

Asterophryinae Microbiome Bibliography

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Skin Microbiome

Belden, L. K., Hughey, M. C., Rebollar, E. A., Umile, T. P., Loftus, S. C., Burzynski, E. A., Minbiole, K. P. C., House, L. L., Jensen, R. V., Becker, M. H., Walke, J. B., Medina, D., Ibanez, R., & Harris, R. N. (2015). Panamanian frog species host unique skin bacterial communities [Article]. *FRONTIERS IN MICROBIOLOGY*, 6. <https://doi.org/10.3389/fmicb.2015.01171>

- Overall, our field survey data suggest that different bacterial communities might be producing broadly similar sets of metabolites across frog hosts and sites. Community structure and function may not be as tightly coupled in these skin symbiont microbial systems as it is in many macro systems. Bierlich, K. C., Miller, C., DeForce, E., Friedlaender, A. S., Johnston, D. W., & Apprill, A. (2018). Temporal and regional variability in the skin microbiome of humpback whales along the western antarctic peninsula. *Applied and Environmental Microbiology*, 84(5), e02574–17. <https://doi.org/10.1128/AEM.02574-17>
- Humpback Whale study about seasonal changes with skin microbiome. Calf to Mother interaction. Microbial diversity increases during foraging season.

Callewaert, C., Ravard Helffer, K., & Lebaron, P. (2020). Skin microbiome and its interplay with the environment. *American Journal of Clinical Dermatology*, 21, 4–11.

- sequencing, bioinformatics, and multidisciplinary research are transforming our understanding of skin-associated microbial communities across diverse environments and species. It explores how microbes colonize the skin of humans, large mammals like humpback whales, and aquatic organisms, while emphasizing the influence of environmental factors such as water and air.

Larsen, A., Tao, Z., Bullard, S. A., & Arias, C. R. (2013). Diversity of the skin microbiota of fishes: Evidence for host species specificity. *FEMS Microbiology Ecology*, 85, 483–494.

- Skin microbiota of fishes good oints towards host species specificity. extensive detail on cr and sequencing and data analysis of what can be done. interesting concet of the donninant microbiota. discusses seasonal changes.

Kruger, A. (2020). Frog skin microbiota vary with host species and environment but not chytrid infection. *Frontiers in Microbiology*, 11, 1330. <https://doi.org/10.3389/fmicb.2020.01330>

- frog skin microbiota vary by host species and environment, but not chytrid infection, highlighting the role of microbial composition in disease dynamics and resistance.

McCormack, J. E., Rodriguez-Gomez, F., Tsai, W. L. E., Faircloth, B. C., & Weckstein, J. D. (2018). Transforming museum specimens into genomic resources. In M. S. Webster (Ed.), *The extended specimen: Emerging frontiers in collections-based ornithological research* (p. 14). Taylor & Francis. <https://doi.org/10.1201/9781315120454>

- Skin microbiome study using feather tip and preserved skin, slight destructive sampling on museum sample. Focused on western scrub jays. Used SNPs. Proved sampling can be long term success in museum samples.

Sylvain, F.-É., Holland, A., Bouslama, S., Audet-Gilbert, Émie, Lavoie, C., Val, A. L., & Derome, N. (2020). Fish skin and gut microbiomes show contrasting signatures of host species and habitat. *Applied and Environmental Microbiology*, 86(16), e00789–20. <https://doi.org/10.1128/AEM.00789-20>

- gut microbiome of teleost fish is shaped by species-specific factors, while the skin mucus microbiome is more influenced by environmental conditions, making it a potential biomarker for ecosystem changes.

Tarnecki, A., Tao, Z., & Arias, C. (2013). Diversity of the skin microbiota of fishes: Evidence for host species specificity. *FEMS Microbiology Ecology*, 85. <https://doi.org/10.1111/1574-6941.12136>

- The study found that the skin microbiota of fish is highly species-specific, with Proteobacteria being the most abundant group. Certain bacteria, like Aeribacillus, were common across all species, while others, such as Neorickettsia and Microbacterium, were unique to specific fish species.

Zheng, Y., Shi, J., Chen, Q., Deng, C., Yang, F., & Wang, Y. (2022). Identifying individual-specific microbial DNA fingerprints from skin microbiomes. *FRONTIERS IN MICROBIOLOGY*, 13. <https://doi.org/10.3389/fmicb.2022.960043>

- Human study ID's individual-specific microbial DNA fingerprints from skin microbiomes using metagenomic sequencing data. These fingerprints are stable over time, independent of body site, and can accurately identify donors with 89.78% accuracy. The analysis revealed that 10 out of 12 individual-specific fingerprints could be aligned to Cutibacterium acnes, proving the potential of these microbial markers for personal identification.

Skowron, K., Bauza-Kaszewska, J., Kraszewska, Z., Wiktorczyk-Kapischke, N., Grudlewska-Buda, K., Kwiecińska-Piróg, J., Walecka-Zacharska, E., Radtke, L., & Gospodarek-Komkowska, E. (2021). Human skin microbiome: Impact of intrinsic and extrinsic factors on skin microbiota. *Microorganisms*, 9.

- study of human skin microbiome in maintaining skin health, emphasizing how its complex microbial community—including bacteria, fungi, viruses, archaea, mites, and phages—interacts with the immune system and responds to internal and external environmental factors. It highlights the impact of microbiome imbalances (dysbiosis) on skin diseases, discusses molecular identification techniques for studying these microorganisms, and underscores the broader systemic consequences of skin microbiome disturbances beyond dermatological conditions

Environmental Factors - Skin Microbiome

Hughey, M. C., Pena, J. A., Reyes, R., Medina, D., Belden, L. K., & Burrowes, P. A. (2017). Skin bacterial microbiome of a generalist puerto rican frog varies along elevation and land use gradients [Article]. *PEERJ*, 5. <https://doi.org/10.7717/peerj.3688>

- Skin microbiome of *Elutherodactylus coqui* along an altitudinal gradient and two land use categories (intact forest vs. disturbed forest). Alpha diversity varied but not with altitude nor land use. Beta diversity (community structure), varied with site, elevation and land use, primarily due to changes in the relative abundance of certain bacterial OTUs.

Ellison, S., Rovito, S., Parra-Olea, G., Vasquez-Almazan, C., Flechas, S. V., Bi, K., & Vredenburg, V. T. (2019). The influence of habitat and phylogeny on the skin microbiome of amphibians in guatemala and mexico [Article]. *MICROBIAL ECOLOGY*, 78(1), 257–267. <https://doi.org/10.1007/s00248-018-1288-8>

- Compared skin microbiome of 2 genera of plethodontid salamander and 1 genus of frogs in montane Mexico and Guatemala. phylogenetic history strongly influences the diversity and community structure of the total bacterial microbiome (between orders), but on lower scales (within genera and species), the effect of habitat predominates. Growing consensus that habitat exerts a strong effect on microbiome structure and composition, particularly at shallow phylogenetic scales.

Gajewski, Z., Johnson, L. R., Medina, D., Crainer, W. W., Nagy, C. M., & Belden, L. K. (2023). Skin bacterial community differences among three species of co-occurring ranid frogs [Article]. *PEERJ*, 11. <https://doi.org/10.7717/peerj.15556>

- Host and environmental factors in 3 species of sympatric ranid frogs. Skin swabs from tadpoles and adults. 16S bacterial communities change across developmental stage, found

microbiome communities from skin of frogs in streams or bogs differed from terrestrial. Effect of habitat use on host-associated microbiome.

Garcia-Recinos, L., Burrowes, P. A., & Dominguez-Bello, M. (2019). The skin microbiota of *eleutherodactylus* frogs: Effects of host ecology, phylogeny, and local environment [Article]. *FRONTIERS IN MICROBIOLOGY*, 10. <https://doi.org/10.3389/fmicb.2019.02571>

- Elutherodactylus frogs skin microbiome hypothesized to be mostly related to microhabitat use but differ by locality. Sequenced V4 region of 16S rRNA gene. Locality had greatest effect on composition (presence/absence) rather than structure (abundance). But some suggestion that ecological disparity translates into differences in microbiome.

Barcoding with MinION

Srivathsan, A., Lee, L., Katoh, K., Hartop, E., Kutty, S. N., Wong, J., Yeo, D., & Meier, R. (2021). ONTbarcoder and MinION barcodes aid biodiversity discovery and identification by everyone, for everyone [Article]. *BMC BIOLOGY*, 19(1). <https://doi.org/10.1186/s12915-021-01141-x>

Vasilita, C., Feng, V., Hansen, A. K., Hartop, E., Srivathsan, A., Struijk, R., & Meier, R. (2024). Express barcoding with NextGenPCR and MinION for species-level sorting of ecological samples [Article]. *MOLECULAR ECOLOGY RESOURCES*, 24(3). <https://doi.org/10.1111/1755-0998.13922>

Gut Microbiome

Chalifour, B. N., Elder, L. E., & Li, J. (2022). Gut microbiome of century-old snail specimens stable across time in preservation. *Microbiome*, 10(1), 99. <https://doi.org/10.1186/s40168-022-01286-z>

- Century old specimen successful gutmicrobe extraction w/o destructive sampling. Methods:
- Alcohol specimens. No problem obtaining gut microbiome from century old snail specimens, but they were never formalin fixed.
- Location of collection more sig factor in gut microbiome composition of communities than what era snail came from (didn't compare species to species). "The effects of decades-long museum preservation on host-microbial communities have not been systematically assessed."

##Formalin Fixed Sample DNA Collection

Ramesh, G., Katiyar, A., Sujatha, R., Raj, A., Gupta, B., & Kumar, A. (2017). Detection of microorganisms on formalin-fixed and stored pathology tissues: A microbiological study.

Journal of Oral and Maxillofacial Pathology : JOMFP, 21, 64–69. <https://doi.org/10.4103/0973-029x.203788>

- Successful detect of formalin-fix tissue; destructive sampling; able to successfully sequence.

Museum and Historical DNA

Wandeler, P., Hoeck, P. E. A., & Keller, L. F. (2007). Back to the future: Museum specimens in population genetics. *Trends in Ecology & Evolution*, 22(12), 634–642. <https://doi.org/https://doi.org/10.1016/j.tree.2007.08.017>

- Guidelines for working with degraded DNA from museum specimens, including tips on selecting samples, optimizing extraction methods, and using short PCR amplicons for better amplification. It also suggests sequencing strategies and bioinformatics tools designed to handle fragmented DNA, helping researchers unlock valuable genetic data from older specimens.

Heyn, P., Stenzel, U., Briggs, A. W., Kircher, M., Hofreiter, M., & Meyer, M. (2010). Road blocks on paleogenomes—polymerase extension profiling reveals the frequency of blocking lesions in ancient DNA. *Nucleic Acids Research*, 38, e161–e161. <https://api.semanticscholar.org/CorpusID:11149446>

- Issues with using aDNA. Good methods paper. Look into blocking lesions mentioned because they were able to work around them but I want to understand more there.

Heindler, F. M., Christiansen, H., Frédérick, B., Dettai, A., Lepoint, G., Maes, G. E., Van de Putte, A. P., & Volckaert, F. A. M. (2018). Historical DNA metabarcoding of the prey and microbiome of trematomid fishes using museum samples. *Frontiers in Ecology and Evolution*, 6. <https://doi.org/10.3389/fevo.2018.00151>

- **Gut microbiome and prey identification from fish that have been formalin fixed.** Between 20 and 100 years old. Sequenced cytochrome c oxidase subunit I (COI) 313bp from vertebrates and 16S rRNA from bacteria 450bp but had large dropout rates. Did not keep any COI, but able to characterize microbiomes from **26 samples out of 225 starting samples**.

Madison, B. C. A. W., Joseph D. AND LaBumbard. (2023). Shotgun metagenomics captures more microbial diversity than targeted 16S rRNA gene sequencing for field specimens and preserved museum specimens. *PLOS ONE*, 18(9), 1–18. <https://doi.org/10.1371/journal.pone.0291540>

- Comparison of **16S rRNA gene sequencing** and **short-read shotgun metagenomics** methods for examining museum specimen-associated gut microbiomes.

Raxworthy, C. J., & Smith, B. T. (2021). Mining museums for historical DNA: Advances and challenges in museomics [Doi: 10.1016/j.tree.2021.07.009]. *Trends in Ecology & Evolution*, 36(11), 1049–1060. <https://doi.org/10.1016/j.tree.2021.07.009>

- Review of challenges with and recent advances in obtaining DNA sequence data from historical (museum) specimens.

Hykin, K. A. M., Sarah M. AND Bi. (2015). Fixing formalin: A method to recover genomic-scale DNA sequence data from formalin-fixed museum specimens using high-throughput sequencing. *PLOS ONE*, 10(10), 1–16. <https://doi.org/10.1371/journal.pone.0141579>

- Comparison of DNA sequencing of formalin-fixed *Anolis carolinensis* museum specimens 30 and 100 years old. Used Illumina high throughput sequencing to obtain massive amounts of short reads. Compared liver, leg muscle, and tail tips. Took care to avoid contamination, best yield was from phenol-chloroform protocol. Minimal PCR cycles. Used 100-bp paired-end Illumina sequencing, pooling both samples on one lane of a HiSeq2000. The older sample failed to provide usable data. For the younger sample, nuclear data did not have sufficient read depth, but they were able to get the whole mitochondrial genome (aided by the high copy number).
- Three tissue types subsampled from formalin-fixed specimens of *Anolis carolinensis*, After trimming, successfully mapped 27.93% of the cleaned reads to the reference genome, were able to reconstruct the complete mitochondrial genome, and recovered an accurate phylogenetic placement for our specimen. Conclude amount of DNA available, which can vary depending on specimen age and preservation conditions

Yeates, D. K., Zwick, A., & Mikheyev, A. S. (2016). Museums are biobanks: Unlocking the genetic potential of the three billion specimens in the world’s biological collections. *Current Opinion in Insect Science*, 18, 83–88. <https://doi.org/10.1016/j.cois.2016.09.009>

- One of the earlier papers reviewing the issues with museum specimens as DNA sources. Focuses on the promise of high throughput methods. Short and sweet.

Zimmermann, J., Hajibabaei, M., Blackburn, D. C., Hanken, J., Cantin, E., Posfai, J., & Evans, T. C. (2008). DNA damage in preserved specimens and tissue samples: A molecular assessment. *Frontiers in Zoology*, 5(1), 18. <https://doi.org/10.1186/1742-9994-5-18>

- A sobering accounting of the DNA damage induced by formalin fixation. They assess average fragment length as a function of age, it is around 50-70bp, with younger specimens longer.

Sampaio, F. L., Day, J. J., Mendis Wickramasinghe, L. J., Cyriac, V. P., Papadopoulou, A., Brace, S., Rajendran, A., Simon-Nutbrown, C., Flouris, T., Kapli, P., Ranga Vidanapathirana,

D., Kotharambath, R., Kodandaramaiah, U., & Gower, D. J. (2023). A near-complete species-level phylogeny of uropeltid snakes harnessing historical museum collections as a DNA source. *Molecular Phylogenetics and Evolution*, 178, 107651. <https://doi.org/10.1016/j.ympev.2022.107651>

- Phylogenetic study conducted using uropeltid snakes and hDNA. Able to work with swabs of nondestructive and destructive DNA sampling.

Pääbo, S., Poinar, H., Serre, D., Jaenicke-Despres, V., Hebler, J., Rohland, N., Kuch, M., Krause, J., Vigilant, L., & Hofreiter, M. (2004). Genetic analyses from ancient DNA. *Annual Review of Genetics*, 38, 645–679. <https://doi.org/10.1146/annurev.genet.37.110801.143214>

- ancient DNA vs h DNA and the advances made in detecting both. Application. Parent paper to Zimmermann 2008.

Staats, R. H. J. A. van de V., Martijn AND Erkens. (2013). Genomic treasure troves: Complete genome sequencing of herbarium and insect museum specimens. *PLOS ONE*, 8(7), 1–11. <https://doi.org/10.1371/journal.pone.0069189>

- Using Beetle soaking method found in Heindler, F. M., Christiansen, H., Frédéric, B., Dettai, A., Lepoint, G., Maes, G. E., Van de Putte, A. P., & Volckaert, F. A. M. (2018). Historical DNA metabarcoding of the prey and microbiome of trematomid fishes using museum samples. *Frontiers in Ecology and Evolution*, 6. <https://doi.org/10.3389/fevo.2018.00151>. Detailed how genomic sequencing was used on non-destructive sampling of items and what info was able to be gained off non-destructive/desicated plant samples

Raxworthy, C. J., & Smith, B. T. (2021). Mining museums for historical DNA: Advances and challenges in museomics [Doi: 10.1016/j.tree.2021.07.009]. *Trends in Ecology & Evolution*, 36(11), 1049–1060. <https://doi.org/10.1016/j.tree.2021.07.009>

-hDNA paper concerning advances in genomic studies in museum samples; useful for work cited paper and review summary of where we are somewhat currently

Tin, M. M.-Y., Economo, E. P., & Mikheyev, A. S. (2014). Sequencing degraded DNA from non-destructively sampled museum specimens for RAD-tagging and low-coverage shotgun phylogenetics. *PloS One*, 9, e96793. <https://doi.org/10.1371/journal.pone.0096793>

- Addresses working with degraded DNA using RAD Tag system, helpful for methods should contamination be high

Madison, B. C. A. W., Joseph D. AND LaBumbard. (2023). Shotgun metagenomics captures more microbial diversity than targeted 16S rRNA gene sequencing for field specimens and preserved museum specimens. *PLOS ONE*, 18(9), 1–18. <https://doi.org/10.1371/journal.pone.0291540>

- Shotgun metagenomic to capture microbial diversity in museum specimens that were fixed in formalin, utilized destructive sampling

Helpful guide to format annotated bibliography (or a CV):

Heiss, A. (2023, January 9). *One Simple TrickTM to Create Inline Bibliography Entries with Markdown and Pandoc*. <https://doi.org/10.59350/hwwgk-v9636>