Asterophryinae Microbiome Bibliography

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Skin Microbiome

Gut Microbiome

Environmental Factors

Community

Museum and Historical DNA

Heindler, F. M., Christiansen, H., Frédérich, B., Dettaï, 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-chloriform protcol. 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).

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/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.

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

- Alcohol specimens. No problem obtaining gut microbiome from century old snail specimens, but they were never formalin fixed.

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

Heiss, A. (2023, January 9). *One Simple Trick^{TM} to Create Inline Bibliography Entries with Markdown and Pandoc*. https://doi.org/10.59350/hwwgk-v9636.