Pea and Canola Intercropping (Peaola) Causes Minor Shifts in the Microbiome

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Is the microbiome contributing to overyielding observed in peaola?

1. Shifts could be occurring in the microbiome of peaola compared to monoculture pea and canola leading to there being greater functional diversity in peaola.
2. Pea could be providing biologically available nitrogen to canola through its symbiosis with rhizobia and arbuscular mycorrhizal fungi.

Soil, rhizosphere, and root samples collected in 2020 near Colfax, WA

- Soil collected from top 10 cm (12 samples per cropping system)
- Rhizosphere collected from roots into rhizosphere buffer (24 samples per cropping system)

No Significant Differences in the Number of Taxa Observed Across Cropping Systems

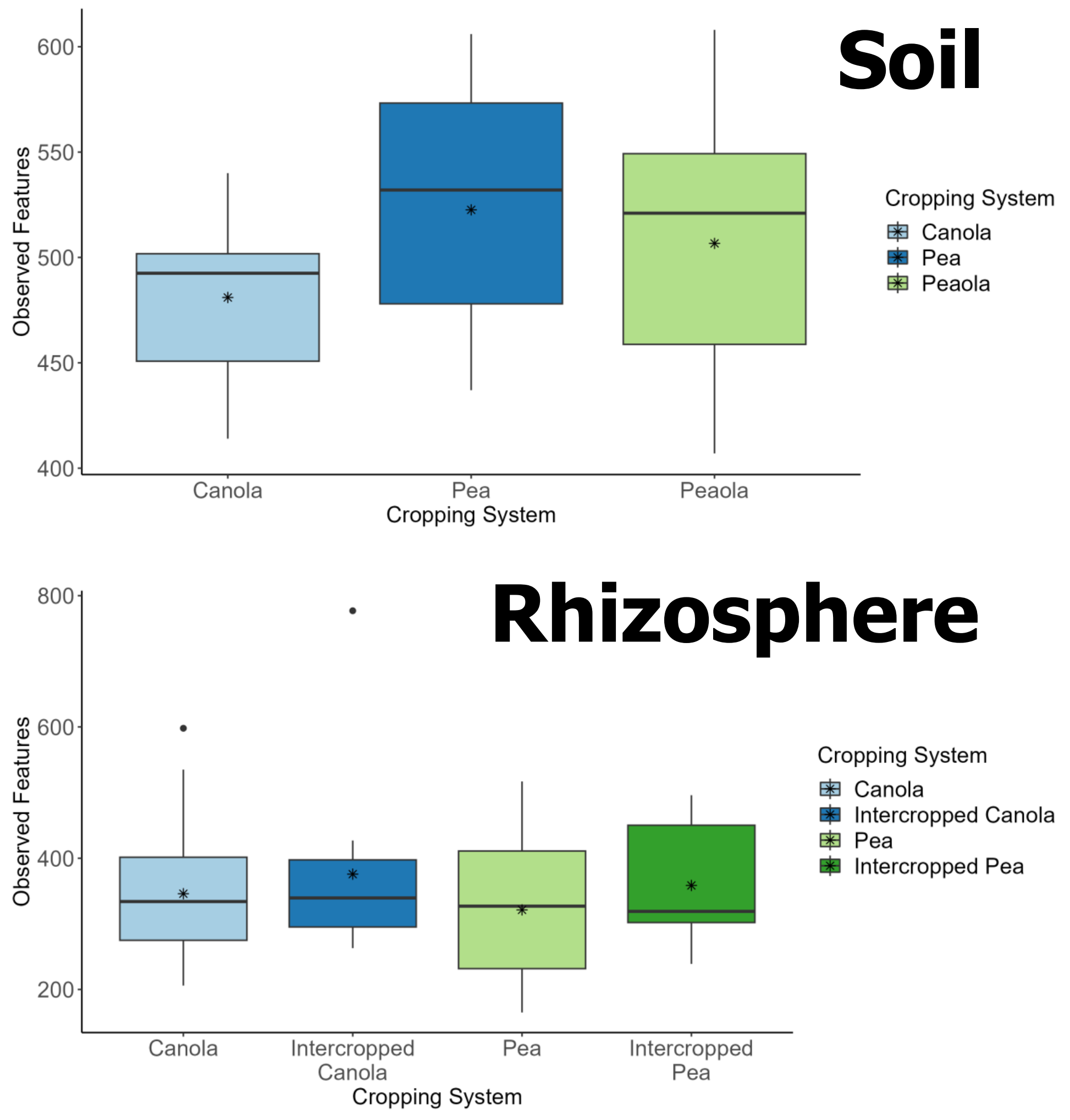

Figure 1. Boxplots showing the number of different taxa (observed features) across cropping systems.

Pea and canola maintain unique rhizosphere community compositions when intercropped

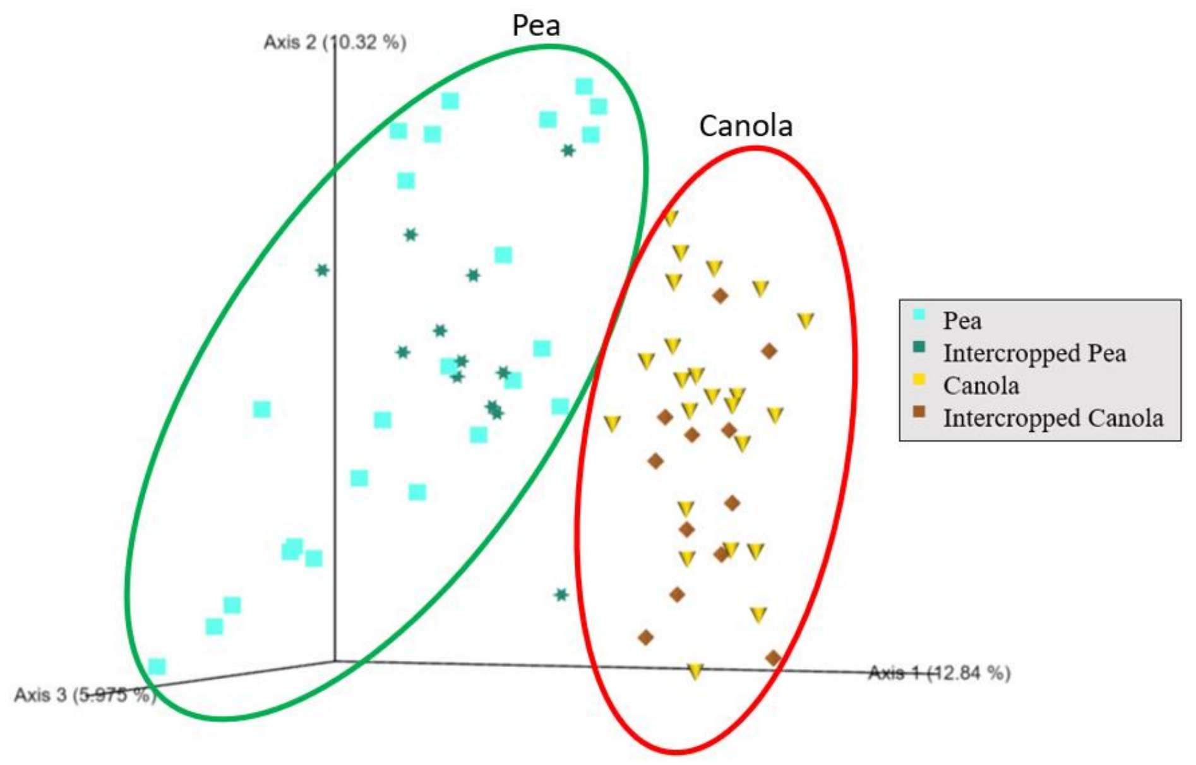

Figure 2. PCoA showing the community composition of the rhizosphere samples across cropping systems using Bray-Curtis distance. Canola and pea are significantly different from each other regardless of cropping system (PERMANOVA, $P < 0.05$).

Shifts are seen in the strict core microbiome across cropping systems in the soil and rhizosphere

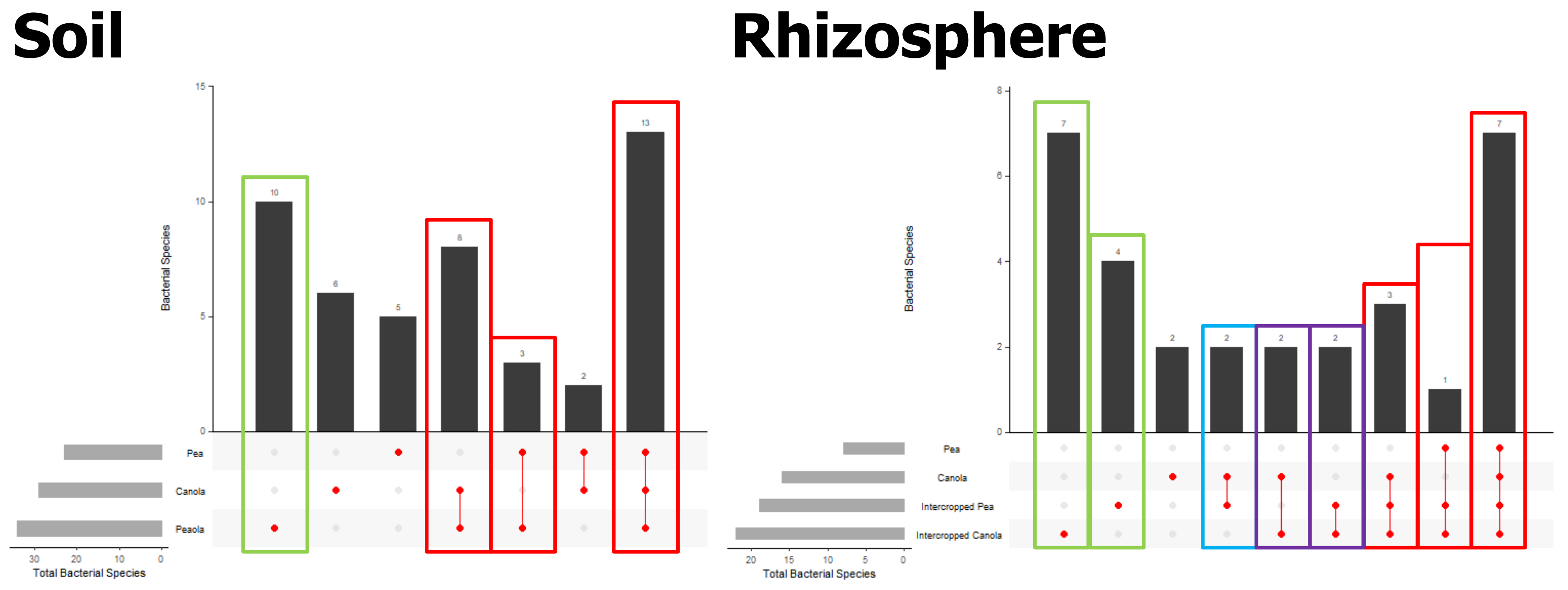

Figure 3. UpSet plots showing how taxa are both found uniquely in some microbiomes, but also shared amongst others. It is possible that peaola is creating a unique soil environment which could be why the peaola microbiome has unique core members. Green = only found in peaola, Blue = only shared with intercropped pea, Purple = only shared with intercropped canola, and Red = shared with peaola.

Bacteria in the rhizosphere are differentially abundant between pea and canola, but bacteria are not differentially abundant between like crops (i.e. canola vs. intercropped canola)

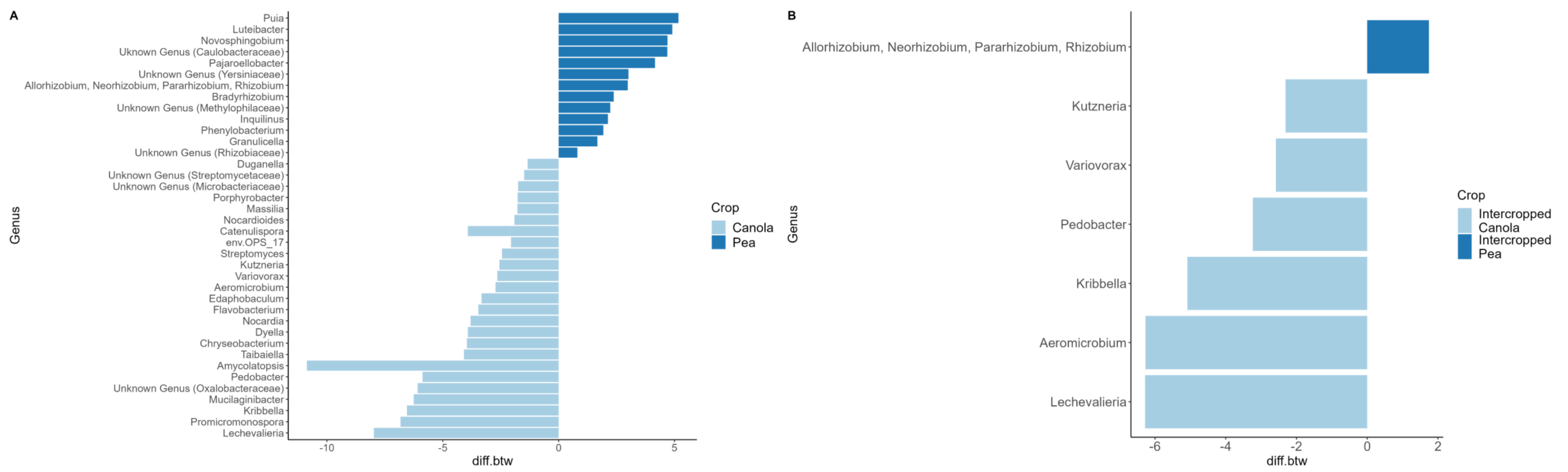

Figure 4. Differentially abundant bacteria between A) canola and pea and B) intercropped canola and intercropped pea. The x-axis shows the differences in the relative abundance between the compared crops. There are 33 fewer differentially abundant taxa when intercropping.

Take Home Messages

- Intercropping alone does not appear to cause significant shifts in the microbiome from monoculture
- Small changes are occurring which can be seen in the core microbiome and in the different abundance analyses
  - Fewer bacteria are differentially abundant between intercropped pea and intercropped canola showing their microbiomes are becoming more similar

Further Information

Janice Parks' LinkedIn

Further Reading