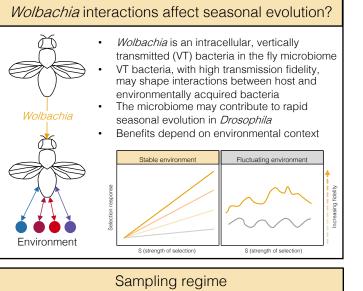
Wolbachia effects on Drosophila microbiome and metabolic phenotypes v

Lucas P. Henry & Julien F. Ayroles Ecology and Evolutionary Biology + Lewis-Sigler Institute @ Princeton Univers

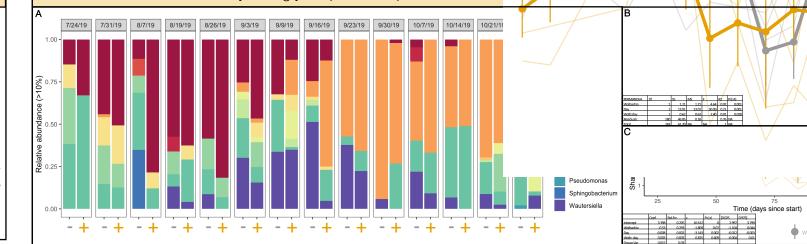
Seasonality strongly shapes Drosophila microbiom



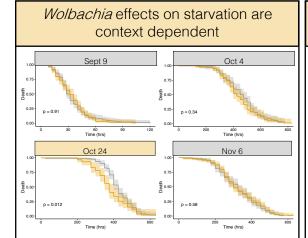


- 4 *Wolbachia* + and 4 *Wolbachia* cages derived from same large, outbred fly population
- Sampled weekly for Wolbachia status and microbiome
- 4X for age-matched flies for metabolic phenotypes
- At the end (~5-6 generations), fecundity + lifespan

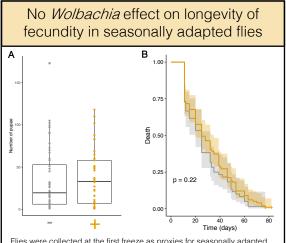




A: Relative abundance of bacteria genera across all time points for W- and W+ cages. Acetobacter increases until Sept, then Commensalibacter dominates. B: PCoA plot for Bray-Curtis distance, colored over season. Each point represents pool of flies. Seasonality strongly shaped betadiversity, with weak Wolbachia effects. C: Volatility plot for change in Shannon diversity differs over time and Wolbachia infection, but there was no significant interaction.



Starvation survival across the four different sampling points. Agematched flies were starved, and then time to death was measured. *Wolbachia* infection status only affected starvation time for Oct 24. Here, W+ flies starved faster than W- flies. This suggests Wolbachia effects are frequently context dependent.



Flies were collected at the first freeze as proxies for seasonally adapted flies. A: *Wolbachia* infection did not affect fecundity (pupae produced per female) for seasonally adapted flies (Kruskal-Wallis X²=0..44, p=0.50). B: *Wolbachia* infection also did not affect longevity. While nearly 25% died in first 15 days, both W+ and W- had similar lifespans (p=0.22).

Conclusions & Future directions

- Seasonality strongly shapes the microbiome
- Wolbachia modulates, but minimal effects on phenotypes
- Fitness benefits will depend on the ecoevolutionary context
- Future directions will focus on additional characterization of microbial variation and metabolomics

Acknowledgements

We acknowledge funding from Princeton University, NIH, and NSF. We thank Michael Fernandez, Elena Filapova, Gordon Gray, and Princeton Facilities for assistance in the field.

