A Longitudinal Study of the Alder Root Nodule Microbiome

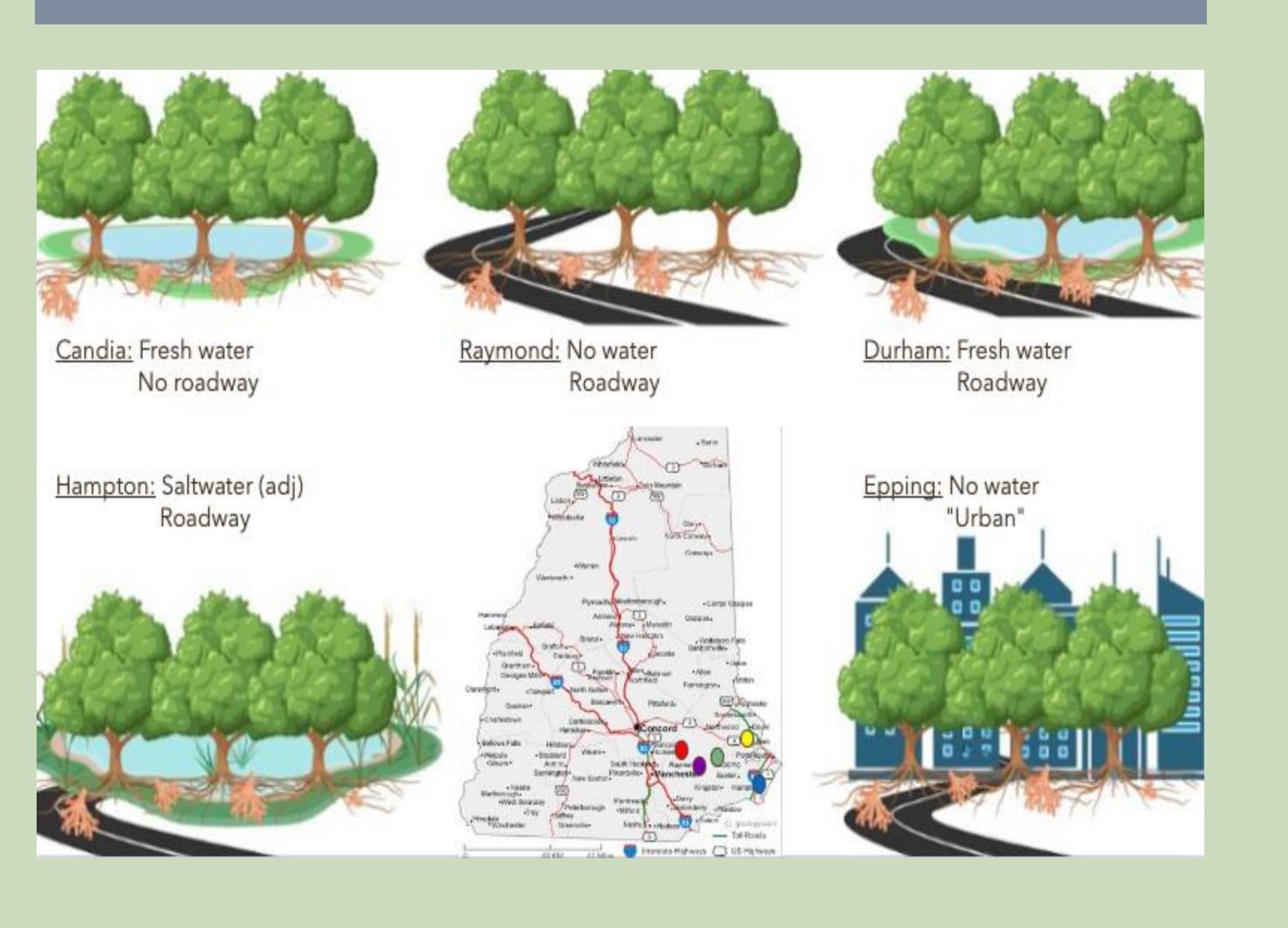
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BACKGROUND

- Soil microbes can help or hinder plants depending on environmental conditions, so understanding the seasonal ebbs and flows of microbial soil communities is necessary for maintaining global soil integrity
- The soil bacteria Frankia can form root nodules with host plants to supply the plant and the surrounding soil with nitrogen, thus allowing degraded lands to be recolonized by plant life
- Previous studies have shown that the nodule microbiomes have different community compositions and different levels of *Frankia* depending on the environment
- More longitudinal studies are needed of the actinorhizal root nodule microbiome in different sites and seasons to be able to better predict nodule community dynamics for future remediation and companion planting projects
- This project aims to unveil:
 - If there are differences between the root nodule bacterial and fungal communities in New Hampshire alders at the different sampling sites
 - If there are seasonal influences in the root nodule bacterial and fungal communities

SAMPLING DESIGN



RESULTS

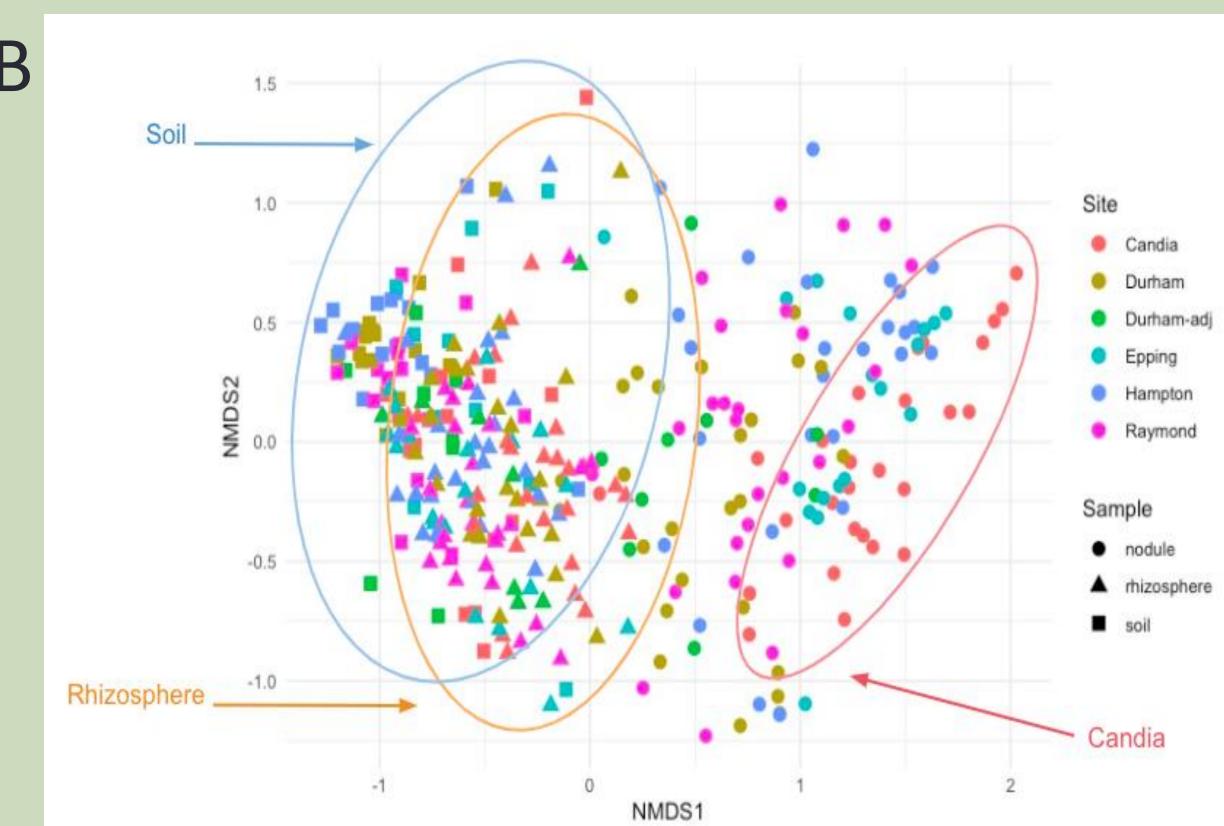


CONCLUSIONS

The alder nodule communities are dynamic niches that are as pliant with the seasons as their plant hosts. *Frankia* abundance peaks during the summer, and these peaks result in troughs in the abundance of fungal root endophytes, possibly due to the high expense of the actinorhizal symbiosis.

The Candia nodules, farthest from a roadway, cluster the tightest within the NMDS, but the nodule communities are not showing as stark differences between the soil samples as has been previously published.

Future work into the metagenomic profiles of these communities will give us insight into the potential interactions within these roadway sites over the different seasons.



Variables	Df	SumofSqs	R ²	F	<i>p</i> -value
Site	5	2.857	0.075	2.069	1e-04
Month	2	1.529	0.04	2.73	4e-04
Year	1	0.832	0.022	2.94	0.002
Site:Month	10	3.843	0.10	1.487	0.002
Site:Year	4	1.741	0.046	1.628	0.0086
Month:Year	4	1.942	0.051	1.819	0.001

- **A.** Relative abundance of the top 5 taxa from each sampling site over the duration of the sampling study. Note the inverse relationships between *Frankiaceae* and the other plotted nodule neighbors. Data is from 16S and ITS sequenced communities.
- **B.** NMDS ordination (stress = 0.12) of the sampled 16S and ITS communities. Shape represents sample type while color represents one of the 6 sampling sites.
- **C.** Results of PERMANOVA of sampling variables. All samples were tested individually except when analyzing possible interactions.

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