

BIBLIOGRAFÍA

- Agnarsson, I., Zambrana-Torrel, C. M., Flores-Saldana, N. P., & May-Collado, L. J. (2011). A time-calibrated species-level phylogeny of bats (Chiroptera, Mammalia). *PLoS Currents*, 3, RRN1212. <https://doi.org/10.1371/currents.RRN1212>
- Alpizar, P., Risely, A., Tschapka, M., & Sommer, S. (2021). Agricultural Fast Food: Bats Feeding in Banana Monocultures Are Heavier but Have Less Diverse Gut Microbiota. *Frontiers in Ecology and Evolution*, 9. <https://www.frontiersin.org/articles/10.3389/fevo.2021.746783>
- Avena, C. V., Parfrey, L. W., Leff, J. W., Archer, H. M., Frick, W. F., Langwig, K. E., Kilpatrick, A. M., Powers, K. E., Foster, J. T., & McKenzie, V. J. (2016). Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. *Frontiers in Microbiology*, 7. <https://doi.org/10.3389/fmicb.2016.01753>
- Ball, H. C., levari-Shariati, S., Cooper, L. N., & Aliani, M. (2018). Comparative metabolomics of aging in a long-lived bat: Insights into the physiology of extreme longevity. *PLOS ONE*, 13(5), e0196154. <https://doi.org/10.1371/journal.pone.0196154>
- Burgin, C. J., Colella, J. P., Kahn, P. L., & Upham, N. S. (2018). How many species of mammals are there? *Journal of Mammalogy*, 99(1), 1-14. <https://doi.org/10.1093/jmammal/gyx147>
- Carrillo-Araujo, M., Taş, N., Alcántara-Hernández, R. J., Gaona, O., Schondube, J. E., Medellín, R. A., Jansson, J. K., & Falcón, L. I. (2015). Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. *Frontiers in Microbiology*, 6. <https://doi.org/10.3389/fmicb.2015.00447>
- Castillo-Figueroa, D. (2020). Why bats matters: A critical assessment of bat-mediated ecological processes in the Neotropics. *European Journal of Ecology*, 6(1), 77-101. <https://doi.org/10.17161/euroj ecol.v6i1.13824>
- Cawthen, L. (2014). *A preliminary survey of the bats of King Island* (BirdLife Technical Report).
- Cláudio, V. C., Gonzalez, I., Barbosa, G., Rocha, V., Moratelli, R., & Rassy, F. (2018). Bacteria richness and antibiotic-resistance in bats from a protected area in the Atlantic Forest of Southeastern Brazil. *PLOS ONE*, 13(9), e0203411. <https://doi.org/10.1371/journal.pone.0203411>
- Cusick, J. A., Wellman, C. L., & Demas, G. E. (2021). The call of the wild: Using non-model systems to investigate microbiome-behaviour relationships. *Journal of Experimental Biology*, 224(10), jeb224485. <https://doi.org/10.1242/jeb.224485>
- Dietrich, M., & Markotter, W. (2019). Studying the microbiota of bats: Accuracy of direct and indirect samplings. *Ecology and Evolution*, 9(4), 1730-1735. <https://doi.org/10.1002/ece3.4842>
- Edenborough, K. M., Mu, A., Mühldorfer, K., Lechner, J., Lander, A., Bokelmann, M., Couacy-Hymann, E., Radonic, A., & Kurth, A. (2020). Microbiomes in the insectivorous bat species *Mops condylurus* rapidly converge in captivity. *PLOS ONE*, 15(3), e0223629. <https://doi.org/10.1371/journal.pone.0223629>
- Eisenhofer, R., Minich, J. J., Marotz, C., Cooper, A., Knight, R., & Weyrich, L. S. (2019). Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. *Trends in Microbiology*, 27(2), 105-117. <https://doi.org/10.1016/j.tim.2018.11.003>

- Foo, J. L., Ling, H., Lee, Y. S., & Chang, M. W. (2017). Microbiome engineering: Current applications and its future. *Biotechnology Journal*, 12(3), 1600099. <https://doi.org/10.1002/biot.201600099>
- Forsythe, A., Fontaine, N., Bissonnette, J., Hayashi, B., Insuk, C., Ghosh, S., Kam, G., Wong, A., Lausen, C., Xu, J., & Cheeptham, N. (2022). Microbial isolates with Anti-Pseudogymnoascus destructans activities from Western Canadian bat wings. *Scientific Reports*, 12(1), 9895. <https://doi.org/10.1038/s41598-022-14223-9>
- Ghosh, S., Kuisiene, N., & Cheeptham, N. (2017). The cave microbiome as a source for drug discovery: Reality or pipe dream? *Biochemical Pharmacology*, 134, 18-34. <https://doi.org/10.1016/j.bcp.2016.11.018>
- Grisnik, M., Bowers, O., Moore, A. J., Jones, B. F., Campbell, J. R., & Walker, D. M. (2020). The cutaneous microbiota of bats has in vitro antifungal activity against the white nose pathogen. *FEMS Microbiology Ecology*, 96(2), fiz193. <https://doi.org/10.1093/femsec/fiz193>
- Hoyt, J. R., Cheng, T. L., Langwig, K. E., Hee, M. M., Frick, W. F., & Kilpatrick, A. M. (2015). Bacteria Isolated from Bats Inhibit the Growth of Pseudogymnoascus destructans, the Causative Agent of White-Nose Syndrome. *PLOS ONE*, 10(4), e0121329. <https://doi.org/10.1371/journal.pone.0121329>
- Ingala, M. R., Becker, D. J., Bak Holm, J., Kristiansen, K., & Simmons, N. B. (2019). Habitat fragmentation is associated with dietary shifts and microbiota variability in common vampire bats. *Ecology and Evolution*, 9(11), 6508-6523. <https://doi.org/10.1002/ece3.5228>
- Ingala, M. R., Simmons, N. B., & Perkins, S. L. (2018). Bats Are an Untapped System for Understanding Microbiome Evolution in Mammals. *MSphere*, 3(5), e00397-18. <https://doi.org/10.1128/mSphere.00397-18>
- Ingala, M. R., Simmons, N. B., Wultsch, C., Krampis, K., Speer, K. A., & Perkins, S. L. (2018). Comparing Microbiome Sampling Methods in a Wild Mammal: Fecal and Intestinal Samples Record Different Signals of Host Ecology, Evolution. *Frontiers in Microbiology*, 9. <https://www.frontiersin.org/articles/10.3389/fmicb.2018.00803>
- Jones, D. N., Ravelomanantsoa, N. A. F., Yeoman, C. J., Plowright, R. K., & Brook, C. E. (2022). Do gastrointestinal microbiomes play a role in bats' unique viral hosting capacity? *Trends in Microbiology*, 30(7), 632-642. <https://doi.org/10.1016/j.tim.2021.12.009>
- Karczewski, K. J., & Snyder, M. P. (2018). Integrative omics for health and disease. *Nature Reviews Genetics*, 19(5), 299-310. <https://doi.org/10.1038/nrg.2018.4>
- Kunz, T. H., Braun de Torrez, E., Bauer, D., Lobova, T., & Fleming, T. H. (2011). Ecosystem services provided by bats: Ecosystem services provided by bats. *Annals of the New York Academy of Sciences*, 1223(1), 1-38. <https://doi.org/10.1111/j.1749-6632.2011.06004.x>
- Lemieux-Labonté, V., Tromas, N., Shapiro, B. J., & Lapointe, F.-J. (2016). Environment and host species shape the skin microbiome of captive neotropical bats. *PeerJ*, 4, e2430. <https://doi.org/10.7717/peerj.2430>

Liu, Y.-X., Qin, Y., Chen, T., Lu, M., Qian, X., Guo, X., & Bai, Y. (2021). A practical guide to amplicon and metagenomic analysis of microbiome data. *Protein & Cell*, 12(5), 315-330. <https://doi.org/10.1007/s13238-020-00724-8>

Mardis, E. R. (2017). DNA sequencing technologies: 2006–2016. *Nature Protocols*, 12(2), 213-218. <https://doi.org/10.1038/nprot.2016.182>

McKenzie, V. J., Song, S. J., Delsuc, F., Prest, T. L., Oliverio, A. M., Korpita, T. M., Alexiev, A., Amato, K. R., Metcalf, J. L., Kowalewski, M., Avenant, N. L., Link, A., Di Fiore, A., Seguin-Orlando, A., Feh, C., Orlando, L., Mendelson, J. R., Sanders, J., & Knight, R. (2017). The Effects of Captivity on the Mammalian Gut Microbiome. *Integrative and Comparative Biology*, 57(4), 690-704. <https://doi.org/10.1093/icb/ix090>

Medellín, R., & Viquez-R, L. (2014). Los murciélagos como bioindicadores de la perturbación ambiental. En *Bioindicadores: Guardianes de nuestro futuro ambiental* (1.a ed., pp. 521-539).

Mehl, C., Schoeman, M. C., Sanko, T. J., Bezuidenhout, C., Mienie, C. M. S., Preiser, W., & Vosloo, D. (2021). Wastewater treatment works change the intestinal microbiomes of insectivorous bats. *PLOS ONE*, 16(3), e0247475. <https://doi.org/10.1371/journal.pone.0247475>

Moreno-Indias, I., Lahti, L., Nedyalkova, M., Elbere, I., Roshchupkin, G., Adilovic, M., Aydemir, O., Bakir-Gungor, B., Santa Pau, E. C., D'Elia, D., Desai, M. S., Falquet, L., Gundogdu, A., Hron, K., Klammersteiner, T., Lopes, M. B., Marcos-Zambrano, L. J., Marques, C., Mason, M., ... Claesson, M. J. (2021). Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. *Frontiers in Microbiology*, 12. <https://www.frontiersin.org/articles/10.3389/fmicb.2021.635781>

Namkung, J. (2020). Machine learning methods for microbiome studies. *Journal of Microbiology*, 58(3), 206-216. <https://doi.org/10.1007/s12275-020-0066-8>

Park, K. J. (2015). Mitigating the impacts of agriculture on biodiversity: Bats and their potential role as bioindicators. *Mammalian Biology*, 80(3), 191-204. <https://doi.org/10.1016/j.mambio.2014.10.004>

Phillips, C. D., Phelan, G., Dowd, S. E., McDONOUGH, M. M., Ferguson, A. W., Delton Hanson, J., Siles, L., Ordóñez-Garza, N., San Francisco, M., & Baker, R. J. (2012). Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. *Molecular Ecology*, 21(11), 2617-2627. <https://doi.org/10.1111/j.1365-294X.2012.05568.x>

Presley, S. J., Graf, J., Hassan, A. F., Sjodin, A. R., & Willig, M. R. (2021). Effects of Host Species Identity and Diet on the Biodiversity of the Microbiota in Puerto Rican Bats. *Current Microbiology*, 78(9), 3526-3540. <https://doi.org/10.1007/s00284-021-02607-5>

Russo, D., & Ancillotto, L. (2015). Sensitivity of bats to urbanization: A review. *Mammalian Biology*, 80(3), 205-212. <https://doi.org/10.1016/j.mambio.2014.10.003>

Russo, D., Salinas-Ramos, V. B., Cistrone, L., Smeraldo, S., Bosso, L., & Ancillotto, L. (2021). Do We Need to Use Bats as Bioindicators? *Biology*, 10(8), 693. <https://doi.org/10.3390/biology10080693>

Sakoui, S., Derdak, R., Addoum, B., Serrano-Delgado, A., Soukri, A., & El Khalfi, B. (2020). The Life Hidden Inside Caves: Ecological and Economic Importance of Bat Guano. *International Journal of Ecology*, 2020, 1-7. <https://doi.org/10.1155/2020/9872532>

Salazar-Hamm, P. S., Hathaway, J. J. M., Winter, A. S., Caimi, N. A., Buecher, D. C., Valdez, E. W., & Northup, D. E. (2022). Great diversity of KS α sequences from bat-associated microbiota suggests novel sources of uncharacterized natural products. *FEMS Microbes*, 3, xtac012. <https://doi.org/10.1093/femsmc/xtac012>

Song, S. J., Sanders, J. G., Delsuc, F., Metcalf, J., Amato, K., Taylor, M. W., Mazel, F., Lutz, H. L., Winker, K., Graves, G. R., Humphrey, G., Gilbert, J. A., Hackett, S. J., White, K. P., Skeen, H. R., Kurtis, S. M., Withrow, J., Braile, T., Miller, M., ... Knight, R. (2020). Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. *mBio*, 11(1), e02901-19. <https://doi.org/10.1128/mBio.02901-19>

Stulberg, E., Fravel, D., Proctor, L. M., Murray, D. M., LoTempio, J., Chrisey, L., Garland, J., Goodwin, K., Graber, J., Harris, M. C., Jackson, S., Mishkind, M., Porterfield, D. M., & Records, A. (2016). An assessment of US microbiome research. *Nature Microbiology*, 1(1), 15015. <https://doi.org/10.1038/nmicrobiol.2015.15>

Trevelline, B. K., Fontaine, S. S., Hartup, B. K., & Kohl, K. D. (2019). Conservation biology needs a microbial renaissance: A call for the consideration of host-associated microbiota in wildlife management practices. *Proceedings of the Royal Society B: Biological Sciences*, 286(1895), 20182448. <https://doi.org/10.1098/rspb.2018.2448>

Wang, Q., Wang, K., Wu, W., Giannoulatou, E., Ho, J. W. K., & Li, L. (2019). Host and microbiome multi-omics integration: Applications and methodologies. *Biophysical Reviews*, 11(1), 55-65. <https://doi.org/10.1007/s12551-018-0491-7>

Yarlagadda, K., Razik, I., Malhi, R. S., & Carter, G. G. (2021). Social convergence of gut microbiomes in vampire bats. *Biology Letters*, 17(11), 20210389. <https://doi.org/10.1098/rsbl.2021.0389>