

The impact of long-term different dietary regimes on microbiota communities in *Drosophila melanogaster*

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INTRODUCTION & AIM

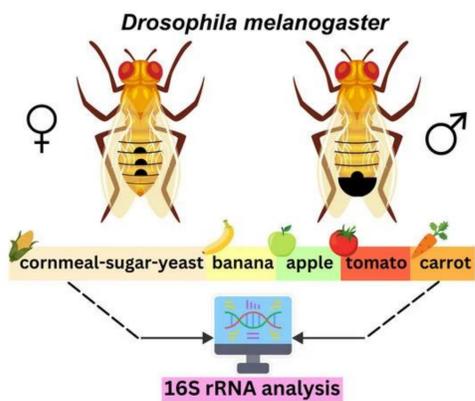
- ✓ *Drosophila* gut microbiota (GM) is critical for host physiology, development, behavior, and overall fitness
- ✓ GM aids nutrient catabolism, immune defense, stress tolerance, longevity, reproduction, and development (1)
- ✓ Laboratory-reared *Drosophila* offers a simplified model (~8 species) compared to wild flies (~30 species), mainly *Proteobacteria* & *Firmicutes* (2)
- ✓ Core genera (*Lactobacillus*, *Acetobacter*) shape gut community, but less common microbes also play key functional roles
- ✓ Lab-maintained GM is largely transient, relying on continuous microbial influx from diet
- ✓ Past studies have mostly explored how **diet composition affects fly fitness and traits** (3), but less is known about **how diet shapes microbiota itself**

👉 **Goal:** Examine how long-term diets shape adult *Drosophila* microbiota and its metabolic potential

Why It Matters

- 🔬 *Drosophila* is a key model organism for studying human disease mechanisms and host-microbe interactions
- 🔗 Understanding diet-microbiota links helps reveal mechanisms on the **nutrition-behavior axis**
- ⚙️ Shows how microbiota complements **host metabolic needs**
- 🌐 Provides insights into **broader principles of symbiosis and microbial community function**

METHODS



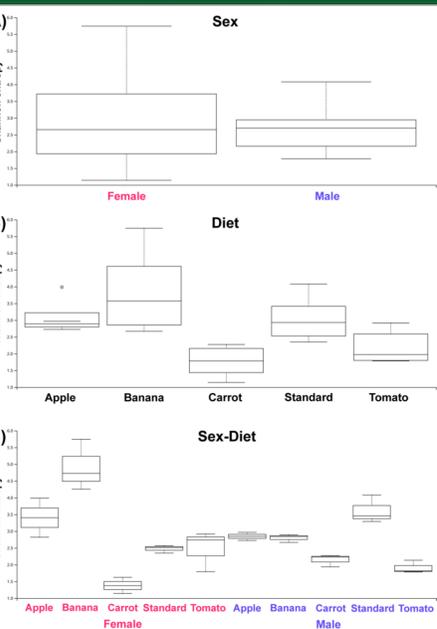
What we did:

- Tested **five diets** → cornmeal, apple, banana, carrot, tomato
- Used **16S rRNA sequencing** → to profile gut microbial communities
- Applied **functional prediction** → to assess microbial metabolic capacity
- Employed **machine learning** → to predict fly diet and sex from microbiota profiles

🏠 **Origin:** Natural population

🏠 **Rearing:** >450 generations under standard laboratory conditions

RESULTS & DISCUSSION



Alpha Diversity Highlights

- ✓ **Sex comparison (A):**
 - Similar diversity in males and females
 - More variation among female samples
- ✓ **Diet comparison (B):**
 - High-sugar diets (banana, standard, apple) → higher microbial diversity
 - Carrot & tomato diets → lower diversity
 - Banana diet shows the highest overall diversity
- ✓ **Sex × Diet (C):**
 - Clear differences across groups
 - Sugar-rich diets boost diversity, especially in females

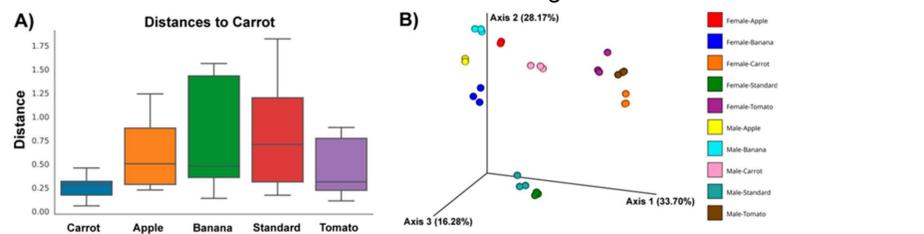
🔗 **Diet has a stronger impact on gut microbiota diversity than sex, with sugar-rich diets driving higher microbial richness, especially in female flies.**

CONCLUSION

- ✓ Sugar-rich diets increase microbial richness, but not overall community performance
- ✓ Core phyla consistent across diets, with varying key family abundances
- ✓ Low-abundance bacterial families differ between diets, adding distinct community signatures
- ✓ Functional predictions point to fermentation as a key metabolic process influenced by diet
- ✓ Diet plays a critical role in shaping microbiota composition and host phenotype interactions

Beta Diversity Highlights

- ✓ **Sex comparison:**
 - No significant differences in microbial composition
- ✓ **Diet comparison (A):**
 - Diet has a strong impact on microbiota composition
 - Carrot diet (C) stands out as most distinct
- ✓ **Sex × Diet (B):**
 - Combined sex and diet grouping shows stronger overall differences
 - Clustering mainly driven by diet, with some sex-based separation
 - Only male & female flies on carrot diet **do not** cluster together



🥕 **Diet** — especially carrot — shapes microbiota composition more than sex, driving distinct community structures across groups.

Taxonomic Composition Highlights

✓ Dominant phyla: **Proteobacteria & Firmicutes**;

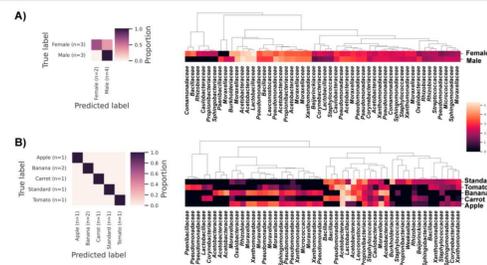
Rare families: *Actinobacteriota*, *Bacteroidota*

✓ **Top families:** *Acetobacteraceae*, *Lactobacillaceae*, *Moraxellaceae*

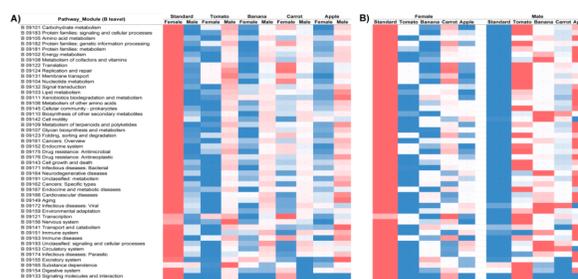
✓ **Key group differences:**

- **A (apple) diet:**
 - Females → mostly *Acetobacteraceae*
 - Males → mostly *Moraxellaceae*, then *Acetobacteraceae*
- **B (banana) diet:**
 - Females → high *Moraxellaceae*
 - Males → dominant *Acetobacteraceae*
- **S (standard) diet:**
 - Both sexes → *Acetobacteraceae* dominant
 - Females → *Burkholderiaceae* next
 - Males → *Propionibacteriaceae* next
- **C (carrot) diet:**
 - Females → *Lactobacillaceae* dominant
 - Males → *Acetobacteraceae* dominant
- **T (tomato) diet:**
 - Females → more *Lactobacillaceae*
 - Males → more *Pseudomonadaceae*

🔗 **Diet shapes which bacterial families dominate, with notable sex-based shifts in community structure across diets.**



🔍 **Machine learning reveals that both major and minor bacterial players contribute to group-specific microbiota patterns, with diet being the strongest differentiator.**



Predictive Features (ML Analysis)

- ✓ **Predictive strength:**
 - **Highest performance:** predicting diet from GM composition
 - **Moderate performance:** predicting sex from GM composition
- ✓ **Key insights:**
 - Distinctive features span both abundant and less abundant bacterial families
 - **Non-core microbes** critically shape fly gut ecosystems

Metabolic Potential Prediction

- Female S-diet microbiota → **high predicted metabolic activity**
- Male S-diet microbiota → **low activity**
- Opposite trend in A, B, T diets (males higher than females)
- C-diet microbiota → most distinct, highest sex-based differences

🔗 **Diet and sex jointly shape the functional capacity of fly microbiota, with unique patterns emerging especially under carrot (C) and standard (S) diets.**

1. Grenier, T.; Leulier, F. *Curr. Opin. Insect Sci.* **2020**, *41*, 92–99.
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3. Wong, A.C.-N.; et al. *J. Exp. Biol.* **2014**, *217*, 1894–1901.