

ALYSSA GOLDPENNY



PROJECT RAISE

The Role of Microbiota in *Drosophila* Evolution

Alyssa Goldpenny, Citrus College, Mentor Courtney Mueller,
PI Dr. Parvin Shahrestani, Department of Biological Sciences, California State University, Fullerton

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 1976.
- 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.

Methods

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.

Background

Phylogeny:

Legend:
 - 10 days (blue)
 - 14 days (green)
 - 28 days (orange)
 - 70 days (red)

Fig. 1
 $\chi^2 = 1975, df = 4, N = 4391, p < 10^{-15}$

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

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

Results

Fig. 2

Whole Genome

16s rRNA

Common bacterial species found:

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

Fig. 3

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Hypothesis

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

Acknowledgements

- 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.

References

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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"