Plant beneficial bacteria dominate a multispecies *Populus* root endosphere core microbiome

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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?
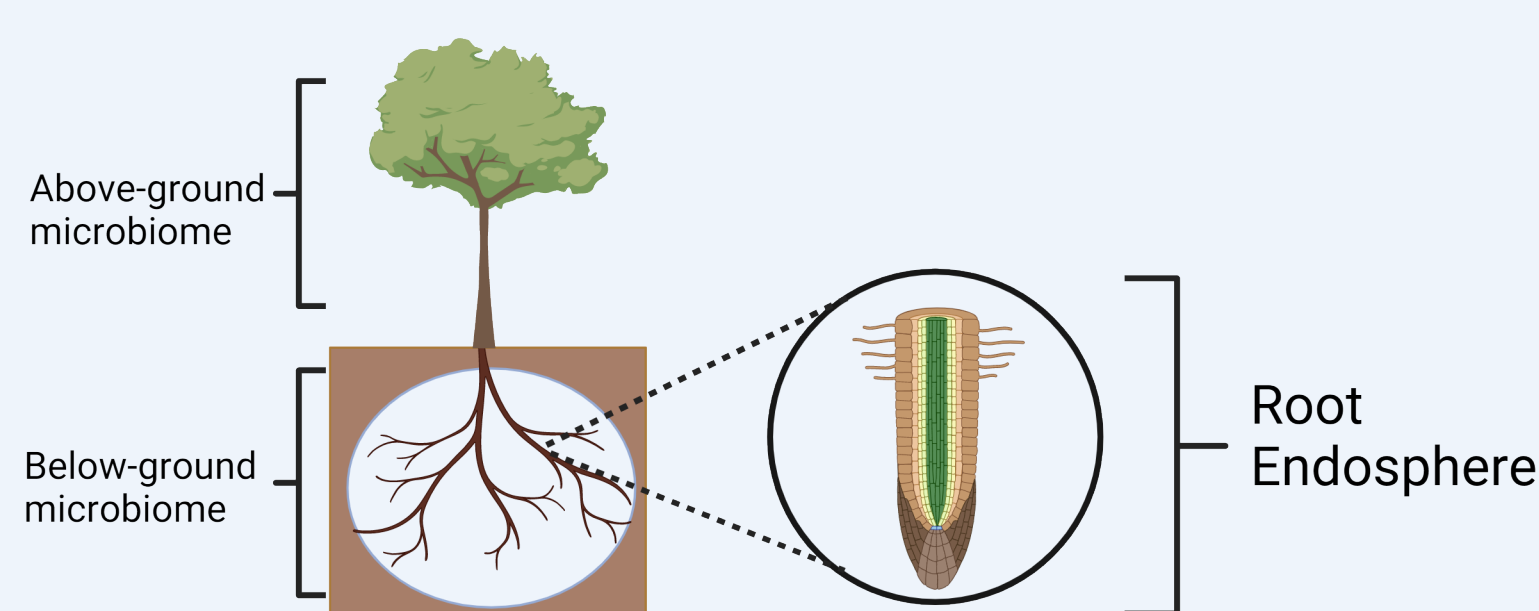3) What biological functions do the core taxa have?

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.

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.
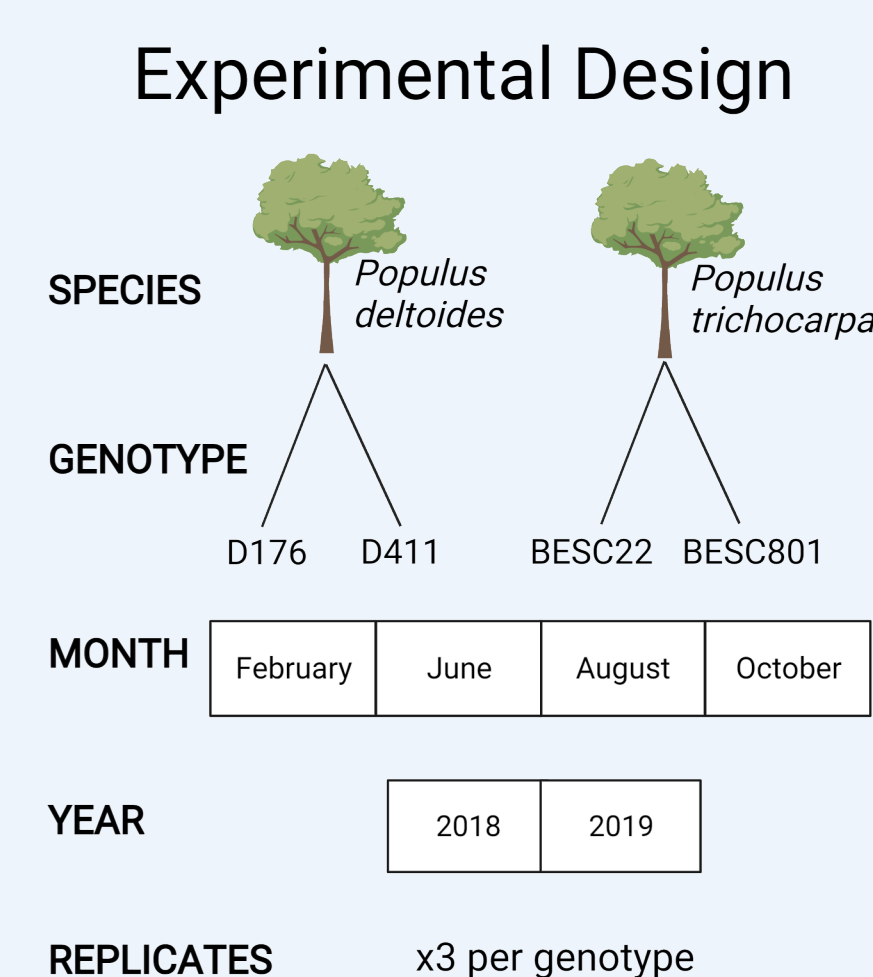

Figure 2. Experimental design.

Figure 3. Data collection and analytical pipeline overview.

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.
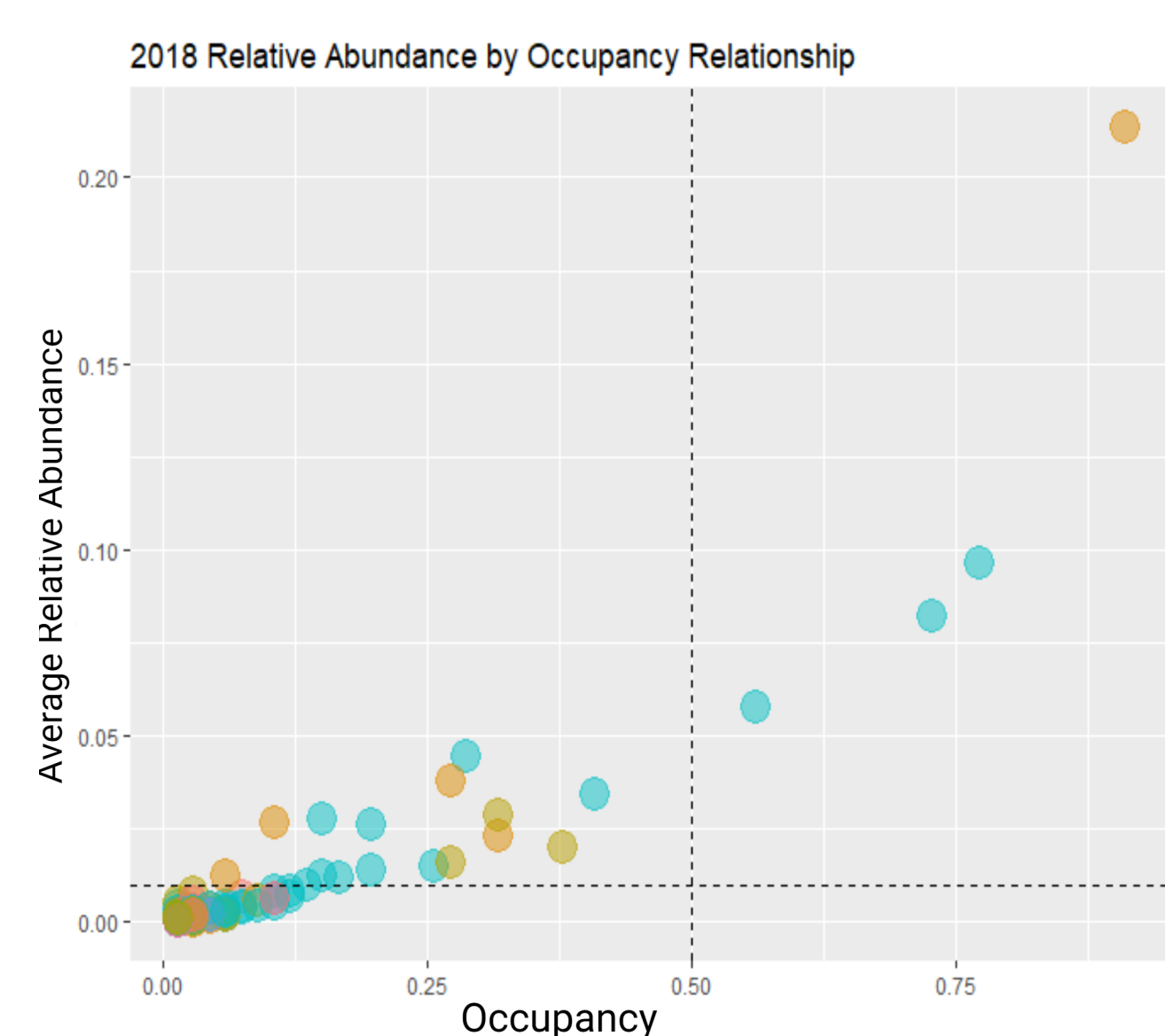
RESULTS

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.
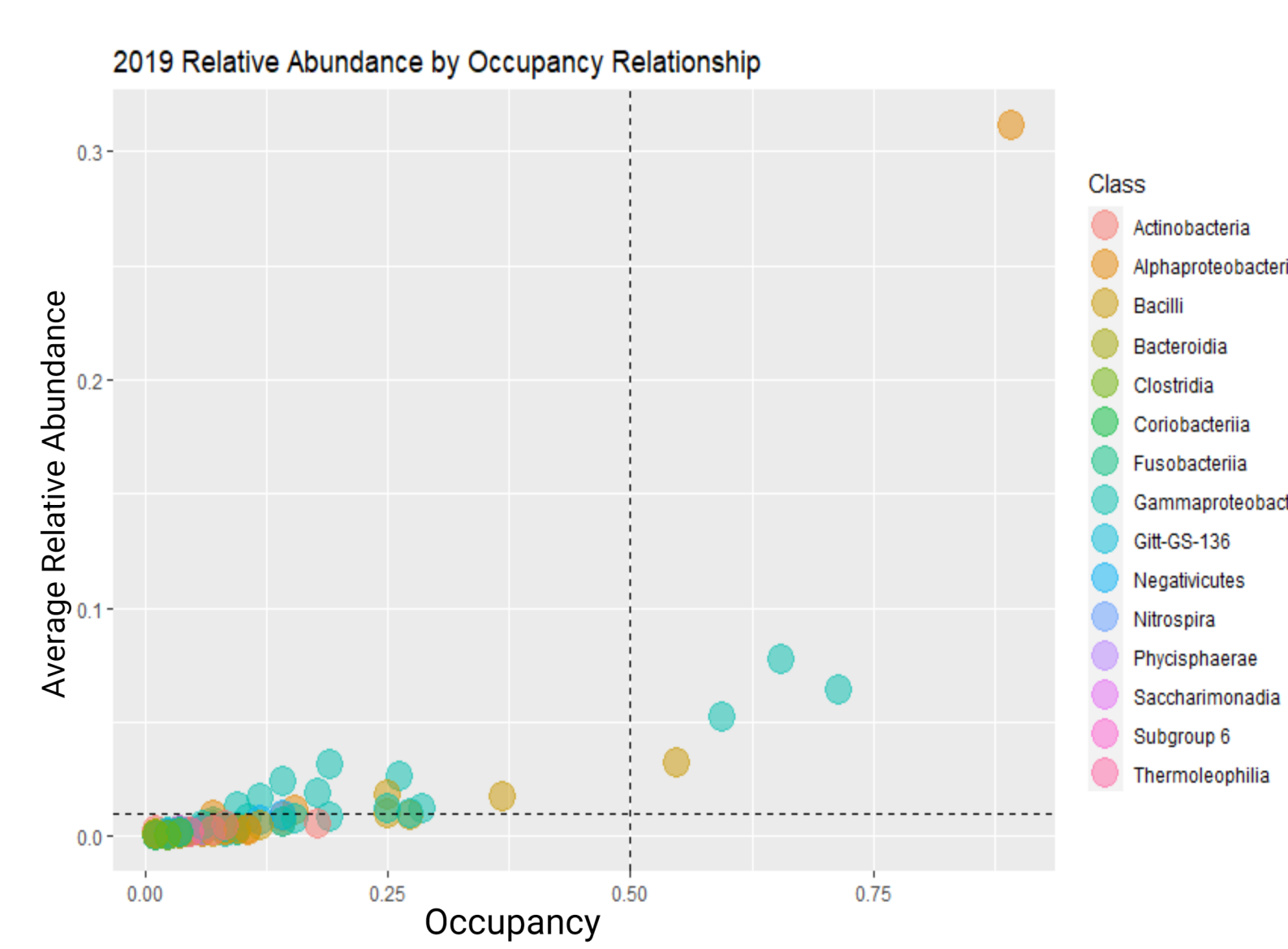

Figure 5. Occupancy-abundance relationship for 2019. Each point is an ASV. Dashed lines represent 1% relative abundance and 50% occupancy thresholds.
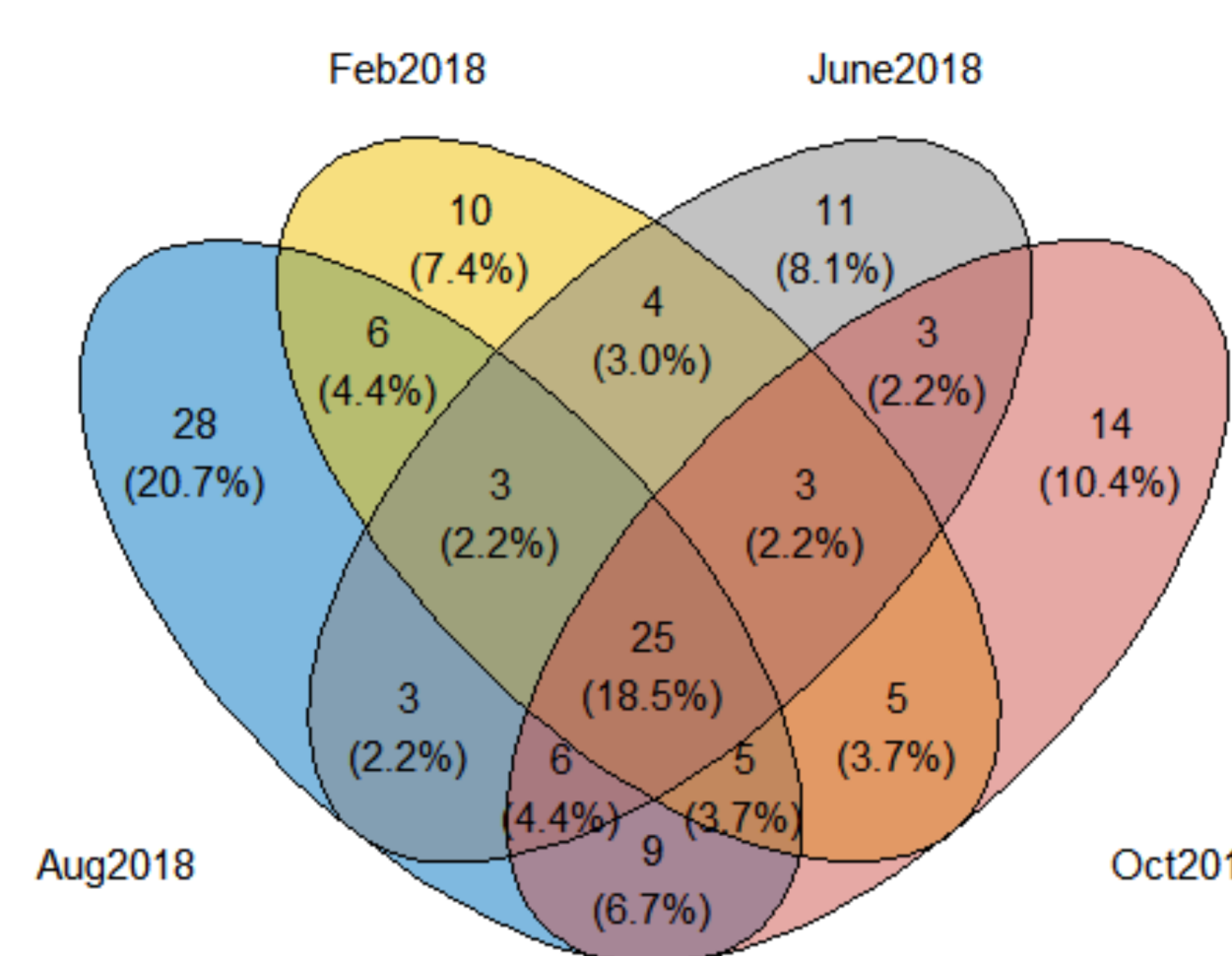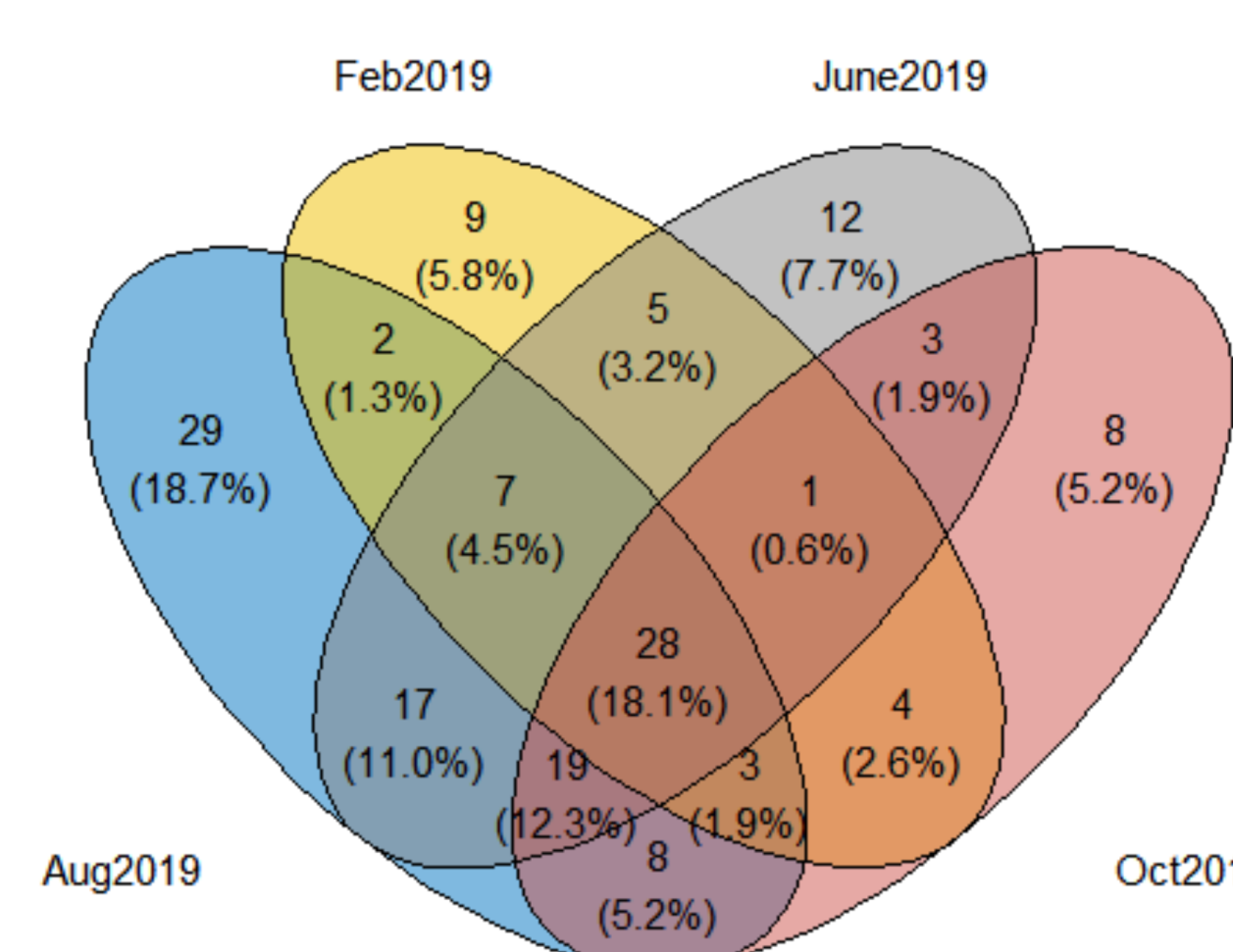

Figure 6. 2018 shared ASVs between months.

Figure 7. 2019 shared ASVs between months.

ASV	Occupancy	Abundance	Phylum	Class	Order	Family	Genus
ASV 9	0.900	0.213	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
ASV 26	0.720	0.082	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia-Shigella
ASV 23	0.707	0.096	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
ASV 18	0.580	0.058	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter

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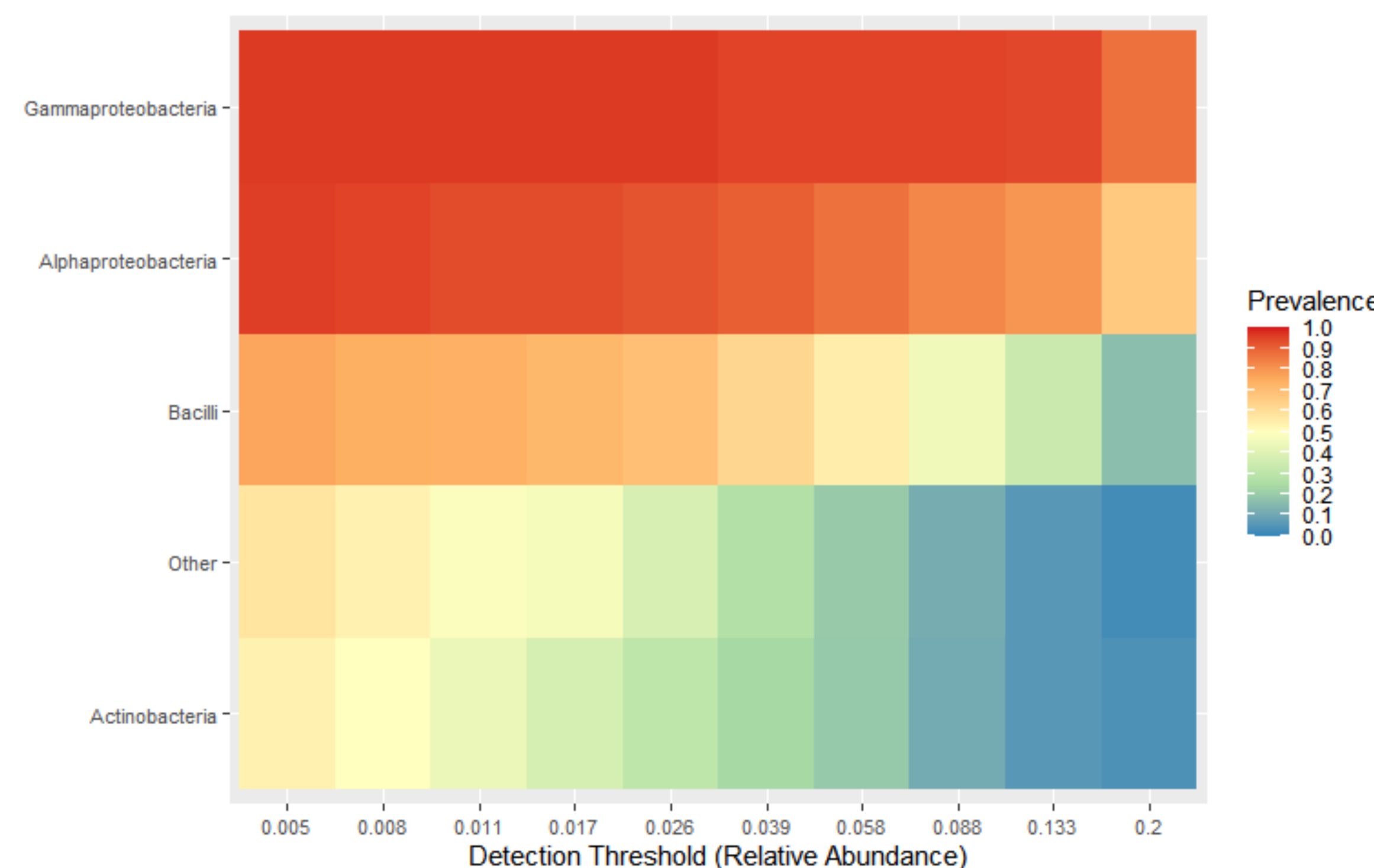

Figure 8. Heat map of 2018 and 2019 core taxa at the Class taxonomic level. Prevalence is equivalent to occupancy.
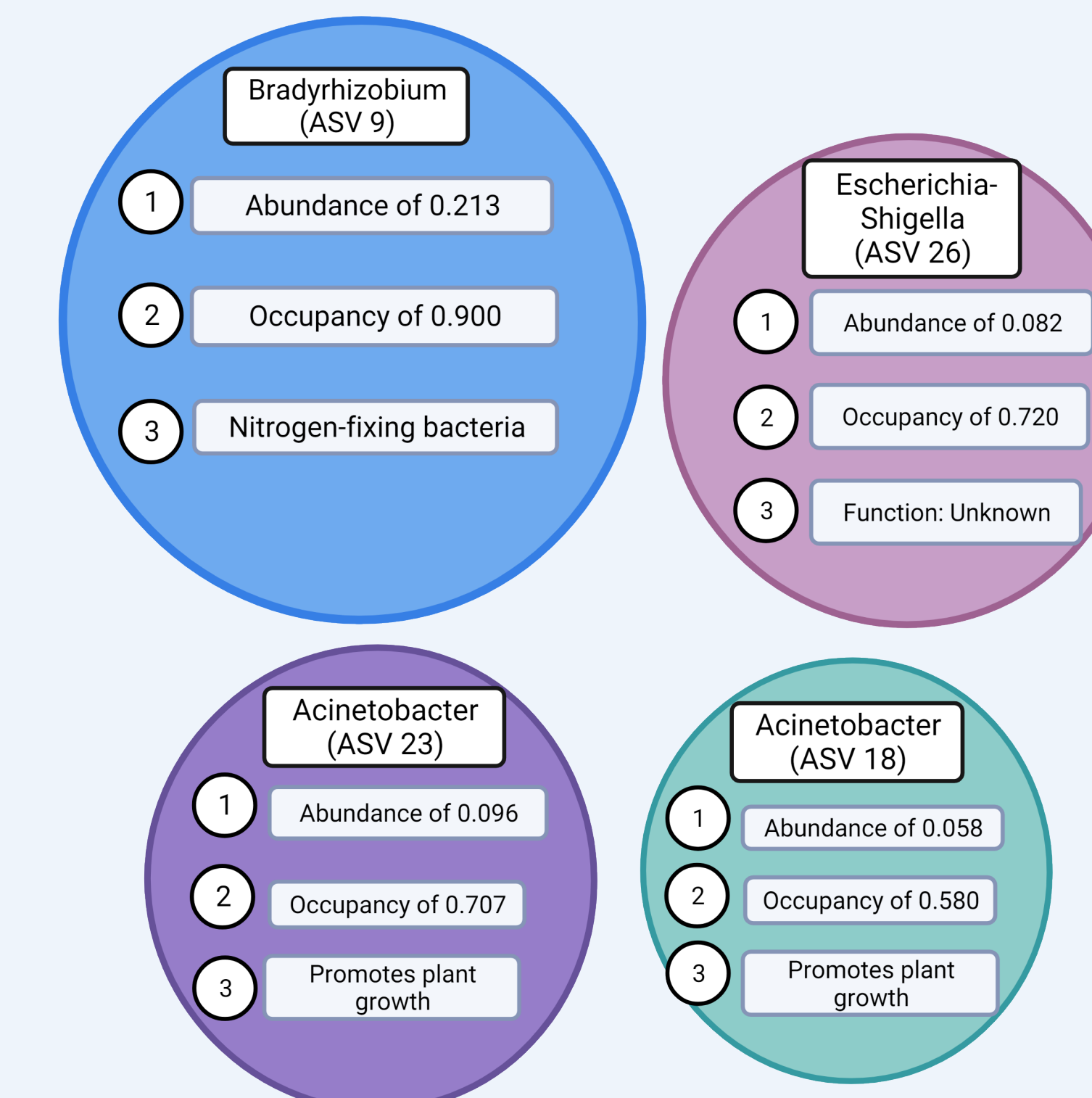
CONCLUSIONS

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

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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R packages used: DADA2, phyloseq, and microbiome

ACKNOWLEDGEMENTS