INTRODUCTION

Populus trees are economically and ecologically important in the United States.

The plant microbiome impacts plant health, and plant microbiomes can change over time. The core microbiome represents a set of taxa characteristic of the host and consistently present across samples.

So, a healthy core microbiome = healthy plant

Experimental Questions:
1) What is the root endosphere core microbiome?
2) How does the core microbiome change over time and between species?
3) What biological functions do the core taxa have?

RESULTS

Figure 1. The plant microbiome is made up of above-ground and below-ground microbiomes. The root endosphere (RE) microbiome lies below-ground within the roots.

We defined core taxa based on 1% relative abundance and 50% occupancy thresholds; relative abundance is the proportion of abundance in all samples and occupancy is the proportion of presence in all samples. Core microbial taxa were investigated for possible functional roles in plant health.

METHODS

We characterized variation of the RE microbiome across four genotypes of two Populus species (Populus deltoides and P. trichocarpa) using 16S rRNA gene amplicon sequencing. We sampled the RE microbiome 8 times over two years.

Figure 3. Data collection and analytical pipeline overview.

Figure 4. Occupancy-abundance relationship for 2018. Each point is an amplicon sequence variant (ASV). Dashed lines represent 1% relative abundance and 50% occupancy thresholds.

Table 1. Dominant core taxa from 2018 and 2019 with the highest occupancy and average relative abundance.

Table:| ASV         | Occupancy | Abundance | Phylum          | Class           | Order  | Family            | Genus              |
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</thead>
<tbody>
<tr>
<td>ASV 0</td>
<td>0.900</td>
<td>0.233</td>
<td>Proteobacteria</td>
<td>Alphaproteobacteria</td>
<td>Rhizobiales</td>
<td>Xanthobacteraceae</td>
<td>Bradyrhizobium</td>
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<tr>
<td>ASV 16</td>
<td>0.720</td>
<td>0.082</td>
<td>Proteobacteria</td>
<td>Gammaproteobacteria</td>
<td>Enterobacteriales</td>
<td>Escherichia shigella</td>
<td>Bradyrhizobium</td>
</tr>
<tr>
<td>ASV 23</td>
<td>0.707</td>
<td>0.096</td>
<td>Proteobacteria</td>
<td>Gammaproteobacteria</td>
<td>Pseudomonadales</td>
<td>Moraxellaceae</td>
<td>Acinetobacter</td>
</tr>
<tr>
<td>ASV 18</td>
<td>0.580</td>
<td>0.058</td>
<td>Proteobacteria</td>
<td>Gammaproteobacteria</td>
<td>Pseudomonadales</td>
<td>Moraxellaceae</td>
<td>Acinetobacter</td>
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</table>

Figure 5. Occupancy-abundance relationship for 2019. Each point is an ASV. Dashed lines represent 1% relative abundance and 50% occupancy thresholds.

Figure 6. 2018 shared ASVs between months.

Figure 7. 2019 shared ASVs between months.

Figure 8. Heat map of 2018 and 2019 core taxa at the Class taxonomic level. Prevalence is equivalent to occupancy.

Figure 9. Four most dominant core taxa and their biological function. Circle sizes reflect level of abundance and occupancy.

CONCLUSIONS

1) There is a subset of core taxa that are potentially beneficial to the plant. Bradyrhizobium is a diazotroph (nitrogen-fixing bacteria). Acinetobacter (ASVs 18 and 23) may promote plant growth.

2) Core taxa that are shared between the two Populus species have similar abundance and occupancy.

3) The core microbiome is limited but contains beneficial taxa that are found over multiple years, possibly providing support for its importance.

We recommend further research on the functional significance of the core microbiome taxa.

REFERENCES

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