

Eating Cactus Takes Guts

Exploring the contributions of host evolutionary history and diet in shaping the gut microbiota of cactophilic flies

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Background

Gut microbial communities often provide functions that have significant implications for their host's fitness. However, understanding how a host's gut microbiome has been shaped by its evolutionary history can be difficult because **the influence of diet can be lesser than, equal to, or greater than host genetic background.**

Flies in the genus *Drosophila* have been previously used as model systems for understanding various factors pertaining to gut microbial community shape and function. We propose that the various species of **cactophilic *Drosophila* native to North America could be a powerful comparative model system** for discerning the contributions of host evolutionary and diet in shaping host gut microbial communities. In this study, we characterize the bacterial gut microbiome from five cactophilic *Drosophila* species and compare their diversity and composition to *D. melanogaster*.

Questions

Study Design

Compare the gut bacterial communities of generalist and cactus specialist flies across the *D. repleta* species group

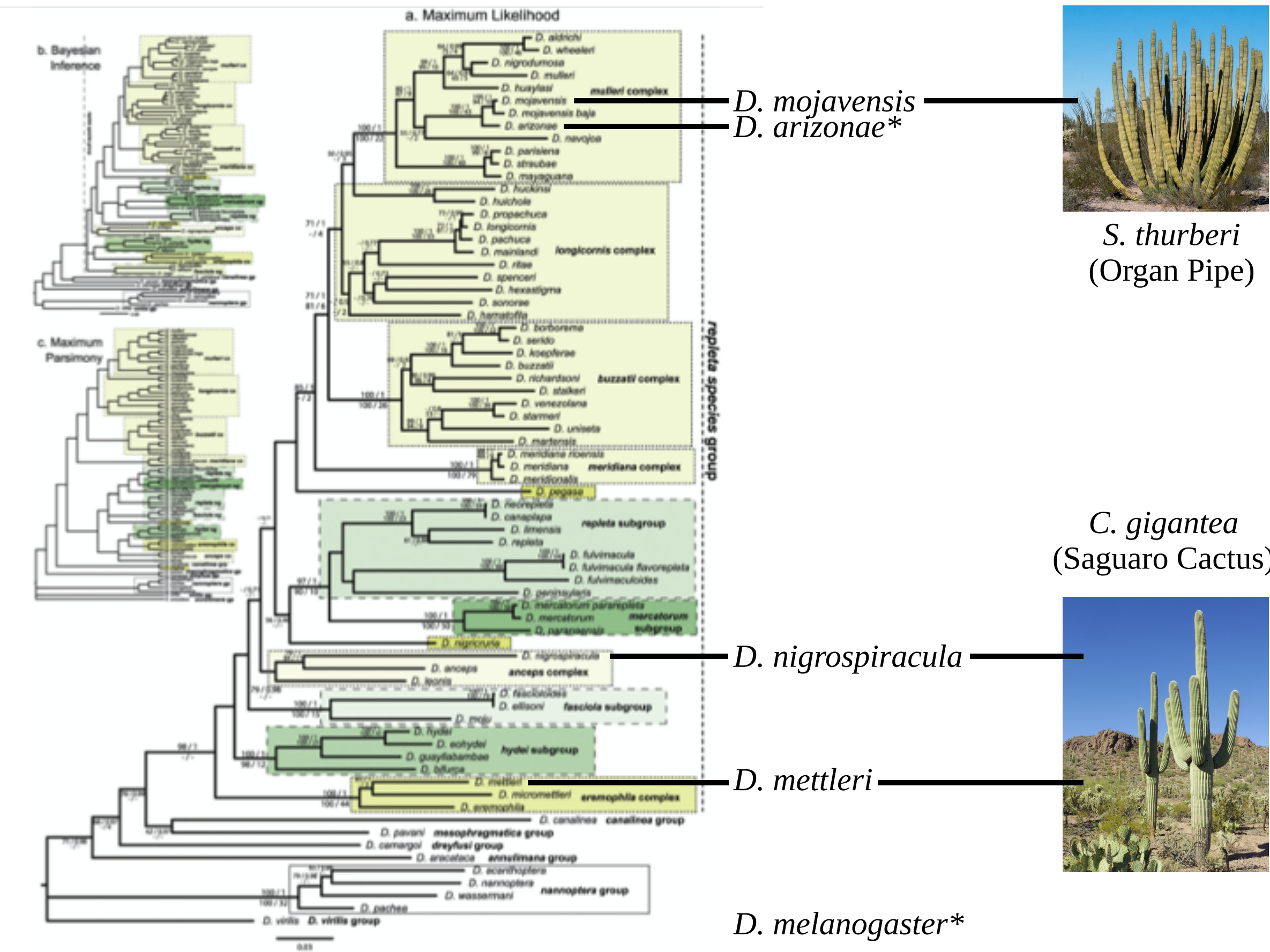


Figure 1: Phylogeny of the *D. repleta* species group (1). Lines indicate the species sampled in this study, as well as the cactus they specialize on. Species marked with an * indicate generalist species.

Alpha-Diversity Comparisons

Generalist flies do not have more diverse bacterial microbiomes

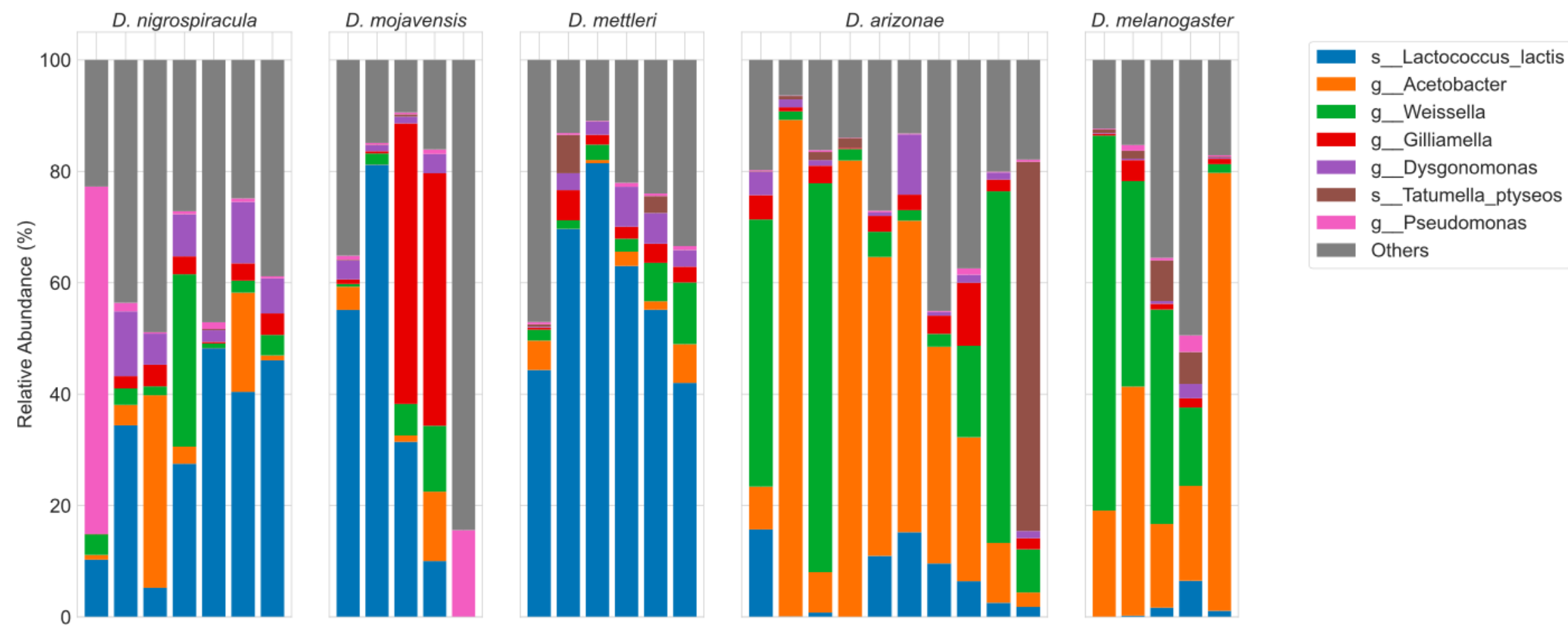


Figure 2: Taxonomy barplot showing the bacterial taxa and their relative abundances in each fly gut microbiome.

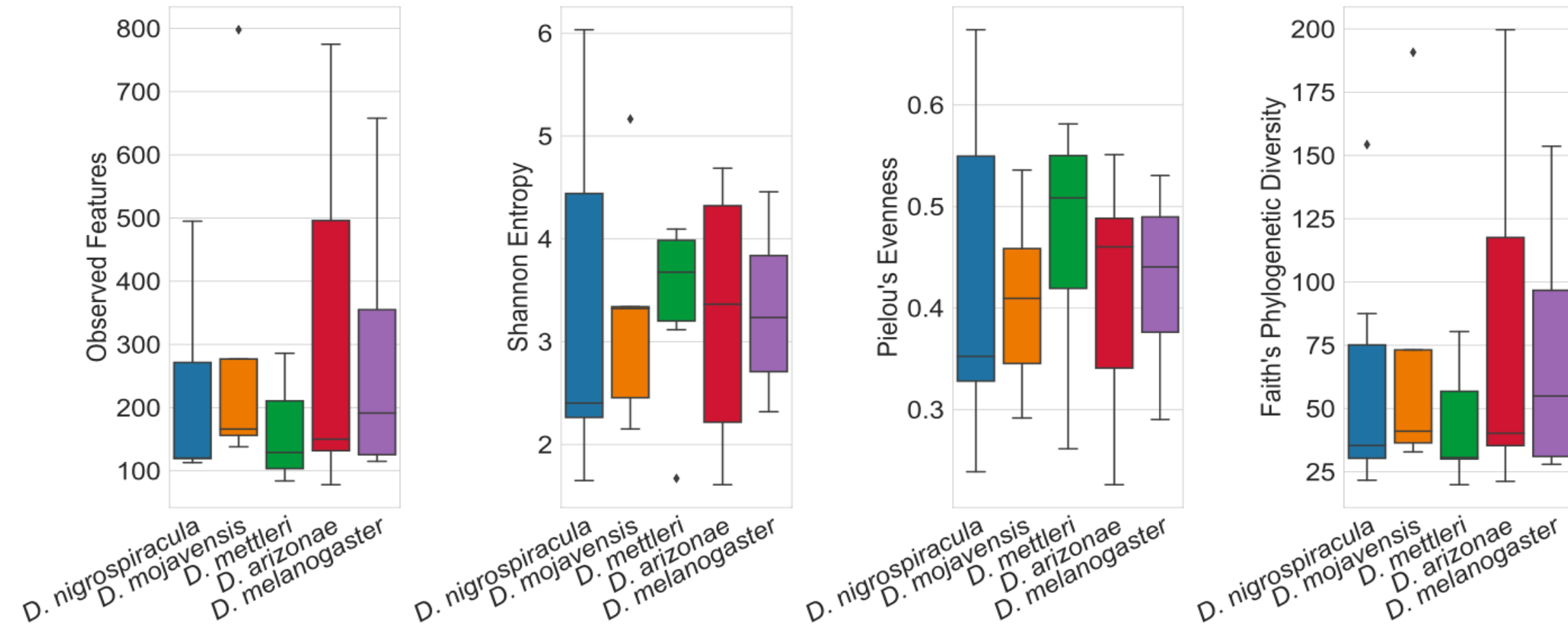


Figure 3: Boxplots showing the alpha-diversity of each fly species using different metrics. No statistically significant differences were observed (KW: p ≥ 0.13)

Beta-Diversity: Compositional and Structural Comparisons

Generalist and specialist fly microbiomes are compositionally similar but structurally distinct

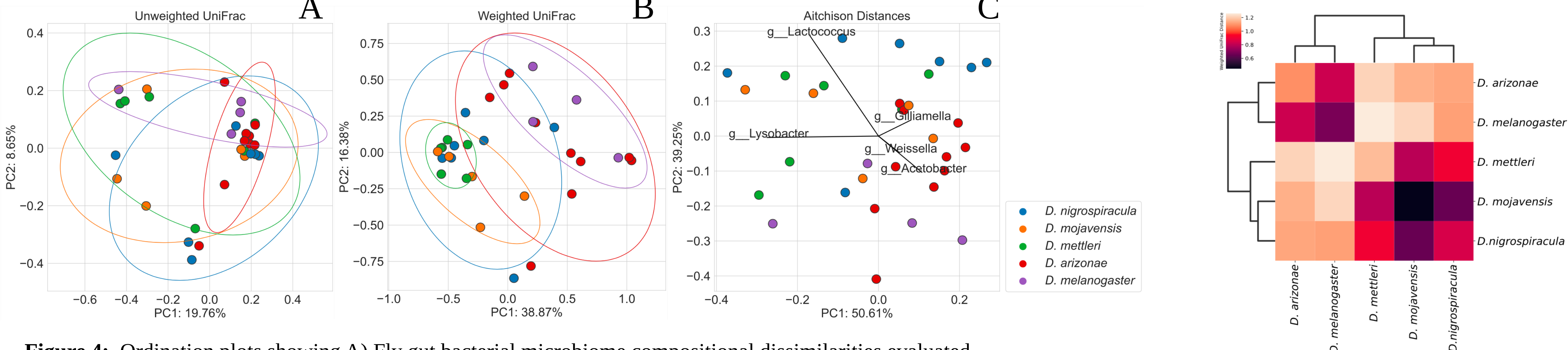


Figure 4: Ordination plots showing A) Fly gut bacterial microbiome compositional dissimilarities evaluated using Unweighted UniFrac distances. No significant differences between any fly species were found (PERMANOVA: p=0.116) B) Fly gut bacterial microbiome structural dissimilarities using weighted UniFrac distances. Significant differences between generalist and specialist flies were found (PERMANOVA: p=0.001, PERMDISP: p=0.086), and pairwise differences are highlighted in figure 5. C) Fly gut bacterial microbiome structural dissimilarities using Aitchison distances. The same significant results were found as described in B (PERMANOVA: p=0.001, PERMDISP: p=0.379). Vectors indicate bacterial taxa that have significant roles in sample clustering.

- Compositional comparisons showed no differences between any fly species
- Strucural comparisons showed differences between generalist and specialist flies

Discussion