approach" the forward individuals. This suggests that the bats, which use sound to understand their environment, are also influenced by rear individuals, which are not captured by sight. Our results suggest that bats may have a unique swarming behavior mechanism that differs from model animals of collective behavior, mainly visual animals.

RAM Evaluation Using a Carollia Genome
Sarah Vaca-Puente[1], Austin Osmanski[1], Robert Hubley[2], Arian Smit[2] and David Ray[1]
1 Department of Biological Sciences, Texas Tech University, Lubbock, USA; 2 Institute for Systems Biology, Seattle, USA

Transposable elements (TEs) are repetitive and ubiquitous DNA sequences abundant in vertebrate genomes, sometimes occupying more than half of mammalian genomes. Their de novo identification has been enabled by RepeatModeler, one of the most common bioinformatics tools to produce libraries of TE families. However, RepeatModeler often produces redundant or incomplete consensus sequences, potentially falsely increasing the observed number of TE families and insertions and requiring extensive manual curation. This process takes some weeks for a de novo genome assembly, and longer for several. To overcome these issues, the software RepeatAfterMe (RAM) was designed. We use RAM to examine TE diversity in *Carollia perspicillata* in comparison to previously described manual curation methods. A total of 860 TE consensus sequences were obtained, of which 493 were considered "complete" (TEs with a clear random sequence in both flanks). The total proportion of TEs obtained in the *C. perspicillata* genome was approximately 30% of the genome, with a high proportion of LINEs. The diversity of TEs found in this Phyllostomid species is lower in relation to TE diversity in Vespertilionid bats, however, it covers almost one-third of this species genome which is representative. Unlike manual curation methods, the RAM analysis was completed in a few hours, compared to several days using manual curation. The resulting TE library was highly accurate, with minimal manual corrections required.

Temporal Variation in Diets of Bats from the Southwestern United States
Ernest W. Valdez[1], Mollie K. Hanttula[2] and Michael F. Medrano[3]
1 U.S. Geological Survey Fort Collins Science Center, University of New Mexico, Albuquerque, USA; 2 Department of Biology, University of New Mexico, Albuquerque, USA; 3 Guadalupe Mountains National Park, Salt Flat, USA

The Southwest has the greatest diversity of bats in the United States. Most of the bat species in this area are insectivorous. Despite decades of study on these bats, there remains a paucity of information on their feeding behavior. In addition, when information is available, it is either outdated or limited to one night of sampling. Although many bat species are opportunistic in their feeding behavior, there tends to be some preferred selection on what foods are available. During 2020 and 2021, we examined diets of several species of bats at Guadalupe Mountains National Park (GUMO) and Pecos National Historical Park (PECO). From these analyses, we found trends in food habits related to opportunism and selective feeding, relative to sampling over time. For example, at GUMO, *Antrozous pallidus* shifted their diets from beetles during June to August 2020, to centipedes during August to November 2020. Whereas at PECO, we found at least two genera (i.e., *Lasionycteris* and *Myotis*) consuming the same food item (i.e., caddisflies) that were seasonally abundant. As to be expected, much of the food availability is likely attributed to insect and plant phenology and relative to climate data. We suggest that future studies investigate the diets of bats over a period of time to allow for a better understanding of their feeding ecology. Understanding these trends will allow for better management decision relative to impacts from various threats such as wildlife diseases, alternative energy and climate change.

Balancing Bat Conservation with Renewable Energy Production
Gillian Vallejo, *C. Jared Quillen and Devin Sawyers
Natural Power Consultants, LLC., USA

Smart curtailment at wind farms builds on the relationship between low blade rotation and lower bat fatality rates. Implementing any curtailment strategy to reduce bat fatalities results in the loss of energy production, and revenue, which is why it is important to optimize curtailment strategies to maximize conservation benefits while minimizing loss of energy production when possible. The US Department of Energy (DOE) is currently funding several Bat Smart Curtailment studies evaluating the effectiveness of approaches to reduce bat fatalities and minimize associated power loss. Natural Power has built a consortium of collaborators (DOE, Wind Wildlife Research Fund, Alliant Energy) to evaluate a Detection and Active Response Curtailment (DARC) strategy at Alliant's English Farms wind energy center (170 MW) in Iowa. We present the results of the first year of a two-year case-study comparing the DARC system with a blanket curtailment approach in terms of both the financial benefits and the fatality rates associated with each. A control treatment was also included in which turbines were only curtailed below manufacturer cut in. We found that the average number of carcasses detected were lower for both the blanket curtailed and DARC curtailed treatment than for the control treatment. However, a statistically significant difference among treatment groups was not detected, most likely due to a lack of statistical power. The DARC system provided a 41% reduction in energy loss associated with the minimization compared to the blanket curtailment strategy. This would translate into a considerable increase in revenue compared to blanket curtailment.

Bat to the Future: Bat Biology Beyond Genomes
Juan Manuel Vazquez
Department of Integrative Biology, University of California, Berkeley, USA

The fields of genomics and comparative biology have changed drastically since the first bat genomes were published in 2011. Our ability to quantify and understand the link between genotype and phenotype has progressed at a scale and speed beyond what we thought possible 10 years ago, going from candidate studies of single genes and individuals to population-scale, multi-omic studies with single-cell resolution. While the evolution of sequencing technology has made high-quality genome assemblies feasible for all organisms, less has been said and done about the datasets and tools needed to functionally validate our new genomic insights. Recent advances in allied technologies, such as single-cell sequencing, linked read sequencing, and CRISPR genome editing provides a unique opportunity to leapfrog the state of bat genomics onto the cutting-edge of functional genomics by leveraging the lessons learned from prior efforts in other organisms. Through investment in equitable collaborations and research capacity, we can begin an active effort to curate resources that will not only be useful for today's researchers, but will allow us to stumble across tomorrow's questions, and drive the next generation of bat research.

Exploring the Neurogenetics of Vocal Learning in Bats to Shed Light on the Evolution of Speech
Sonja Vernes
University of St Andrews, St Andrews, GBR

Vocal learning, the ability to produce modified vocalizations as a result of learning from acoustic signals, is a key trait in the evolution of speech. While extensively studied in songbirds, mammalian models for vocal learning are rare. Bats present a promising study system given their

gregarious natures, small size, and maintenance in captive colonies. We utilize the pale spear-nosed bat (*Phyllostomus discolor*) as a tractable model for understanding vocal learning mechanisms. We take an interdisciplinary approach to provide an integrated understanding across genomics, neurobiology and transgenics. We generated new, high-quality genome annotations of genes and non-coding microRNAs, used gene expression patterns and neuroimaging to explore the brain, and report creation of transgenic bats by manipulating expression of FoxP2, a speech related gene. These interdisciplinary approaches are facilitating mechanistic and evolutionary understanding of mammalian vocal learning and can contribute to other areas of investigation that utilize *P. discolor* as a study species.

Disentangling the Effects of Anthropogenic Disturbance and Community Structure on Multi-pathogen Dynamics in Cave-dwelling Bat Communities

Amanda Vicente-Santos[1], Paula Ledezma-Campos[2], Bernal Rodríguez-Herrera[2], Eugenia Corrales-Aguilar[3], Gábor Á. Czirják[4], David J. Civitello[1] and Thomas R. Gillespie1

1 Population Biology, Ecology and Evolution, Emory University, Atlanta, USA; 2 Biology, University of Costa Rica, San José, CRI; 3 Virology, University of Costa Rica, San José, CRI; 4 Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research, Berlin, DEU

Despite the established linkages among anthropogenic disturbance, biodiversity loss, and increased risk of emerging infectious diseases (EIDs), predicting the direction, magnitude, and mechanisms driving emergence events remains challenging. As reservoirs for high-profile EIDs, bats have featured prominently in studies examining risks of disease emergence; however, that cave-dwelling bats present a unique study system to disentangle the dual effects of disturbance on species composition and disease prevalence remains overlooked. Here, we evaluated how anthropogenic disturbance and cave complexity influence bat community composition and the prevalence of multiple pathogens at the bat community level. We conducted our study in 15 caves in Costa Rica along a gradient of human disturbance. Surveys were repeated in the dry and wet seasons. We collected samples from 1,238 adult individuals, representing 17 species from four families with diverse ecological niches. We determined the infection prevalence of four common and divergent pathogens: *Bartonella* (244/1238), *Leptospira* (93/410), *Trypanosoma* (396/1238), and microfilaria (82/1237). Cave complexity, but not disturbance, predicted bat community composition. However, degraded habitats sustained smaller bat populations. Structural equation modelling revealed that pathogens responded differently to habitat quality, cave complexity, species richness and bat density. By developing a distinctive framework using a multi-host, multi-parasite system, this work provides insight into the complex patterns of pathogen dynamics and bat community ecology in changing environments.

Life on the Run: Migration Patterns and Yearly Variation Shape the Gut Microbiome of Tequila Bats

Luis Víquez-R[1,2], Kelly Speer[3,4,5], Kerstin Wilhelm[1], Nancy Simmons[3,6], Rodrigo A. Medellín[7], Simone Sommer[1] and Marco Tschapka[1,8]

1 Institute of Evolutionary Ecology and Conservation Genomics, Ulm, DEU; 2 UBIS Research Group, Bucknell University, Lewisburg, USA; 3 Richard Gilder Graduate School, American Museum of Natural History, New York, USA; 4 Center for Conservation Genomics, Smithsonian's National Zoological Park & Conservation Biology Institute, Washington D.C., USA; 5 Department of Invertebrate Zoology, National Museum of Natural History, Washington D.C., USA; 6 Department of Mammalogy, American Museum of Natural History, New York, USA; 7 Institute of Ecology, Universidad Nacional Autónoma de México, Mexico City, MEX; 8 Smithsonian Tropical Research Institute, Gamboa, PAN

Migratory animals live in a world of constant change. Animals undergo many physiological changes in preparing themselves for migration. Although this field has been extensively studied over the last decades, we know relatively little about the seasonal changes that occur in the microbial communities that these animals carry in their guts and the extent that this may have on the immune capacity of the animals. We assessed the V4 region of the 16S rRNA high-throughput sequencing to estimate the microbiome diversity of Tequila Bats from fecal pellets and evaluate how the natural process of migration shapes the microbiome composition, and diversity. We collected samples from bats in the Pacific Dry Forest and the Sonoran Desert in Mexico. Firmicutes and Proteobacteria largely dominate the gut microbiome in the Tequila Bats with significant year-year variations across all sites. Our study has demonstrated that locality and year-to-year variation shape the composition, overall diversity, and the 'uniqueness' of the gut microbiome in our study species. We also identified several bacterial taxa that might play essential roles in the immune response of these bats to external pathogens. Our data highlights how the gut microbiome is highly volatile between sites and years and how the immunological "preparedness" of migratory animals needs to be evaluated in the context of the migration stopovers and year-year variation.

Social Information in the Contact Calls of Common Vampire Bats

Julia K. Vrtilek1, Grace Smith-Vidaurre[2,3,4] and Gerald G. Carter[1,5]

1 Department of Evolution, Ecology and Organismal Biology, Ohio State University, Columbus, USA; 2 Laboratory of Neurogenetics of Language, Rockefeller University, New York, USA; 3 Rockefeller University Field Research Center, Rockefeller University, Millbrook, USA; 4 Department of Biological Sciences, University of Cincinnati, Cincinnati, USA; 5 Smithsonian Tropical Research Institute, Panama City, PAN

When adult common vampire bats (*Desmodus rotundus*) are socially isolated, they produce contact calls. These calls contain enough information for individual recognition and can attract past food-sharing partners. However, it remains unclear whether vampire bat contact calls also contain other social information. Other bat species have been shown to produce learned vocalizations that convey group identity and allow them to recognize unrelated groupmates. In primates, heritable similarities in calls might provide information that allows individuals to recognize unfamiliar kin. To identify what social information vampire bat social calls contain, we recorded more than 200,000 contact calls made by 113 individuals from seven colonies. To determine pairwise vocal similarity, we used 27 spectral and temporal measures of calls to classify calls to bats. We then asked whether calls contained three types of social information by testing whether multivariate acoustic distance was predicted by kinship (based on known maternities and 17 microsatellite markers), familiarity (time spent together in captivity), and the strength of social bonds (rates of social grooming and food sharing). Our preliminary results suggest that vampire bats may sound more similar to their kin; other analyses are ongoing.

Bat Species Diversity Linked with Stream Health as Described by Intolerant Insect Diversity

Trevor G. Walker[1], Sarah C. Zirkle[1], Sarah K. Krueger[1], Gene Zirkle[2] and Catherine G. Haase[1]

1 Department of Biology, Austin Peay State University, Clarksville, USA; 2 U.S. Army Fort Campbell, Fort Campbell Fish and Wildlife, Kentucky

Due to the reliance of North American bat species on aquatic insects for forage, we suspect there should be a link between stream health and metrics of bat diversity. This relationship is especially important with the current global declines of insects and with ongoing land-use change. We assessed this hypothesis using metrics of bat diversity and various variables of aquatic insects, specifically those related to aquatic species sensitive

to stream health. We captured bats via mist nets at 25 sampling locations on Fort Campbell Army Base, KY and calculated bat species richness and Simpson's Diversity Index. We collected aquatic insects with Hess samplers, kick nets, dip nets, and light traps. Insects were identified down to the family, dried, and weighed. We assigned each family an average of tolerance values and calculated the Family Biotic Index for each location. We also calculated percent abundance and percent biomass comprised of Ephemeroptera, Plecoptera, and Trichoptera (EPT) at each location. We used a generalized linear model to relate bat diversity indices to aquatic insect metrics and included weather variables (nightly mean temperature, total nightly precipitation) and Julian date as covariates. We found that bat species richness and bat species evenness had a positive response to EPT family richness, but individual bat species key in on other habitat characteristics, such as food availability, weather conditions, and other temporal characteristics when foraging in these areas. These results indicate bat species diversity is linked to healthy streams as represented by these insects being present.

Endangered Gray Bats Use Bridges and Culverts in an Area Lacking Natural Roosts

Joey A. Weber[1,2], Frankie Tousley[1], Brianne L. Walters[1], and *Joy M. O'Keefe[1,3]
1 Center for Bat Research Outreach and Conservation, Indiana State University, Terre Haute, USA; 2 North Carolina Wildlife Resources Commission, Asheville, USA; 3 Natural Resources and Environmental Sciences, University of Illinois, Urbana, USA

To protect populations of rare bats, we must locate and describe essential habitat, such as daytime roost sites. For the federally endangered gray bat (*Myotis grisescens*), caves are critical hibernation and pup rearing sites, and human disturbance is a threat. Gray bats live year-round in eastern Tennessee (TN), but we know of no natural roosting habitat for adjacent areas of North Carolina (NC). After gray bats were found roosting in several bridges and a culvert in western NC, the NC Department of Transportation funded a three-year study of their distribution and evaluated available roosting habitats in this region. We captured bats over two years, surveyed with acoustic detectors, tracked bats via radio telemetry, and searched 268 bridges (mainly randomly selected) and some culverts for bats. Gray bats were active across most of the 733,000-ha French Broad River Basin in NC from March to September. We located 37 gray bat roosts in NC, including 24 bridges (three with >1,000 bats), eight culverts, three buildings, and two trees; tagged bats also used two known caves in TN. Generalized linear models showed that ideal bridge roosts were concrete, with box- or I-beam construction and accessible expansion joints. Gray bats chose bridges near larger streams in less-developed landscapes, typically within 4 km of populous primary roosts. Gray bats exploit large concrete bridges and long culverts in the absence of natural habitat; thus, we suggest systematic searches of such structures within migration distance of their known hibernacula.

How Emerging Technologies Can Inform the Conservation Management of the Grey-headed Flying-fox

Justin A. Welbergen[1], Jessica Meade[1], Eliane McCarthy[1], Samantha Yabsley[1], Sienna Grady[1] and John Martin[2]
1 Hawkesbury Institute for the Environment, Western Sydney University, Richmond, AUS; 2 Institute of Science and Learning, Taronga Conservation Society Australia, Mosman, AUS

The grey-headed flying-fox (*Pteropus poliocephalus*) is a vulnerable, extremely mobile species of bat found in southeastern Australia where it is exposed to a range of anthropogenic threats including habitat loss, urbanization, extreme heat events, and wildfires. However, at present, monitoring is inadequate and information on the impacts of threats is limited, posing key impediments to the sound conservation management of this ecologically important species. In this presentation, we will provide an overview of the findings of our recent research aimed at informing the evidence-base for flying-fox management and conservation in Australia. We show that emerging technologies, such as drone, radar, and satellite remote sensing, along with large-scale applications of animal tracking, hold great promise for radically improving flying-fox monitoring and for facilitating the identification and documentation of population threats. Improved landscape-scale monitoring of the spatiotemporal dynamics of the grey-headed flying-fox, along with improved knowledge of threats, will help us be better equipped to predict and mitigate impacts and so enable more effective, proactive conservation management of the species across jurisdictional boundaries.

There and Back Again: Homing in Bats Revisited

Theodore J. Weller[1], Erin F. Baerwald[2], Dana M. Green[3] and Richard A. Holland[4]
1 Pacific Southwest Research Station, USDA Forest Service, Arcata, USA; 2 Ecosystem Science and Management, University of Northern British Columbia, Prince George, CAN; 3 Department of Biology, University of Regina, Regina, CAN; 4 School of Natural Sciences, Bangor University, Bangor, GBR

At the 1971 North American Society for Bat Research (NASBR) meeting in Albuquerque, Don Wilson and James S. Findley presented "Randomness in Bat Homing." The central tenants of their paper were that homing ability in bats could be explained by chance alone or by some sort of random search (Wilson and Findley 1972). In this retrospective, we assess the knowledge gained from, but also the limitations of, older studies on bat homing and review the advances in our understanding of homing and navigation in bats. Although much has been learned over the last half century about the orientation and navigation of bats, particularly our understanding of cues and spatial orientation, we still do not know if bats are capable of true navigation nor how they learn to do so. Partly because of technological advances, the study of homing has expanded from bats' ability to return to roosts after being displaced short distances to determining how bats navigate and find destinations during long-distance seasonal migrations. We advocate for expansion of the study of navigation to include inter-seasonal movements and tropical areas and highlight the need to apply new knowledge of movement and navigation to the conservation of bats.

Species Composition Changes in Indiana's Bat Populations Since the Arrival of White-nose Syndrome

Bradford Westrich and Timothy A. Shier
Division of Fish & Wildlife, Indiana Department of Natural Resources, Bloomington, USA

The spread of white-nose syndrome (WNS) across North America has caused drastic and perhaps irreversible changes to populations of many cave-hibernating bat species. The presence of WNS in Indiana was confirmed in January 2011. State-wide acoustic bat surveying began in summer 2011 and has continued into 2022. These surveys have used Anabat SD2 bat detectors and associated hardware to record echolocation calls from individuals in the surrounding environment. These data, coupled with data from decades of winter bat counts in hibernacula, were analyzed for changes to Indiana's native bat populations. It was found that the composition of Indiana's bat species has changed significantly since the arrival of WNS, both in terms of total numbers and proportional representation. Hibernaculum surveys have documented pre-WNS (1991–2007) to post-WNS (2015–2019) declines of 92% and 86% in tricolored bats (*Perimyotis subflavus*) and little brown bats (*Myotis lucifugus*), respectively, while changes to Indiana bats (*Myotis sodalis*) remained statistically insignificant. Proportionally, summer acoustic bat surveys documented a combined

decline in tricolored and Myotis spp. bats from 21% to 11% of all species from 2011 to 2021, while tricolored bats alone declined from 17% to 4% of all species across the same period. An understanding of these changes is therefore essential to adapting conservation and management strategies to aid in the recovery of these populations, particularly with the added pressures of climate change, wind energy development, and other large-scale changes to habitat.

Wind Energy Fatality Minimization Efforts and Research in the United States
Michael Whitby
Bat Conservation International, Austin, USA

Bat Conservation International has been involved in studying the impact of wind energy on bats and potential mitigation measures since 2006 when it was a founding member and coordinator of the Bats and Wind Energy Cooperative. For this presentation, we will provide an overview of research on minimization methods in the United States. To begin, we will review past work on minimization focusing on operational minimization and acoustic deterrents. Recent meta-analysis has shown operational minimization to be an effective strategy across multiple widespread North American Species including *Lasiurus cinereus*, *L. borealis*, and *Lasionycteris noctivagans.* We estimate that fatalities are reduced by 33% every 1 m/s increase in speed at which turbine blades start spinning, resulting in an approximately 62% (5469% 95% CI) average decrease in bat fatalities when operational speeds are increased to 5.0 m/s. Additionally we will review past and ongoing investigations of bat deterrents in the United States. Acoustic deterrents have shown mixed effects for *L. cinereus*, and one study has shown an increase in fatalities of *L. borealis*. We will review ongoing work investigating ways to refine operational minimization to minimize both bat fatalities and energy loss. This includes work on real-time acoustic detection and turbine shutdown and modeled risk curtailment.

Can Acoustic Recordings of Cave-exiting Bats in Winter Estimate Bat Abundance in Hibernacula?
Jericho C. Whiting[1], Bill Doering[2] and Ken Aho[3]
1 Department of Biology, Brigham Young University-Idaho, Rexburg, USA; 2 Veolia Nuclear Solutions—Federal Services, Idaho Falls, USA; 3 Department of Biological Sciences, Idaho State University, Pocatello, USA

Counting hibernating bats in caves estimates bat abundance; such counts can be used to understand population fluctuations. Passive acoustic monitoring can record large amounts of long-term data. We acoustically monitored and counted two species of bats in 9 hibernacula from November to March 2011 to 2018. We hypothesized that acoustic data recorded from Townsend's big-eared bats (*Corynorhinus townsendii*) and western small-footed myotis (*Myotis ciliolabrum*) exiting hibernacula could be used to estimate abundance of those species in hibernacula. We conducted 29 hibernacula surveys and simultaneously set passive acoustic detectors during winter. Acoustic monitors recorded for 1,063 nights. Detectors recorded 2,459 files of Townsend's big-eared bats and 9,094 files of western small-footed myotis. Mean number of Townsend's big-eared bats counted in a cave was 96; mean number of western small-footed myotis counted in a cave was 7. For Townsend's big-eared bats, the top model held 43% of model weight and included the variable bat activity (i.e., mean number of Anabat files/night) and cave. For western small-footed myotis, the top model held 55% of model weight and contained the variable bat activity. Mean number of acoustic recordings of bats flying out of a cave across a winter was positively related to the number of hibernating bats counted in a cave for western small-footed myotis; for Townsend's big-eared bats that relationship held for 2 caves with >90 individuals. Our results indicate that researchers can use passive acoustic data as an index of abundance of bats hibernating in caves in temperate climate zones.

In Search of White-nose Tolerance: Whole-genome Positive Selection Analysis Between Two Contrasting Myotis Species
Flora Whiting-Fawcett[1], Thomas M. Lilley[2] and Steve Paterson[1]
1 Department of Evolution, Ecology and Behaviour, University of Liverpool, Liverpool, GBR; 2 Finnish Museum of Natural History, University of Helsinki, Helsinki, FIN

Myotis bat populations across North America have been devastated by white-nose syndrome (WNS), following the introduction of the causative fungus, *Pseudogymnoascus destructans*. In contrast, European species suffer minimal effects from infection, and are thought to have co-evolved with the fungus for thousands of years. The aim of this research is to find evidence for the evolution of WNS tolerance in a European Myotis with lengthy exposure to the fungus. The analysis contrasts positive selection across the genome in this species to an American Myotis, assessing 6777 orthologues in total. The American species, *Myotis lucifugus*, is highly susceptible; the European, *Myotis brandtii*, is tolerant and located in Europe, but is nested within the American *Myotis* clade. This phylogenetic closeness makes *M. brandtii* an ideal contrast to the American bats. Two methods were used to identify genes under positive selection, PAML and McDonald-Kreitman. Only genes with significant results in both tests were put forward for further analysis. Initial results showed significant selection in genes previously highlighted in the WNS literature. These were not restricted to immune-related genes, but had a range of roles, including in hibernation and fat accumulation. Our results support previous findings that tolerance to WNS may have a basis that is not solely due to adaptations in immune genes. The genes highlighted in this analysis provide interesting targets to investigate whether tolerance is evolving through similar mechanisms in persisting American populations. Allelic diversity within these genes could provide a predictive basis for how well naïve populations will survive infection.

Assessing Temporal Use Patterns at Northern Long-Eared Bat Roosts Using Infrared Cameras
Ellen Whittle[1], Ian Abernethy[2] and Anna Chalfoun[3]
1 Department of Zoology and Physiology, University of Wyoming, Laramie, USA; 2 Wyoming Natural Diversity Database, University of Wyoming, Laramie, USA; 3 US Geological Survey, University of Wyoming, Laramie, USA

Site fidelity can increase survival in animals by reducing energy costs of locating suitable habitat for foraging or breeding. The northern long-eared bat (*Myotis septentrionalis*), currently listed as threatened in the United States, has experienced catastrophic population declines from white-nose syndrome. Maternity roosts are critical for sheltering and raising offspring; however, suitable trees are often limited in systems altered by human activities such as timber harvest and cattle grazing. Under current federal regulations, maternity roosts are legally protected in June and July, when young are non-volant and vulnerable to disturbance or removal. These protections may be insufficient in retaining critical habitat if bats rely on prior knowledge of suitable roost trees in subsequent years. Our objectives were to 1) quantify activity of northern long-eared bats at maternity roosts for multiple years, and 2) test the use of infrared trail cameras to record temporal patterns of roost behaviors. We recorded 989 videos of bats at 12 roosts (12/13 total trees) in the Black Hills National Forest. Roost use ranged from 14 years after first documentation, and colony activity was evident as late as August. Bats exhibited numerous behaviors including "touch-and-go" approaches, repeated entering and

exiting of the roost cavity, and infrequently, females carrying pups. Because bat use was largely intermittent, long-term camera monitoring may be the most practical method of determining temporal use patterns, including duration and frequency of bat use. This is especially helpful for rare species, which may benefit from management focused on retaining roosts for multiple years.

Unravelling the Taxonomic Status of Medium-sized Bent-winged Bats (Miniopterus) on the Australian Continent

Sigit Wiantoro[1,3] and Kyle N Armstrong[2,3]
1 Museum Zoologicum Bogoriense, Research Center for Biosystematics & Evolution, National Research & Innovation Agency, Bogor, IDN; 2 South Australian Museum, Adelaide, AUS; 3 School of Biological Sciences, University of Adelaide, Adelaide, AUS

The medium-sized bent-winged bats are abundant and distributed widely ranging from Europe, Africa, Asia to Australia. They are arguably one of the most difficult bat groups to resolve taxonomically due to similar appearance across species. The piecemeal approach to their taxonomy over more than a century by multiple taxonomists using traditional taxonomic methods, who had only limited access to geographic and phylogenetic sampling, has led to a confusing array of names and peculiar distributions. Our study aimed to determine the species level status of the three geographic groups of medium-sized *Miniopterus* that occur on the Australian continent. The null hypothesis that there was a single species of *Miniopterus* present was addressed with a combination of reduced representation genome-scale DNA markers, a single mitochondrial gene and traditional morphometrics. Despite the unavailability of reliable diagnostic morphological characters, this study confirmed the differentiation of the Australian *Miniopterus* from the Palearctic-Ethiopian *M. schreibersii*, and even from *M. fuliginosus* and *M. blepotis* as the senior names of medium-sized *Miniopterus* in the Oriental-Australasian region. Further analysis within Australian species using the single nucleotide polymorphisms (SNPs) generated using a genome-scale DNA sequencing method ('DArTseq') and near the full length of the Cytochrome-b gene revealed three distinct genetic clusters/lineages, each suggesting one putative species. This effectively doubles the number of Australian bent-winged bat species based on past morphological analysis.

Winter Colony Count Status and Trend Analysis for the North American Bat Monitoring Program

Ashton Wiens[1,4], Tina Cheng[2,4], Bradley Udell[3,4], Winifred Frick[2,4], Brian Reichert[3,4], Bethany Straw[3,4] and Wayne Thogmartin[1,4]
1 Upper Midwest Environmental Sciences Center, U.S. Geological Survey, La Crosse, USA; 2 Bat Conservation International, Austin, USA; 3 Fort Collins Science Center, Fort Collins, USA; 4 North American Bat Monitoring Program, Fort Collins, USA

The North American Bat Monitoring Program has garnered contributions from many partners, providing data storage and protection, and this collaboration provides the capacity for continental scale population modeling. Using this collection of data, we detail the inaugural analytical pipeline providing winter colony count status and trend analyses for 12 bat species. We pair a simple exponential interpolation model with a Bayesian hierarchical model, allowing analysis of well- and under-sampled sites and species, those facing environmental stressors and those receiving less attention. Results give predictions of current and historical abundance and trends over any period and at any spatial scale. Using information about the arrival of white-nose syndrome, we are also able to gain insight into the differences in the effects of white-nose syndrome among all monitored species.

Predicting Conservation Behaviors Towards Bats in the USA, Belize, Cambodia, and Uganda: the Importance of Local Context

Adam S. Willcox[1], David R. Ader[2], Mason A. Cordan[3], BreeAnna M. Dell[4], Kirstin E. Fagan[5], Hannah G. Shapiro[6], Marcy J. Souza[7], Mallory Tate[8], Michelle L. Verant[9] and Emma V. Willcox[2]
1 Department of Forestry, Wildlife and Fisheries & The Smith Center for International Sustainable Agriculture, University of Tennessee, Knoxville, USA; 2 The Smith Center for International Sustainable Agriculture, University of Tennessee, Knoxville, USA; 3 Department of Forestry, Wildlife and Fisheries, University of Tennessee, Knoxville, USA; 4 Department of Public Health – Seattle & King County, USA, 5 Department of Wildlife, Fisheries, and Conservation Biology, University of Maine, Orno, USA; 6 Warnell School of Forestry & Natural Resources, University of Georgia, Athens, USA; 7 Department of Biomedical and Diagnostic Sciences, University of Tennessee College of Veterinary Medicine, Knoxville, USA; 8 Biodiversity Division, Tennessee Wildlife Resources Agency, Nashville, USA; 9 Biological Resources Division, National Park Service, Fort Collins

Many assume bats are negatively viewed by the public and that this results in a major barrier to conservation efforts. While negative perceptions of bats have historically been documented in European and North American contexts, there is strong evidence that attitudes and behaviors towards bats vary among cultures and regions of the world. Even in the case of North America, recent research indicates that certain user groups have changed historically negative attitudes towards bats to those that are either neutral or positive. We have developed attitude scales and semi-structured interview guides towards bats that are adaptable to local contexts. Our quantitative surveys and qualitative interviews of people in Belize, Cambodia, Uganda, and the USA support the importance of understanding local context as a driver of attitudes and behaviors towards bats. In this presentation, we will take you around the world to hear different people's and culture's varied and poignant thoughts and attitudes towards bats. We will include cases from visitors and managers of Mammoth Cave and Zion National Parks in the USA to ranchers living in vampire bat ranges in Belize; And bushmeat hunters and cooks in Uganda to guano harvesters in caves and street vendors selling goods nightly at emergence sites in Cambodia. By highlighting the application of varied social science studies in local contexts, we can continue to improve effective bat conservation by connecting biologists and social scientists in the IBRC and NASBR communities.

Spatial Ecology of Ugandan Horseshoe Bats as Reservoirs of Emerging Viral Pathogens

Kalani M. Williams[1], Natalie R. Wickenkamp[1], Emma K. Harris[1], Benard Matovu[2], Betty Nalikka[2], Lillian Nalukenge[2], Jack-Michael Mutebi[2], Aggrey Siya[2], Tanya A. Dewey[3], Kevin Castle[4], Teddy Nakayiki[5], Robert M. Kityo[2] and Rebekah C. Kading[1]
1 Microbiology, Colorado State University, Fort Collins, USA; 2 Zoology, Makerere University, Kampala, UGA; 3 Biology, Colorado State University, Fort Collins, USA; 4 Four Seasons Veterinary Specialists, Fort Collins, USA; 5 Entomology, Uganda Virus Research Institute, Entebbe, UGA

Recently, insectivorous horseshoe bats (*Rhinolophus* spp.) have become known for their association with coronaviruses, including strains closely related to SARS-CoV-2, but they have also been associated with hosting several other important viral families. It is becoming increasingly critical to understand the ecology of these reservoir hosts, along with where and how spillover events could occur. For *Rhinolophus* bats on the African continent, there is currently very little known about their movement patterns. In this study we use GPS tracking to ascertain locations bats select for foraging within the Mount Elgon region of Uganda and determine whether these locations are closer or further from various landscape features than would be expected if their distribution was random. GPS data was acquired by suturing GPS units onto bats and taking fixes once

every hour during periods of low activity and once every six minutes during periods of high activity. Using kernel density algorithms to determine foraging hotspots from the distribution of GPS points, our preliminary data suggest foraging hotspots are significantly closer to rivers/streams and protected areas and significantly further from roads and human settlements than would be expected if their distribution was random. Foraging sites were an average of 13 km away from cave roosts and bats spent an average of 4 h and 50 min at a single foraging site. Moving forward, known foraging sites could be targeted for conservation, as well as monitored for risk of viral spillover.

Use of Bridges as Day Roosts by Bats in the Trans-Pecos Region of West Texas

Holly G. Wilson[1], Stirling J. Roberston[2] and Richard D. Stevens[1,3]
1 Texas Tech University, Lubbock, USA; 2 Texas Department of Transportation, Environmental Affairs Division, Austin, USA; 3 Museum of Texas Tech, Lubbock, USA

Roosts are crucial components of bat habitat that can affect survival and fitness. Finding an appropriate roost can present a challenge, but some road infrastructure presents reliable roost options within an ever-changing environment. The Trans-Pecos region of west Texas hosts great bat diversity, making it an ideal region to study roosting habits in bridges across multiple scales. During the summers of 2018 and 2019, we survey 204 bridges across 10 counties spanning more than 107,500 km^2. In addition to structure surveys, we implemented landscape characteristics using landcover data in GIS as well as microsite characteristics using iButtons. Across habitat scales, we expected microclimate, structure type, and distance to water to be related to use by bats. We analyzed data by applying linear mixed-effects models to determine the relationship between bat presence and abundance within structures. This information, along with continued study, can aid conservation efforts by departments of transportation when planning maintenance and construction of structures, as well as provide a better understanding of the role anthropogenic effects play in bat ecology.

Flying Foxes (*Pteropus* spp.) of Myanmar – With Notes on Taxonomic Status of *P. intermedius*

Hsu Lae Win[1,2], Sara Bumrungsri[2] and Pipat Soisook[3]
1 Zoology Department, Myeik University, Myeik, Tanintharyi Region, Myanmar; 2 Division of Biological Science, Faculty of Science, Prince of Songkla University, Songkhla, THA; 3 Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkla University, Songkhla, THA

Myanmar, although incredibly rich in bat diversity, has a handful of in-country bat taxonomists. This makes the knowledge on bats from this significant zoogeographic region still poor and need support from global bat research community. A recent international collaboration to enhance Myanmar taxonomic capacity has been established for studying flying foxes in the country with a particular interest in the elusive *Pteropus intermedius*. Preliminary results of morphological examination of newly collected and museum specimens, including types, and genetic analyses, show that there are two species of *Pteropus* in Myanmar. The taxon intermedius, earlier known only from the South-Central part of the country, should be considered conspecific with *medius*. The type specimen of intermedius, although with notably, abnormally small body, the craniodental characters and measurements agree with *medius*. The genetic analyses, based on mitochondrial COI, CytB and ND2, of specimens from and around type locality of *intermedius* grouped together with *medius* from elsewhere in the upper part of the country. In the south, specimens from Tanintharyi Region, Myiek and in the archipelago, prove to be *P. hypomelanus*. With no current concrete evidence, the species *P. vampyrus* should be excluded from the list of its occurrence in Myanmar. The results will be useful for future plan and action of bat conservation, not only in the country but in the whole region.

Small Scale Movements of *Rousettus aegyptiacus* in Limpopo Province, South Africa and Implications for Disease Risk

Matthew R. Wood, Wanda Markotter and *J. Low de Vries
Department of Medical Virology, Centre for Viral Zoonoses, Faculty of Health Sciences, University of Pretoria, Pretoria, South Africa

The Egyptian rousette bat (*Rousettus aegyptiacus*) has been associated with numerous potentially zoonotic viruses, including rabies-related lyssa-, paramyxo-, and coronaviruses and has been suggested as the primary reservoir of Marburg virus. The viruses associated with *R. aegyptiacus* could potentially spread to other mammalian species, including humans, livestock, and wildlife when they are in contact or in close proximity to each other. It is important to understand potential overlap between these species. This can occur due to the feeding locations of *R. aegyptiacus*, the areas they traverse nightly, or during migration. We deployed VHF trackers on 26 individual *R. aegyptiacus* during a 12-month period between February 2021 and February 2022 and tracked bats for 9 nights each month. Tracking was commenced at sunset and continued throughout the night until an hour before sunrise. Bats were tracked by driving roads across the study area and walking transects in less accessible areas. During summer months *R. aegyptiacus* centred their feeding around natural occurring Ficus sycomorus trees which are mostly found around the river. However, during the colder winter months activity increased around residential areas where cultivated fruits are grown. Winter months are classified as a high-risk period for virus spill over due to increased viral prevalence in excretions and due to increased feeding by bats in residential areas.

Engaging Volunteers to Deliver Science Outcomes

Lisa Worledge, Claire Boothby, Elisa Fuentes-Montemayor, Ella Browning, Giada Giacomini, Katherine Boughey, Lia Gilmour, Philip Briggs and Sonia Reveley
The Bat Conservation Trust, London, GBR

The Bat Conservation Trust (BCT) could not deliver all that we do in terms of science and conservation outcomes without engaging volunteers and non-bat professionals in our work. Through consideration of four examples, relating to human-bat interactions, species monitoring, habitat surveys, and disease surveillance, we'll highlight how we work with different groups towards our objective of 'Discover: To ensure scientific evidence is in place to support bat conservation.' Churches in the UK have been home to bats for centuries, however, their use of these places of worship, often important heritage sites, can bring conflict with church communities. To better understand the extent of the issues, we're running community science surveys with volunteers from bat, heritage, and church communities. We developed an automated sound classification system for processing large volumes of recordings to underpin our Nightwatch initiative, an accessible way to get more people involved with wildlife data collection, encouraging more diverse participants. In another project, we used Forestry England staff, complete novices with bats, to undertake passive acoustic surveys to inform natural capital accounting and woodland condition monitoring. The outcome was a huge step forward in understanding the behavior of protected species, the health of woodlands and biodiversity more generally. We have used members of the public and bat workers to support our collaborative disease surveillance efforts, working with Governmental and academic partners, and contributing to

several published studies. At BCT we are in no doubt about the valuable contribution that volunteers make to our work in delivering science outcomes.

Bat Declines from White-nose Syndrome Reveal Heterogenous Top-down Influences on Arthropods

Amy K. Wray[1], M. Zachariah Peery[1], Jade M. Kochanski[2,3], Emma Pelton[2,4], Daniel L. Lindner[5] and Claudio Gratton[2]
1 Department of Forest & Wildlife Ecology, University of Wisconsin-Madison, Madison, USA; 2 Department of Entomology, University of Wisconsin-Madison, Madison, USA; 3 Department of Integrative Biology, University of Wisconsin-Madison, Madison, USA; 4 Xerces Society for Invertebrate Conservation, Portland, USA; 5 Center for Forest Mycology Research, Northern Research Station, USDA Forest Service, Madison, USA

Abrupt changes in predator populations provide unique opportunities to test for top-down effects on prey and thus understand trophic relationships. In North America, white-nose syndrome (WNS) has caused precipitous declines in hibernating bat populations, raising the question of whether the rapid loss of arthropodivores may relieve top-down predation pressure and manifest in changes in arthropod abundance. The severe decline of little brown bats (*Myotis lucifugus*) in particular provides a natural predator removal experiment which may clarify the influences of bats on arthropod prey. During the summer periods from 2015–2018, we performed intensive arthropod black-light trapping surveys, ultrasonic acoustic monitoring, and emergence counts at little brown and big brown bat (*Eptesicus fuscus*) maternity roosts in Wisconsin, USA. We found that little brown bat populations at study sites declined by 95%, with corresponding high-frequency acoustic activity declining by 79%. In comparison, big brown bat populations declined by 38%, but corresponding low-frequency acoustic activity did not change. Total arthropod abundance also decreased over the four-year period but showed a relative increase at sites near little brown bat roosts in comparison to sites far from roosts with less bat activity (controls). Trends in arthropod abundance differed within taxonomic and functional groups, with relative increases most noticeable among common little brown bat prey. These results indicate that bat population losses due to WNS can release predation pressure on some arthropod groups. Overall, this study provides further evidence that disease-related declines in predators can exert measurable but heterogenous top-down effects on their prey.

Endoparasite Diversity of Mexican Free-tailed Bats (*Tadarida brasiliensis*) Characterized using Non-invasive DNA Metabarcoding

Khyana N. Yearwood, Andrea Schreier and Ann Holmes
1 Department of Animal Science, University of California, Davis, USA

Understanding parasite communities in bats can provide information on nutrient and energy flow within habitats, population ecology, and health impacts. Parasites are ecologically important but poorly understood. It has been difficult to analyze gastrointestinal endoparasite communities that exist amongst bats without harming them. Studies have used gut dissection to physically remove parasites from bats and characterize them, but this invasive technique results in the death of bats. For this study, I used environmental DNA (eDNA) sampling methods to collect bat guano pellets from three Mexican free-tailed bat (*Tadarida brasiliensis*) communities in the Yolo County, CA region. This form of sampling eliminates major disturbances of bats in their natural habitats. For sample processing, I used DNA metabarcoding, a noninvasive method, to analyze the diversity of parasites that exist in these specific roost populations. DNA was extracted from the guano pellets and analyzed using three different primer types: 18S, 16S, and COI. These primers can detect and amplify a broad range of taxa which is important because bat parasites do not fit into one taxonomic group. Nematodes, Trematodes, and Acarina have been found in other Mexican free-tailed bat populations so it is possible that the bat roosts from these three sites will have similar results. These bat populations in the Yolo County region serve as ecologically important predators of agricultural pests of the large rice fields and corn fields nearby their roosts. Understanding their gastrointestinal endoparasitic composition may provide more information about bats' ecological contribution to this area.

The Developing Bat Brain

Laurel R. Yohe[1], Stevie Clemens[1] and Matteo Fabbri[2]
1 Department of Bioinformatics and Genomics, University of North Carolina Charlotte, Charlotte, USA; 2 Vertebrate Paleontology, Field Museum of Natural History, Chicago, USA

While regions of the bat brain often have demonstrated signatures of specialization and divergence (e.g., enlargement of olfactory bulb regions in frugivores), much less is known of the morphogenesis of these regions and the developmental origins of sensory divergence. To understand how the brain develops, embryonic series of bats from divergent ecologies are necessary but often not possible to collect either feasibly or pose threats to declining bat populations. However, female museum specimens offer a rich set of morphological resources such that some specimens were collected and were unknowingly pregnant. We obtained an in-depth embryo series of twelve species of neotropical bats (between 5–10 stages per species) that exhibit different dietary ecologies. Using diffusible iodine-enhanced contrast μCT-scanning, we visualized the internal anatomy of the developing embryo series in a minimally destructive manner. From these scans, we segmented different brain regions and quantified volumes of each region, which enabled us to visualize and measure how the bat brain develops through time and how these regions may vary across species of divergent diets. Focusing specifically on neotropical Leaf-nosed bats (Phyllostomidae; n = 12 species), which are well known for their diversity in dietary ecologies, we compared plant-visiting versus animal feeding bats. We found that the olfactory bulb deviates allometrically from embryonic growth in all plant-visiting bats observed, emphasizing their reliance on olfaction to find food and how early development contributes the necessary neural resources to facilitate this adaptation.

The Evolution of Acoustic Methods for the Study of Bats

Veronica Zamora-Gutierrez[1], *María Cristina MacSwiney G.[2], Santiago Martínez Balvanera3 and Everardo Robredo Esquivelzeta[3]
1 CONACYT - Centro Interdisciplinario de Investigación para el Desarrollo Integral Regional Unidad Durango, Instituto Politécnico Nacional, Durango, MEX; 2 Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, MEX; 3 Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, Ciudad de México, MEX.

The study of bat acoustic signals requires specialized equipment with microphones capable of recording high frequencies. There has been growing interest in bat acoustics and a rapid evolution in ultrasonic recording equipment, from the pioneering work using detectors weighing several kilograms, to the current pocket-sized and open-source recorders. The increasing accessibility of bat detectors has extended the field of bat acoustics from simple activity detection to acoustic species identification and experimental research, investigations referenced in NASBR meetings from mid-90's until today. Traditional call analysis was based on multivariate statistical techniques such as discriminant function analysis. However,

technological improvements have led to expanding knowledge regarding the complexity and versatility of bat echolocation, and have kindled the evolution of signal processing methods with new approaches (i.e., deep learning) and more powerful computational techniques. Free access to reference libraries that permit adequate and extensive algorithm comparisons have emerged as a cornerstone for the refinement of automated acoustic analysis. Acoustic surveys have provided important insights into the effects of anthropogenic activities and urbanization on bat activity and diversity. Understanding how human activities affect biodiversity is a crucial prerequisite for the development and application of effective species conservation programs.

Migratory Mites: Influence of the Migration of *Leptonycteris yerbabuenae* (Chiroptera) on *Periglischrus paracaligus* (Spinturnicidae)
Daniel Zamora-Mejías[1,2], Rodrigo A. Medellin[1], Juan Bibiano Morales-Malacara[3] and Bernal Rodríguez-Herrera[2]
1 Instituto de Ecología, Universidad Nacional Autónoma de México, Mexico City, MEX; 2 Universidad de Costa Rica, San José, CRI; 3 Unidad Multidisciplinaria de Docencia e Investigacion, Facultad de Ciencias, Universidad Nacional Autónoma de México, Campus Juriquilla, Querétaro, MEX

Latitudinal migration increases the fitness of migrants by exploiting favorable conditions between non-adjacent geographic regions. Other phenomena can consequently be derived from it, such as interactions with parasites. Host behavior, geographical range, spatial movement, and population density may impact parasitic transmission, parasite abundance, and directly influence the morphometric and genetic variation, being important drivers of parasite variability. Our goal was to measure the variability and changes in parasitic loads among the ectoparasites of the migratory *Leptonycteris yerbabuenae*, over their distribution range in Mexico. From 2017 to 2019, we documented ectoparasite loads of wing mites and bat flies in six caves along the migratory route of *L. yerbabuenae*. We inspected a total of 516 bats and collected more than 6,000 ectoparasites. Data on ectoparasite abundance and prevalence were analyzed using General Linear Mixed Models. We used linear and Geometric Morphometric to evaluate morphometric variation on the specific wing mite *Periglischrus paracaligus*. Molecular analyses included three genes to explore the intraspecific and interspecific variation of *P. paracaligus*. Our results showed that migration may decrease ectoparasite abundance. Geometric morphometrics and molecular analyses revealed high variability among populations and evidence of species divergence in *P. paracaligus*, following the phylogeny of its host. However, our knowledge of the main factors that shape the interactions between the bat hosts and their parasites during migration remains elusive, bats and their parasites may play an important role in conservation, providing guidelines for a better understanding of the parasite/pathogen transmission and infectivity.

eDNA Detection of *Leptonycteris nivalis* at Flowering Agave Using Two Sampling Techniques
Julie A. Zeyzus[1], Daniel E. Sanchez[2], Emma L. Federman[2], Kristen M. Lear[3], Heather F. Sahli[1] and Faith M. Walke[r2]
1 Department of Biology, Shippensburg University, Shippensburg, USA; 2 Bat Ecology and Genetics Lab, School of Forestry and Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, USA; 3 Bat Conservation International, Austin, USA

Using environmental DNA (eDNA) to identify the genetic material of organisms in the environment is an emerging method for assessing species presence. This method can be used to detect plant pollinators by collecting contact locations then extracting and amplifying the DNA. We developed a collection protocol and a quantitative Polymerase Chain Reaction (qPCR) assay to detect the presence of the federally listed, and IUCN endangered Mexican long-nosed bat (*Leptonycteris nivalis*) at flowering *Agave havardiana* within a known foraging area of Big Bend National Park, Texas. We monitored *A. havardiana* using infrared camcorders and auxiliary infrared lights to capture *L. nivalis* flower visitation. At known contact areas to Agave flowers, we tested two sample collection techniques, flower removal (n = 26) and flower swabbing (n = 20), then applied the new assay for eDNA detection of *L. nivalis* to confirm presence. *Leptonycteris nivalis* DNA was detected on 74% of the 46 total samples collected between 26 June and 19 July 2021. Of the positive detections, the flower removal sampling technique resulted in more DNA detections (77%) compared to the flower swabbing technique (70%). However, these preliminary results suggest that both flower removal and flower swabbing are feasible techniques to use for detecting eDNA from *L. nivalis*. From qPCR analysis of eDNA left on *A. havardiana* by *L. nivalis*, we intend to efficiently identify plant-pollinator interactions which can, in turn, contribute to essential conservation and management strategies for both species.

Immunocompetence of *Nyctalus noctula* Females During Gestation
Katerina Zukalova[1], Veronika Seidlova[1], Ulmann Vit[2], Pavlik Ivo[3], Jiri Pikula[1] and Jan Zukal[4]
1 Department of Ecology and Diseases of Zoo Animals, Game, Fish and Bees, University of Veterinary Sciences, Brno, CZE; 2 Public Health Institute Ostrava, Ostrava, CZE; 3 Faculty of Regional Development and International Studies, Mendel University in Brno, Brno, CZE; 4 Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZE

Reproduction is the most energy- and nutrition-demanding period throughout the life of bat females. Daily and seasonal fluctuations of ambient temperature and insect availability strongly affect their foraging activity and reproduction success. These factors are especially pronounced in temperate bat species as offspring must grow quickly during the short warm season and accumulate resources to survive the winter. However, individual female reproduction success may influence other factors, including parasite and pathogen load. To assess the immunocompetence of 20 female noctule bat *Nyctalus noctula* during pregnancy we evaluated the presence of mycobacteria in fecal samples using three different methods, i.e., direct microscopy after Ziehl-Neelsen staining, culture examination, and qPCR. The majority of females were positively tested for mycobacteria presence (90%) at least once but two females were negative during all study periods. The prevalence of mycobacteria shading changed during the pregnancy with the highest rate in two periods, i.e., after the hibernation and shortly before the parturition. The pattern of prevalence changes differed between females with twins and singletons and it was influenced by the food freshness. At the same time, the severity of infection (copies/mL DNA of NTM) increased during the course of pregnancy but the female *N. noctula* were able to cope with mycobacteria.

Pluripotent Stem Cells Provide a New Framework for Studying Bat Biology
Thomas Zwaka
Department of Cell, Developmental and Regenerative Biology, Icahn School of Medicine at Mount Sinai, New York, USA

Bats have evolved properties that are unique among mammals, but no comprehensive cellular models of bats have yet been developed, limiting our capacity to learn more about their unique biology. In order to establish bats as a novel model study species, we used a modified Yamanaka technique to create induced pluripotent stem cells (iPSCs) from a wild greater horseshoe bat (*Rhinolophus ferrumequinum*). BiPS cells (bat induced pluripotent stem cells) were shown to be stable in culture, capable of differentiating into all three germ layers, and forming complex embryoid bodies, which included organoids. They were found to have a core pluripotency gene expression program that was comparable to that of other

species, but they also exhibited molecular characteristics that were distinct from those of any other stem cell isolated from other species. Furthermore, we assessed the broader applicability of our protocol by creating iPS cells from the evolutionary distant bat species, *Myotis myotis* (greater mouse-eared bat), which was non-lethally sampled in the wild and exhibited characteristics that were similar to those of the greater horseshoe bat iPS cells, indicating that this unique pluripotent state evolved in the ancestral bat lineage. Bat induced pluripotent stem cells (iPS cells) and their differentiated progeny should advance our understanding of the role bats play as virus hosts and allow for the functional studies required to determine the molecular basis of bats' unique characteristics.

Noctule Females Optimize Their Investment in the Litter Size

Katerina Zukalova[1], Veronika Seidlova[1], Vladimir Piacek[1], Monika Nemcova[1], Michal Pribyl[1], Jiri Pikula[1] and *Jan Zukal[2]
1 Department of Ecology and Diseases of Zoo Animals, Game, Fish and Bees, University of Veterinary Sciences, Brno, CZE; 2 Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, CZE

The success of animal reproduction is impacted by a trade-off between energetic costs and mortality associated with immediate vs. future reproductive attempts. The reproductive strategies of European insectivorous bats differ from common mammalian standards due to the use of delayed fertilization. Phenology of bat reproduction is influenced also by ecological conditions. To assess factors influencing the course of pregnancy we evaluated levels of blood progesterone in 20 female noctule bats *Nyctalus noctula*. The bats were individually tagged and randomly divided into two groups with different hibernation ending points (i.e., a control group vs. a treatment group with a week longer hibernation). Following emergence from hibernation, the bats were kept in a wooden box at a stable temperature of 22 °C. The majority of females gave birth to a single neonate (65%) but one female aborted her pups two days before the first successful births of other females. Based on development of progesterone concentration, we were able to define a number of different reproduction strategies, i.e., females with single offspring or twins, and females with supposed resorption of one embryo (embryonic mortality after implantation of the developing fertilized egg). Length of gestation differed significantly between the two groups, with the longer hibernation (treatment) group having a roughly two-day shorter gestation period. We may conclude. that female *N. noctula* are able to manipulate their litter size to balance immediate and future reproduction success. The estimated gestation length of approx. Forty-nine days appears to be standard for *N. noctula*, with females optimizing their thermoregulatory behavior to keep the length of gestation as close to the standard as possible.