



Effect of larval density of Black Soldier Fly (Diptera: Stratiomyidae) on bacterial succession in diets and larval gut



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Background

Black Soldier Fly larvae (*Hermetia illucens*, BSF) are efficient bioconverters of organic waste, and interact with a complex microbial community. The bacterial community composition varies with waste type (1), but larval feeding can also change bacterial population sizes (2,3).

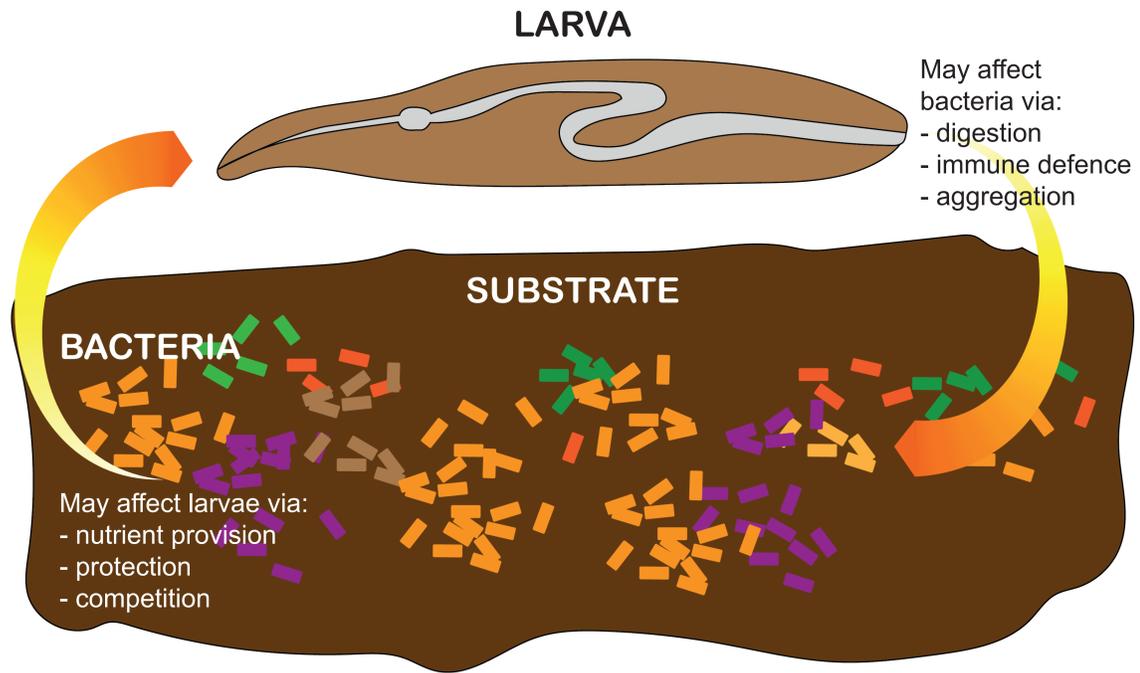
Research question

What is the effect of larval density on bacterial succession in three different diets and the larval gut?

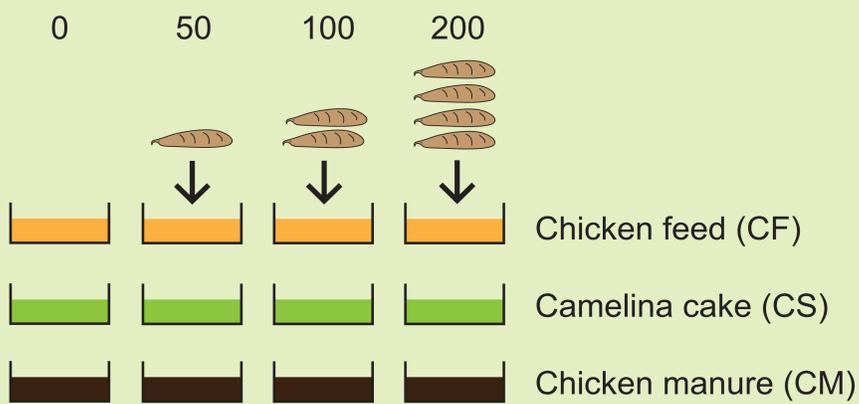
Hypotheses

The effect of larvae on bacterial communities increases with time and larval density. This means that:

1. with increasing larval density, bacterial community composition of substrate is increasingly different from the control without larvae.
2. bacterial community composition of both substrate and larvae converges across diets with increasing larval density.



Methods



12 treatments, 4 replicates each. Sampled total DNA of substrates and larvae at 4 time points. Bacterial 16S rRNA gene (V5-V6) amplicon sequencing, Illumina HiSeq.

Data analyses:

- NG-Tax pipeline
- R microbiome and phyloseq packages
- MDS plots of relative abundance data OTUs
- heatmaps of genera (metagenomeSeq)

Conclusions

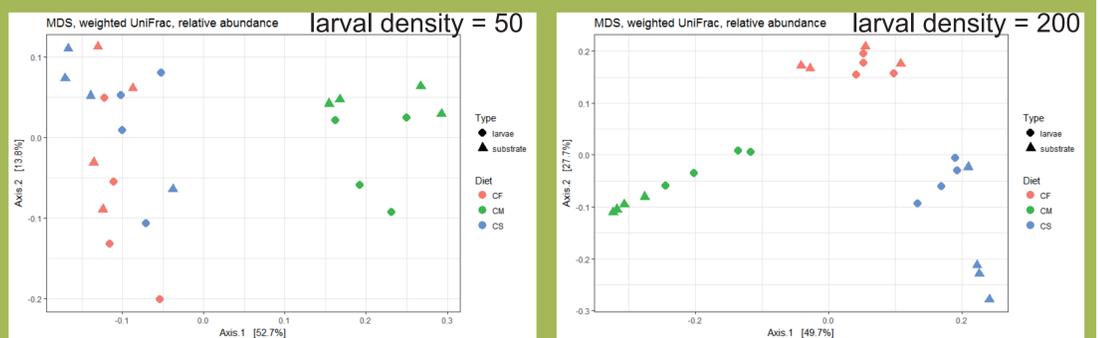
These preliminary results suggest that:

- Both substrate- and larval gut bacterial community composition change with diet and larval density;
- Substrate and larval gut communities are more distinct in chicken manure than in the other two diets.

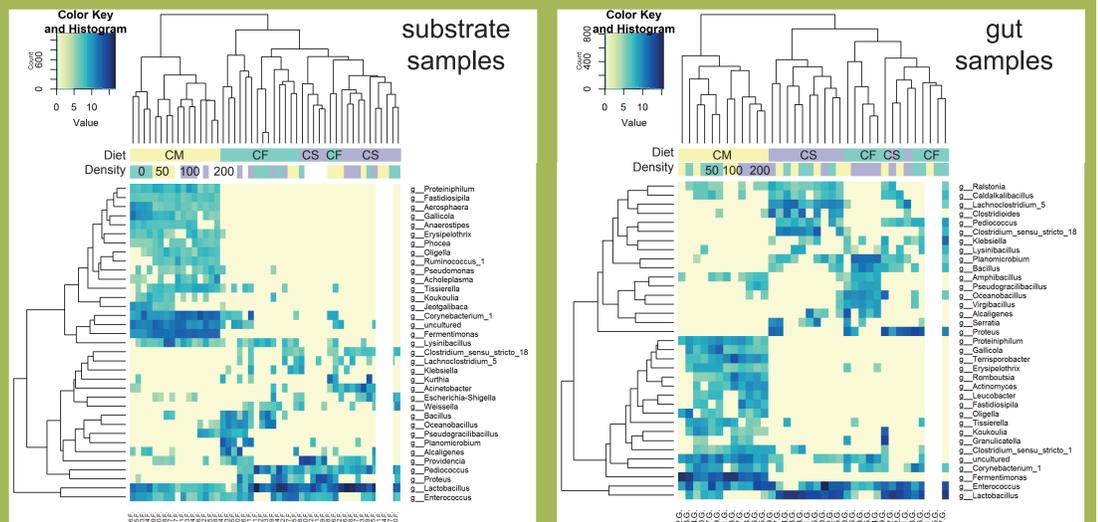
Follow-up questions

- How do the bacterial communities develop over time?
- Can we identify a core microbiome in BSF larvae?
- What is the effect of bacteria on BSF performance?

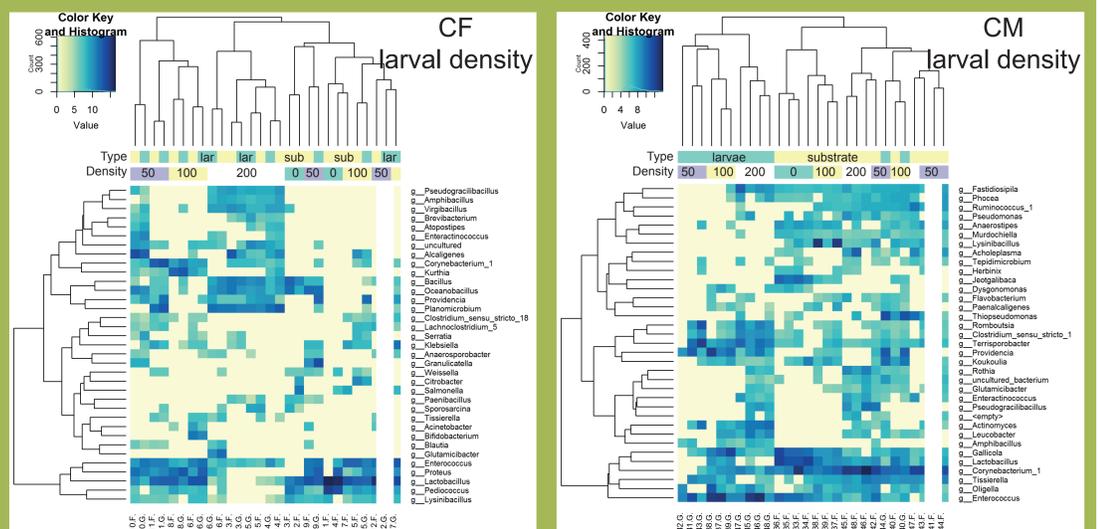
Preliminary results (time point = day 15)



Diets are better separated at higher larval density.



Both substrate and gut samples cluster for diet, in CM for density too.



Substrate and gut samples cluster after density in CF, before in CM.

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References: 1: Jeon et al. 2011, Curr Microbiol, 62(5): 1390-1399; 2: Erickson et al. 2004, J Food Prot 67(4): 685-690; 3: Liu et al. 2008, Env Entomol 37(6): 1525-1530.