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The Role of Microbiota in *Drosophila* Evolution

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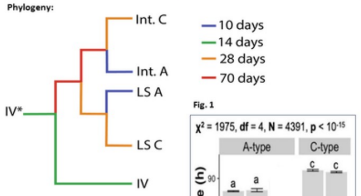
Introduction

- Laboratory selection can lead to phenotypic differentiation among sexual populations through standing genetic variation.
- Past experiments were always missing one large area: microbiota.
- To study the relationship between host and microbiota, we worked with the *Drosophila melanogaster* species of fruit fly.
- Populations are descendants from the Rose populations, originally sampled in Massachusetts in 1975.
- Populations have undergone longevity selection.
  - **A-types:** Our evolved populations with accelerated development cycles of just **10-days.**
  - **C-types:** Our controls with generation cycles of **28 days.**

Background

Phylogeny:



Longstanding (LS) - 23 years
- **Selection Regimes:**
- **A-type: ACOs**
- **C-type: COs**

Intermediate (Int.) - 5-7 years
- **Selection Regimes:**
- **A-type: AOs**
- **C-type: nCOs**

Fig. 1

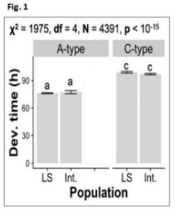
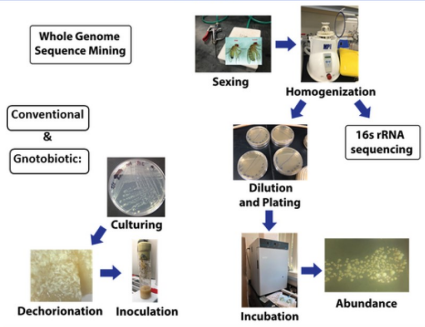


Fig. 1: Shows the difference in development time between A- and C-types. A-types have shorter development times in general.

Hypothesis

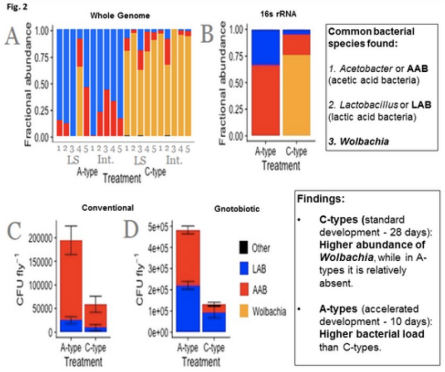
- **Populations selected for faster development become differentiated from founder populations in both development time and microbiota composition.**

Methods



Results

Fig. 2



Common bacterial species found:

1. *Acetobacter* or **AAB** (acetic acid bacteria)
2. *Lactobacillus* or **LAB** (lactic acid bacteria)
3. ***Wolbachia***

Findings:

- **C-types** (standard development - 28 days): **Higher abundance of *Wolbachia***, while in A-types it is relatively absent.
- **A-types** (accelerated development - 10 days): **Higher bacterial load** than C-types.

Conclusion

Major Finding:

This suggests that **populations do select for microbiota**, and specifically that the A-types are more **open to colonization** by bacteria than C-types are.

Overall Conclusion:

Populations selected for faster development did indeed show significant differences from their founder populations in microbiota composition.

References

Burke, M. K. et al. (2010). Genome-Wide Analysis of a Long-Term Evolution Experiment with *Drosophila*. *Nature, 467(7315):* 587-590, doi:10.1038/nature09352

Graves Jr, J. L. et al. (2017). Genomics of Parallel Experimental Evolution in *Drosophila*. *Molecular Biology and Evolution, 34(4):* 831-842, doi:10.1093/molbev/msw282

Rose, M. R. (1984). Laboratory Evolution of Postponed Senescence in Drosophila melanogaster. *Evolution, 38(5):* 1004-1010, doi:10.1111/j.1558-5646.1984.tb00370.x

Shahrestani et al. (2021). Research Strategy. *Research Grant Proposal Summer 2021*, doi: TBD.

Photo: Anonymous. (December 2009). *Sexing Drosophila*. Retrieved from https://arrogantscientist.wordpress.com/sexing-drosophila/

Prabhune, M. (2019). CRISPR: Drosophila Melanogaster as a Model Organism for Biomedical Research. *Sythego: The Bench*. Retrieved from https://www.synthego.com/blog/crispr-drosophila

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In general, we took different populations of Drosophila melanogaster, each one has undergone various levels of longevity selection and compared their microbial compositions. We had a population whose generation cycle was 28 days, which is the standard, and we had a population with an accelerated generation cycle of just 10 days. The two main bacterial genus' we looked for were Acetobacter and Lactobacillus. All in all, it was found that populations who have undergone different selection pressures will have distinctly different bacterial compositions and/or abundances as well.

Alternate Text:

Alyssa Goldpenny

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Image of Alyssa Goldpenny

Image of text and graphic laden project presentation entitled "The Role of Microbiota in Drosophila Evolution. Alyssa Goldpenny, Courtney Mueller"