Overlap between stigma and seed bacterial communities of watermelon (*Citrullus lanatus*)

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Introduction

- Bacterial communities can be transmitted between plant generations through seeds [1].
- Some bacteria may be florally transmitted to developing seeds (Fig. 1) [2], but the overlap between stigma and seed bacterial communities is largely unstudied [3,4].
- Watermelon, with its florally transmitted pathogen *Acidovorax citrulli* [5-6] and large reproductive tissues [7], presents a useful model for studying floral transmission.
- **Research questions:**
  - What percentage of bacterial genera are shared between stigma and seed communities?
  - Is the overlap consistent across commercial watermelon fields?

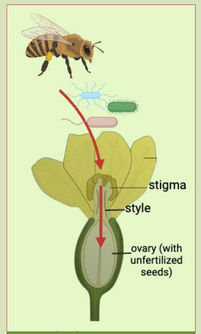
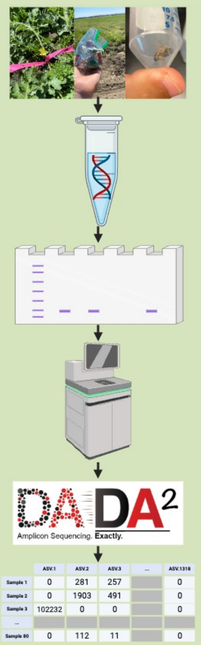


Figure 1. A diagram of floral transmission.

Methods

- Collected stigmas (n=38), 7-day old melons (n=38) and honeybees (n=20) from four commercial fields across the California Central Valley
- Pooled bees by field and seeds by fruit, extracted DNA using Qiagen PowerSoil and Plant Pro kits
- Verified the presence of bacterial DNA with PCR
- Sent DNA extracts to Novogene for library preparation and Novaseq sequencing
- Processed raw sequence data with the DADA2 [8] workflow in R [9]
- Conducted community ecology analyses [10]



Results and conclusions

Stigmas and seeds share many abundant taxa, including *Sphingomonas, Shigella, Cutibacterium* and *Acidovorax* (Fig. 2).

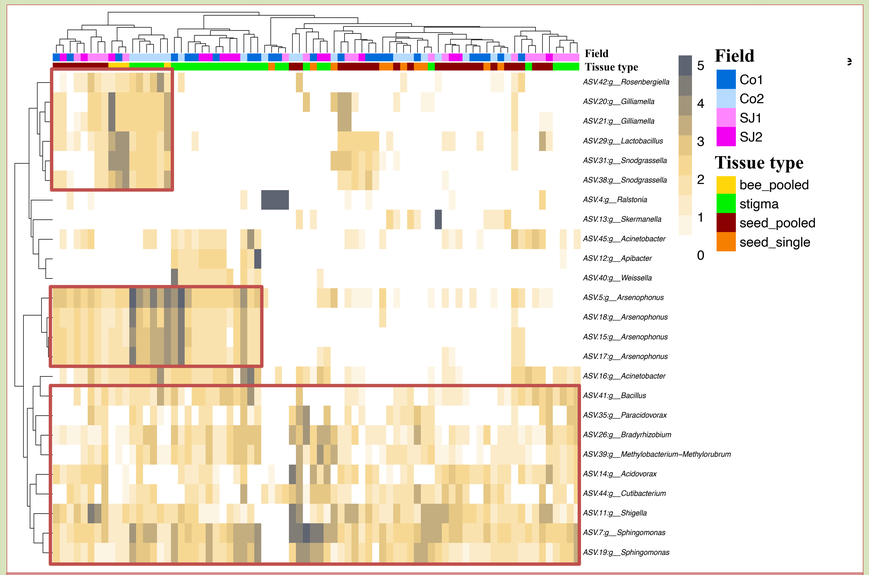


Figure 2. A heatmap of the 25 most abundant amplicon sequence variants (ASVs) across all samples. Colors of the cells represent the log10 abundance of a given ASV. Samples are clustered by their similarity across fields and tissue types, and ASVs are clustered by their co-occurrence. Block highlights represent clusters of interest.

A variable but large proportion of seed ASVs are shared with stigmas across fields (Fig. 3).

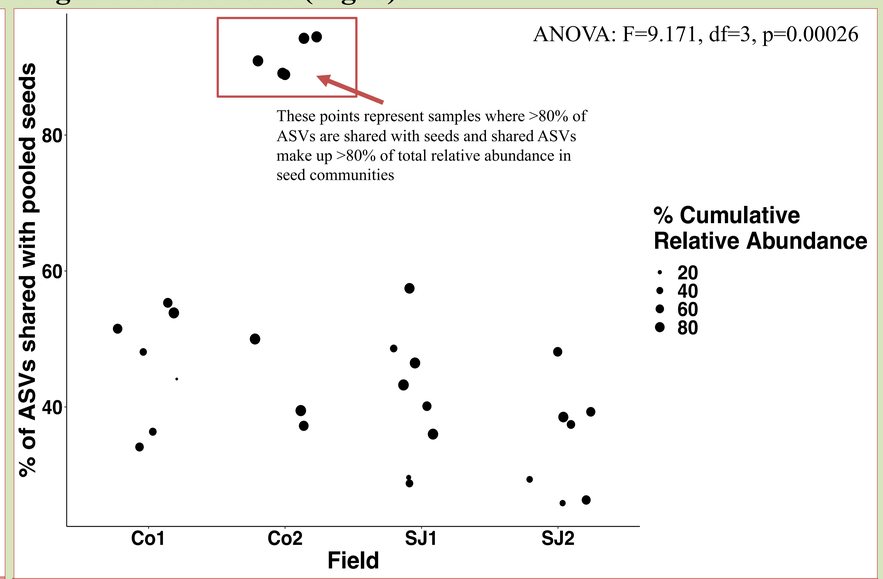


Figure 3. Dotplot of percent of ASVs in pooled seeds that are also found in stigma samples, grouped by field. The size of the points indicates the cumulative relative abundance stigma-transmitted ASVs in the seed samples. Each point represents an individual stigma.

Alpha diversity varied by field but not tissue between stigmas and pooled seeds (Fig. 4).

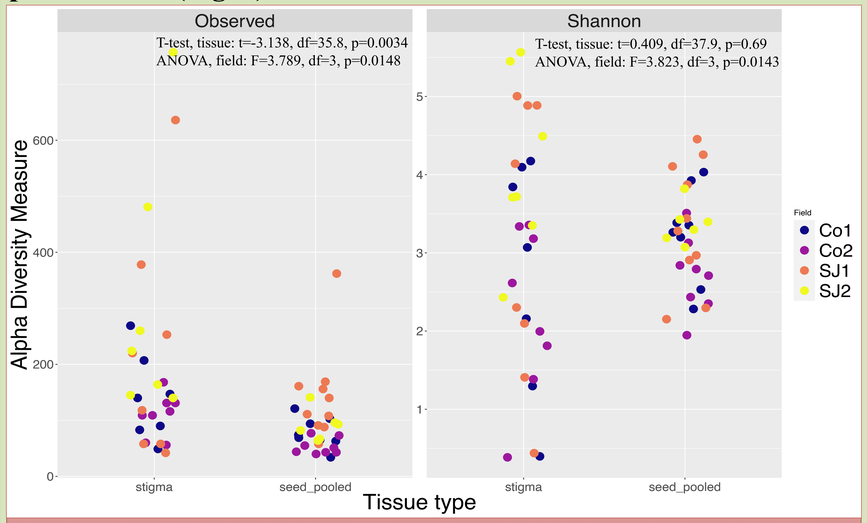


Figure 4. Dotplots of alpha diversity (observed richness, Shannon index) by tissue and color-coded by field.

Community composition varied significantly by tissue and field, with correlations to the abundance of dominant ASVs (Fig. 5).

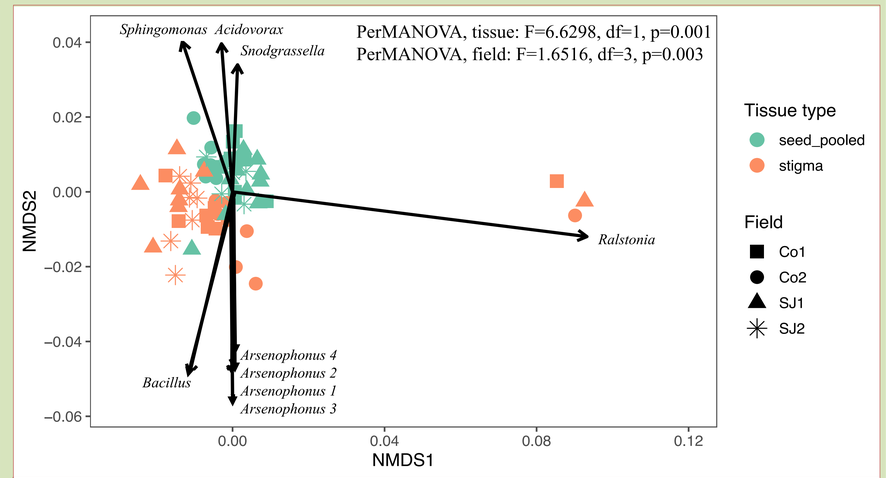


Figure 5. NMDS ordination of communities based on Bray-Curtis dissimilarities, with vector analysis of ASVs. Colors represent the tissue types sampled, and shapes represent the field sampled. Arrows indicate the direction of correlation between community composition and the abundance of a given ASV.

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