

Getting to the Core: 33 Unique Constituents Identified as the Core Microbiome of *Cornus florida*



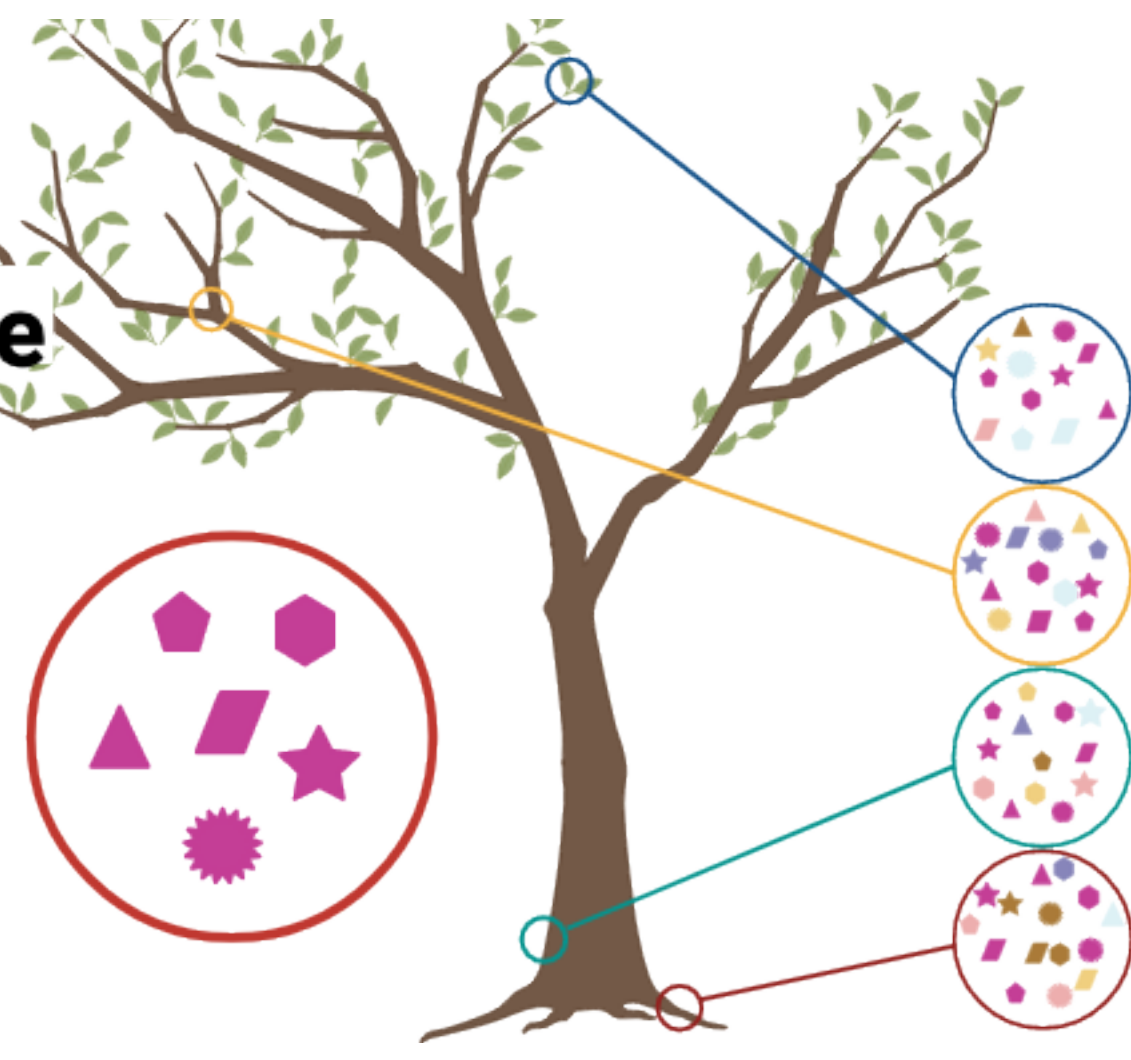
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INTRODUCTION

Core Microbiome

Defined here as the microbial taxa found to occupy all niches (roots, stem, bark, leaves) of *Cornus florida* (dogwood)



Importance - Dogwood is economically valuable to Tennessee as an ornamental and is ecologically important as a native tree.

Discovering dogwood's core microbiome may contribute to clues about stress resilience and fitness.

The Study - We aim to profile the dogwood microbiome using fungal ITS and prokaryotic 16S marker gene sequences sampled from root, stem, bark, and leaf niches

PROKARYOTIC RESULTS

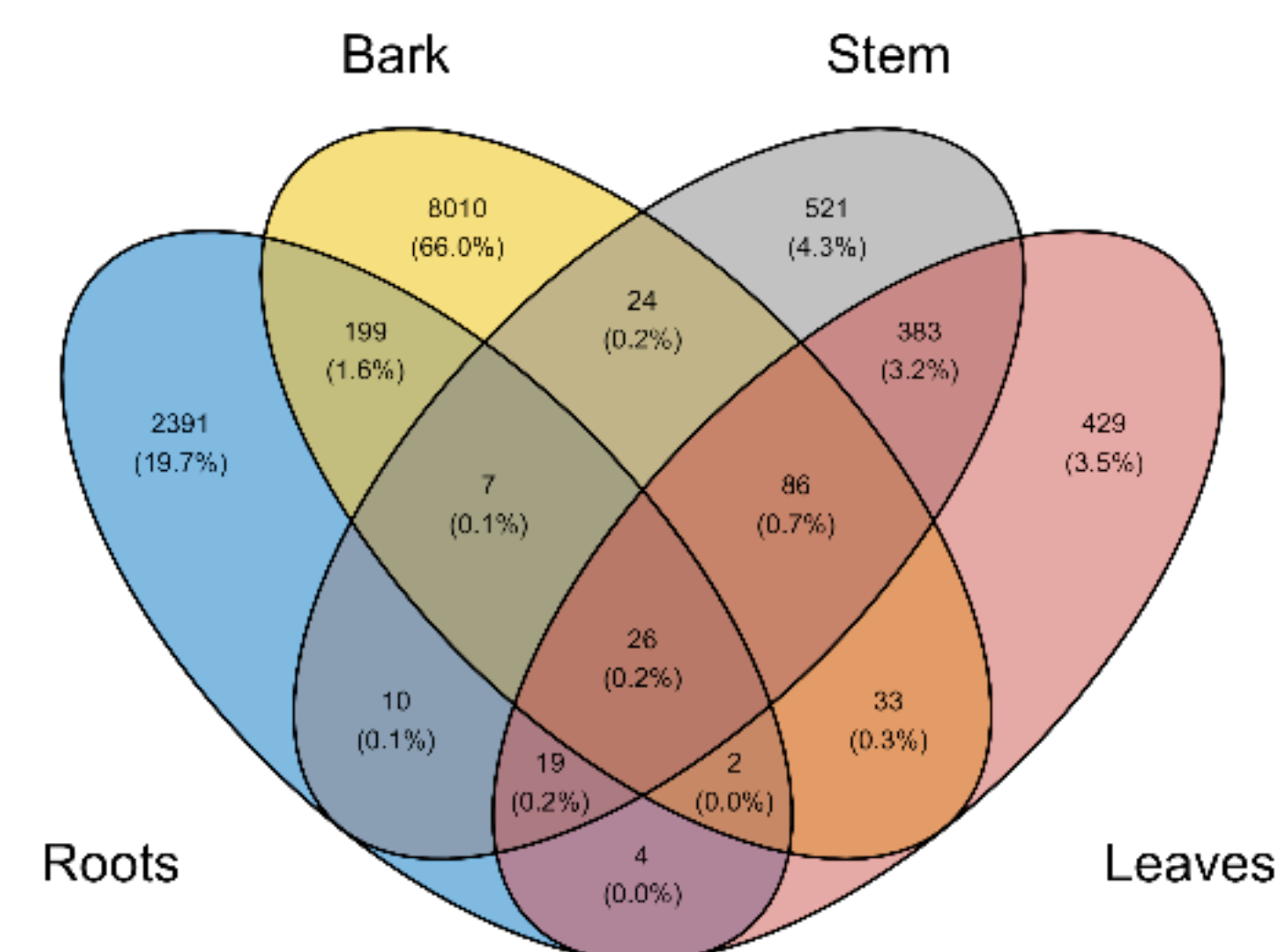


Figure 1: Venn diagram representing the number of bacterial amplicon sequence variants (ASVs) across four dogwood niches, and the intersection of these niches.

FUNGAL RESULTS

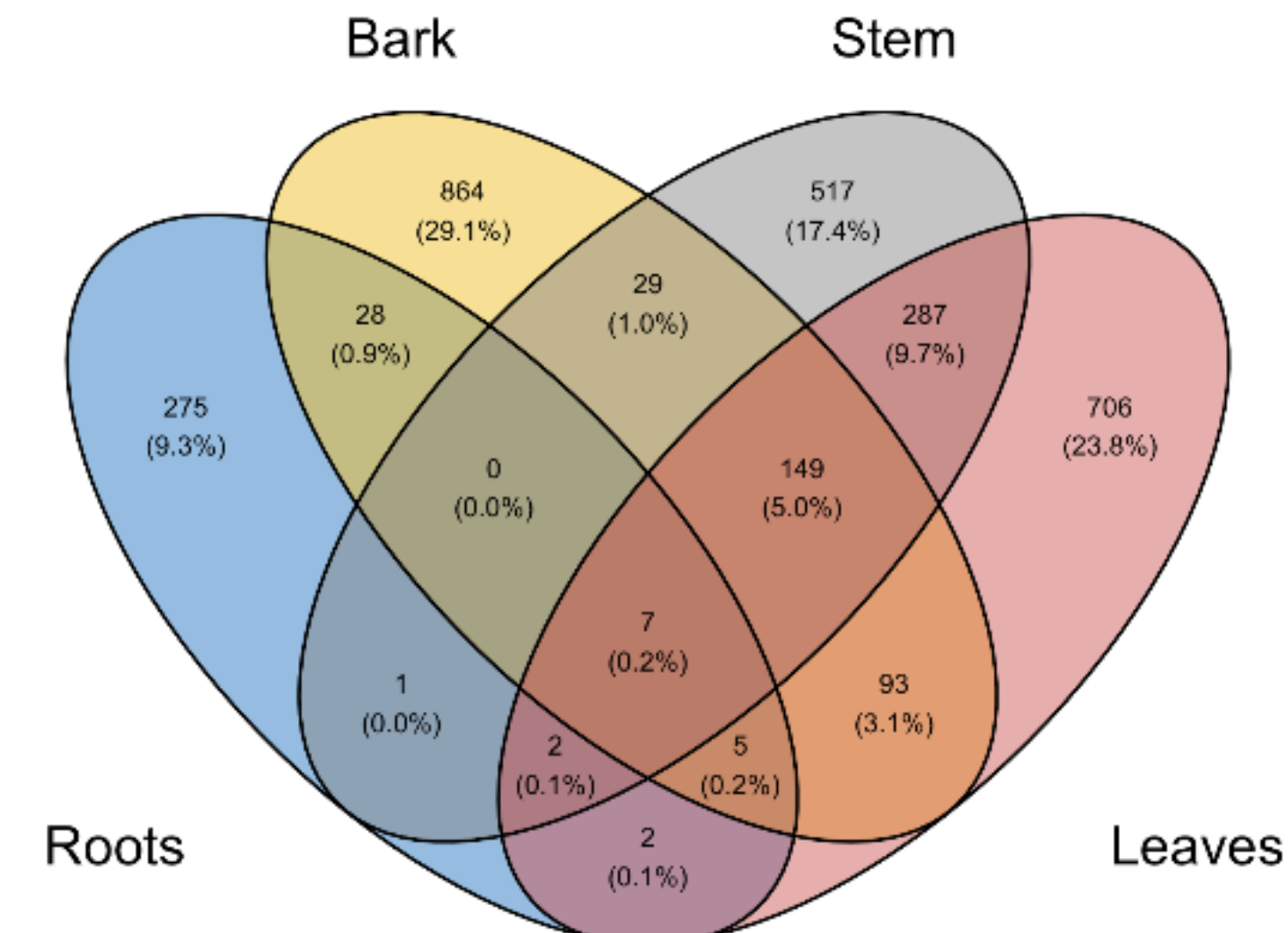


Figure 3: Venn diagram representing the number of fungal ASVs across four dogwood niches, and the intersections of these four niches.

CONCLUSION

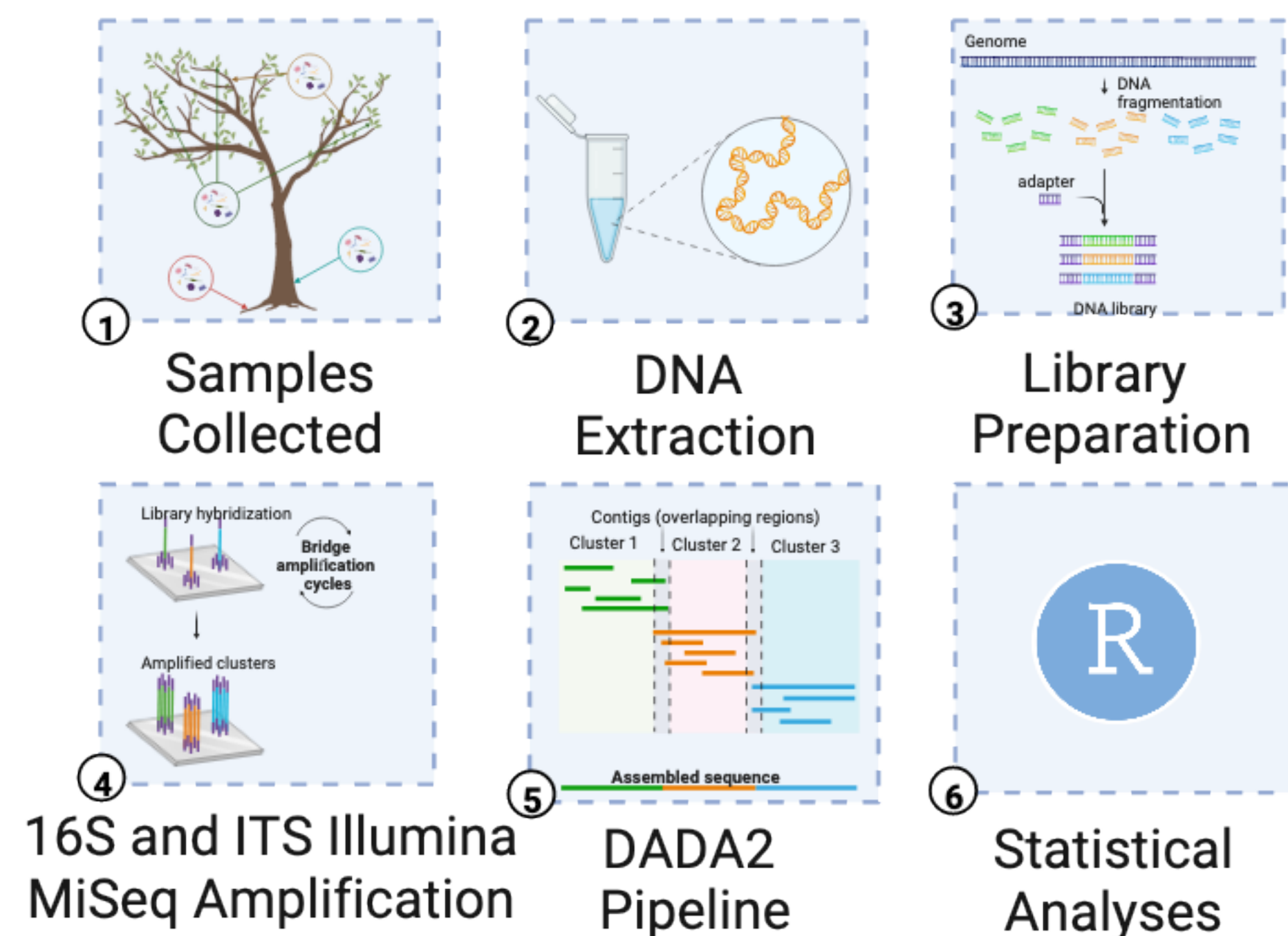
Dogwood's core microbiome consists of **7 fungal** and **26 prokaryotic taxa** that have **occupancy across all four niches.**

These 33 taxa are found in 5 - 94% of the total samples, but are found in at least one sample per niche (roots, stem, bark, and leaves).

Core taxa abundance varies widely.

Heatmaps show that many have less than 0.5% relative abundance, meaning that that taxa accounts for less than 0.5% of the total microbes present in the samples.

METHODS



Samples were collected from **20 dogwood trees growing in Tullahoma, Tennessee** in 2019. **Four samples** collected per tree, **one per each niche:** roots, stem, bark, leaves.

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Kingdom	Phylum	Class	Core ASV Count	% Samples Containing ASV	
Bacteria	Acidobacteriota	Acidobacteriae	2	66%	
		Thermoanaerobaculia	1	23%	
		Vicinamibacteria	1	33%	
	Actinobacteriota	Acidimicrobia	1	43%	
		Thermoleophilia	1	11%	
	Bacteroidota	Bacteroidia	1	94%	
	Chloroflexi	Chloroflexia	1	27%	
		NA	1	54%	
	Bacteria	Cyanobacteria	Cyanobacteriia	1	9%
			Dependentiae	1	8%
		Firmicutes	Bacilli	1	5%
		Myxococcota	Myxococcia	1	6%
		Patescibacteria	Parcubacteria	1	5%
		Planctomycetota	Saccharimonadia	2	9%
			Planctomycetes	2	74%
		Proteobacteria	Alphaproteobacteria	4	18%
Verrucomicrobiota		Verrucomicrobiae	2	9%	
Archaea		Crenarchaeota	Nitrososphaeria	1	13%
	Thermoplasmata	Thermoplasmata	1	14%	

Table 1: Data table showing taxonomic levels of the 26 shared prokaryotic ASVs present in the dogwood core microbiome.

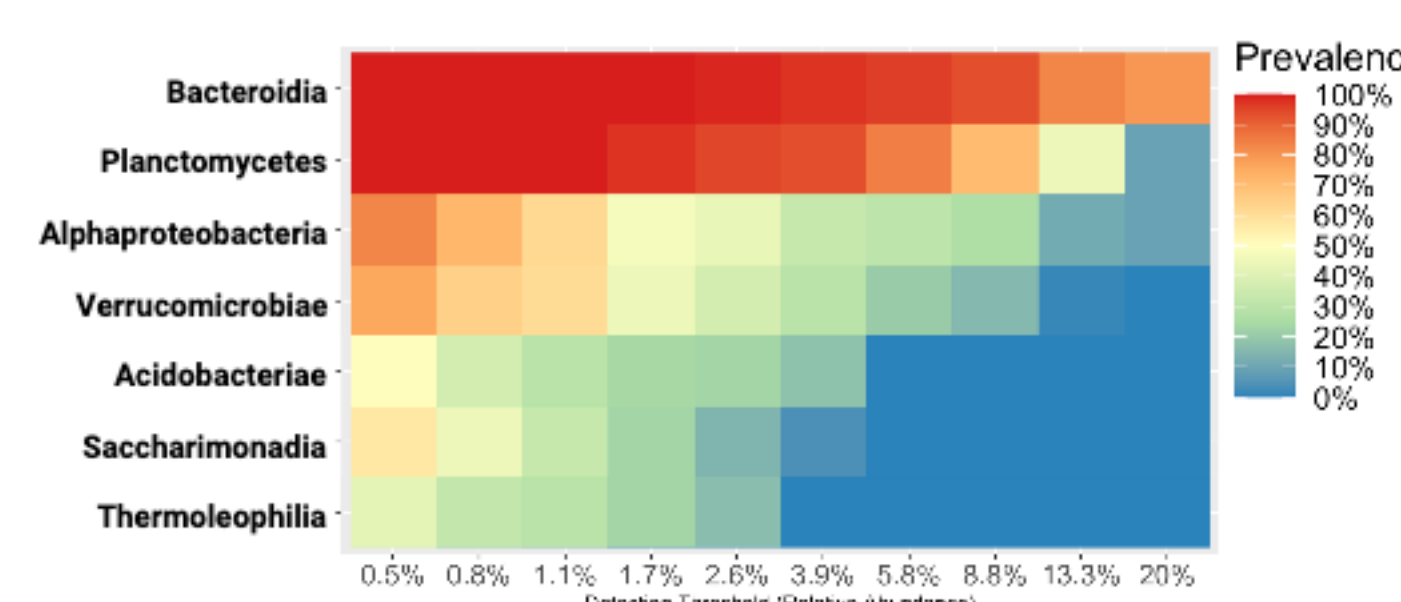


Figure 2: Heat map representing the prevalence (percent of each of the total samples that contain the taxa) of each of the most abundant prokaryotic classes across all samples from all dogwood niches at each specified detection threshold.

Kingdom	Phylum	Class	Core ASV Count	% Samples Containing ASV
Fungi	Ascomycota	Dothideomycetes	4	32%
		Agaricomycetes	1	10%
	Basidiomycota	Tremellomycetes	1	24%
		NA	1	13%

Table 2: Data table showing taxonomic levels of the seven shared fungal ASVs present in the dogwood core microbiome.

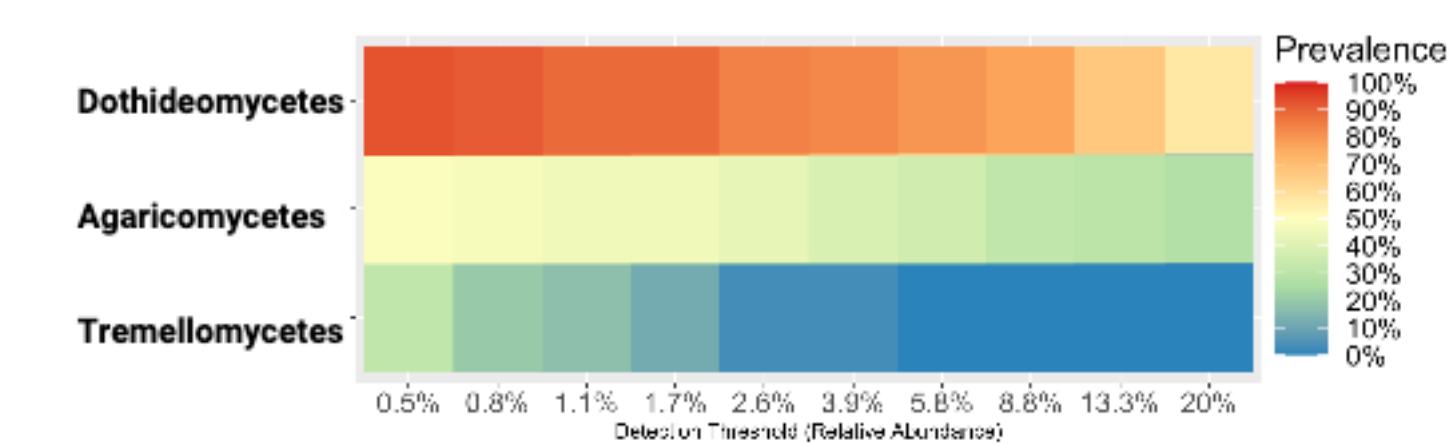


Figure 4: Heat map representing the prevalence (percent of the total samples that contain the taxa) of the most abundant fungal classes across all samples from all dogwood niches at each specified detection threshold.

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FUTURE WORK

- Further exploration to find potential functional roles of core microbes
- Incorporation of datasets from a broader geographic region beyond Tennessee (eastern United States) to refine the results of this study

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