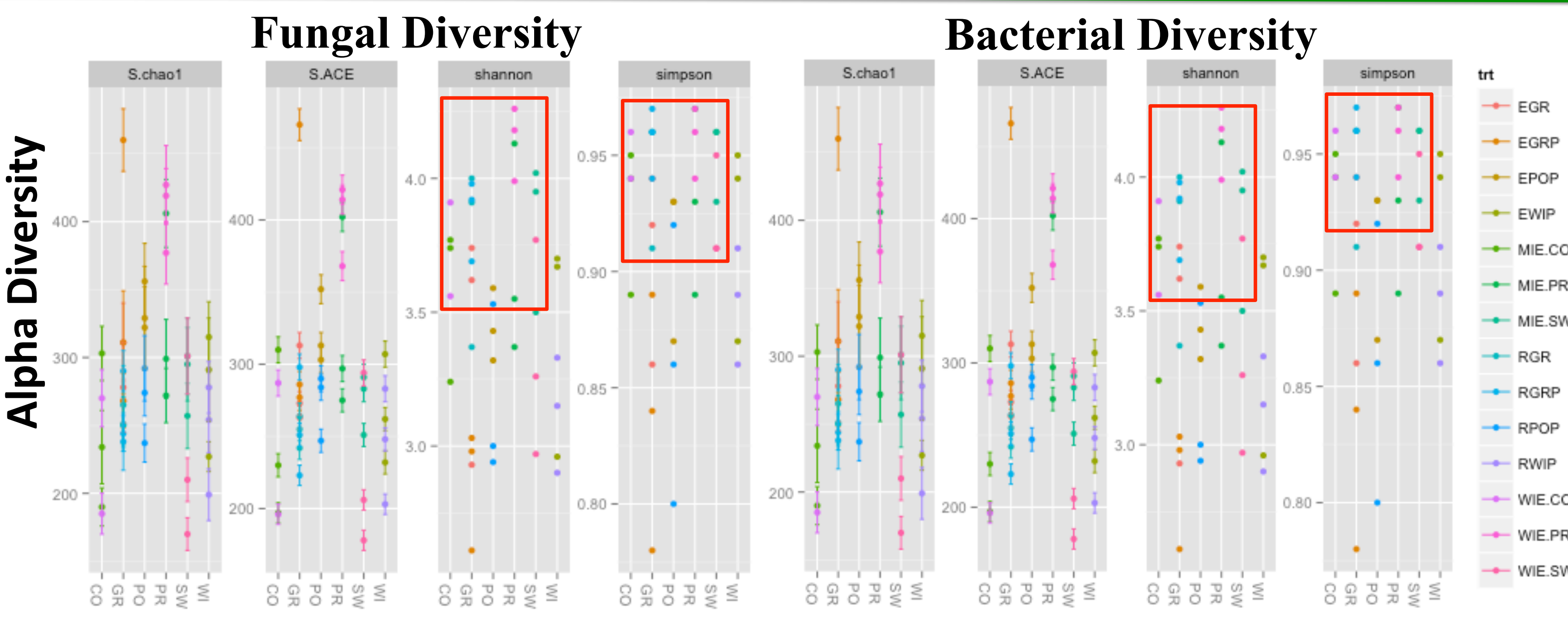
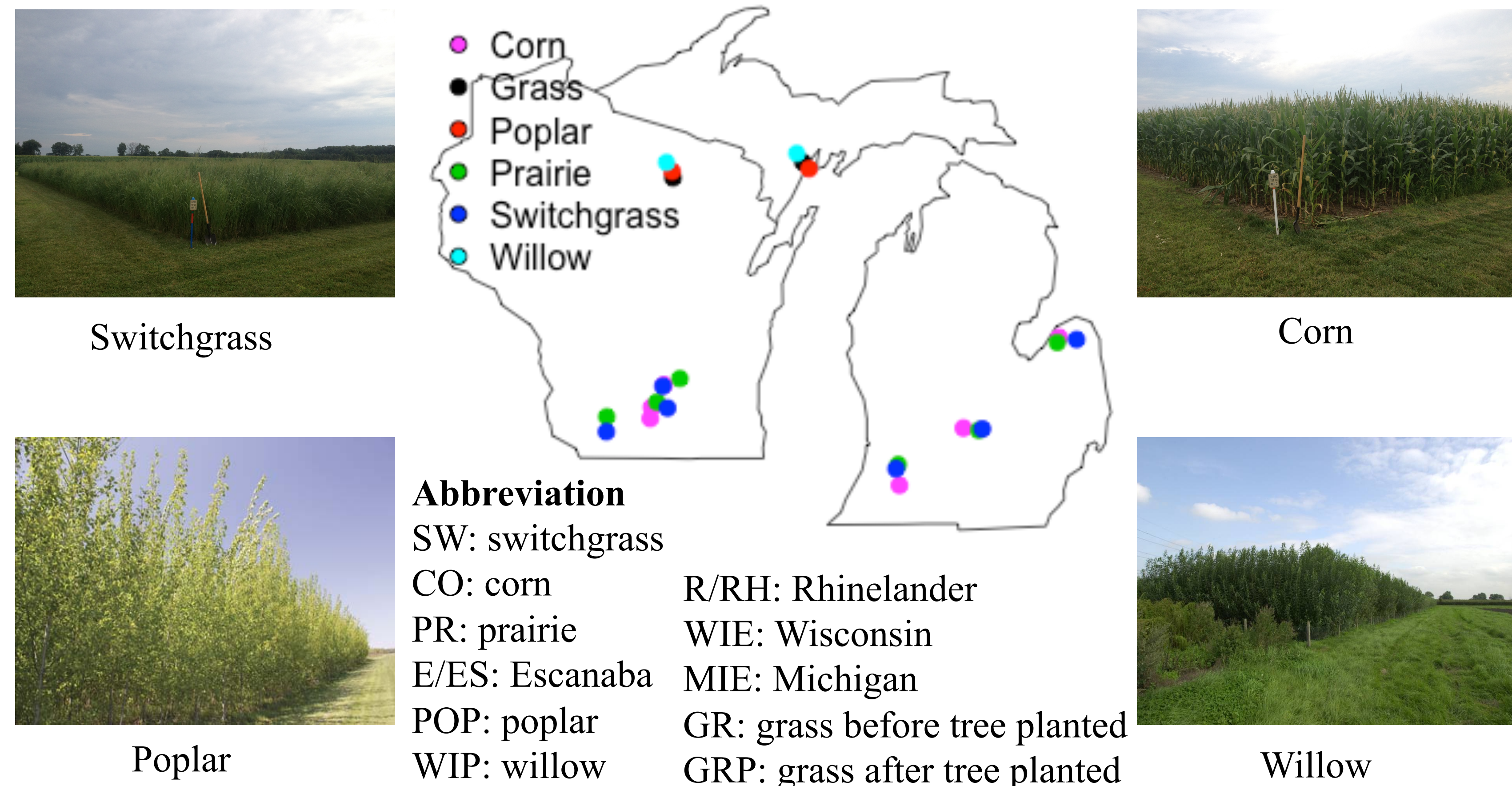
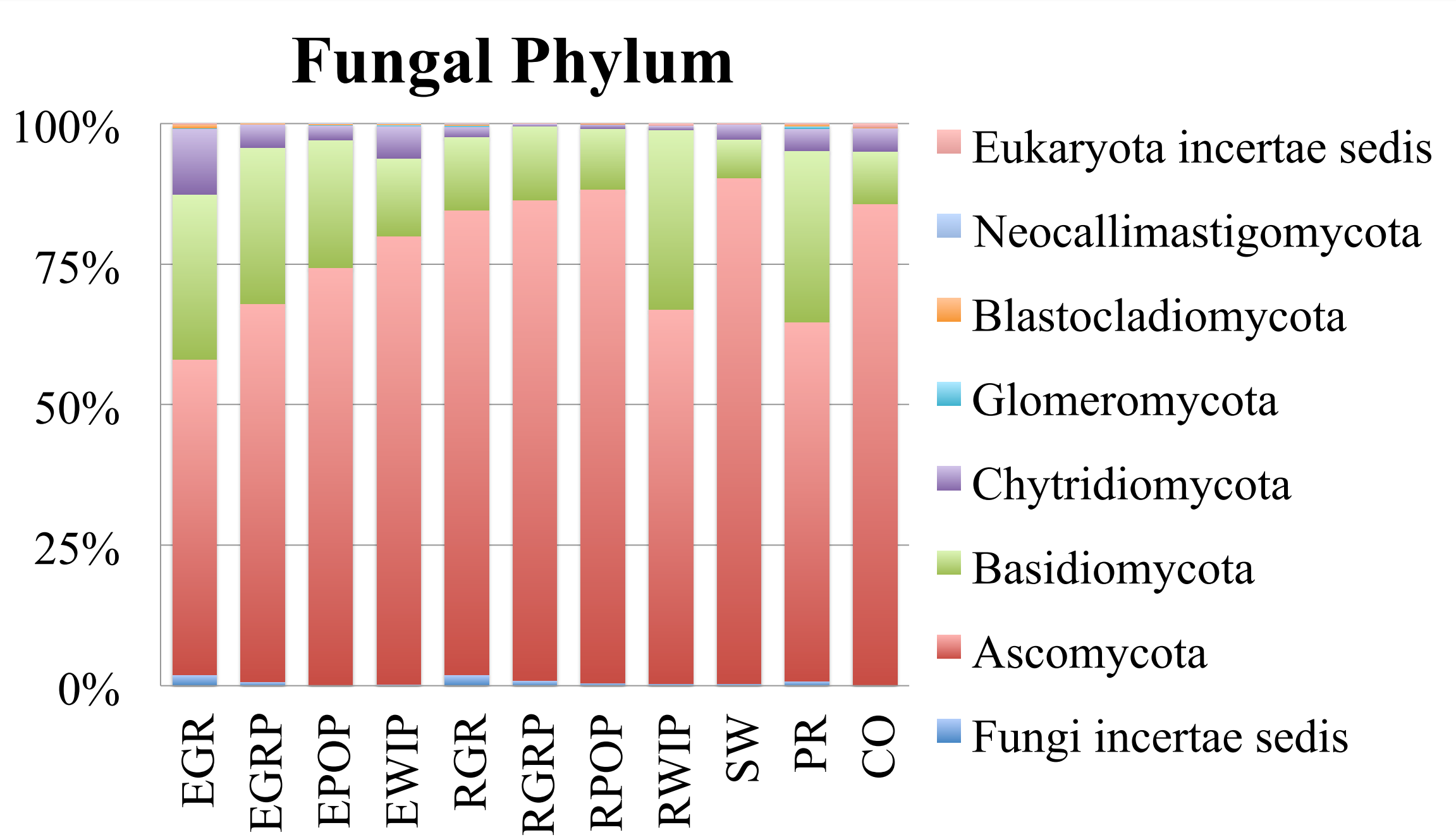


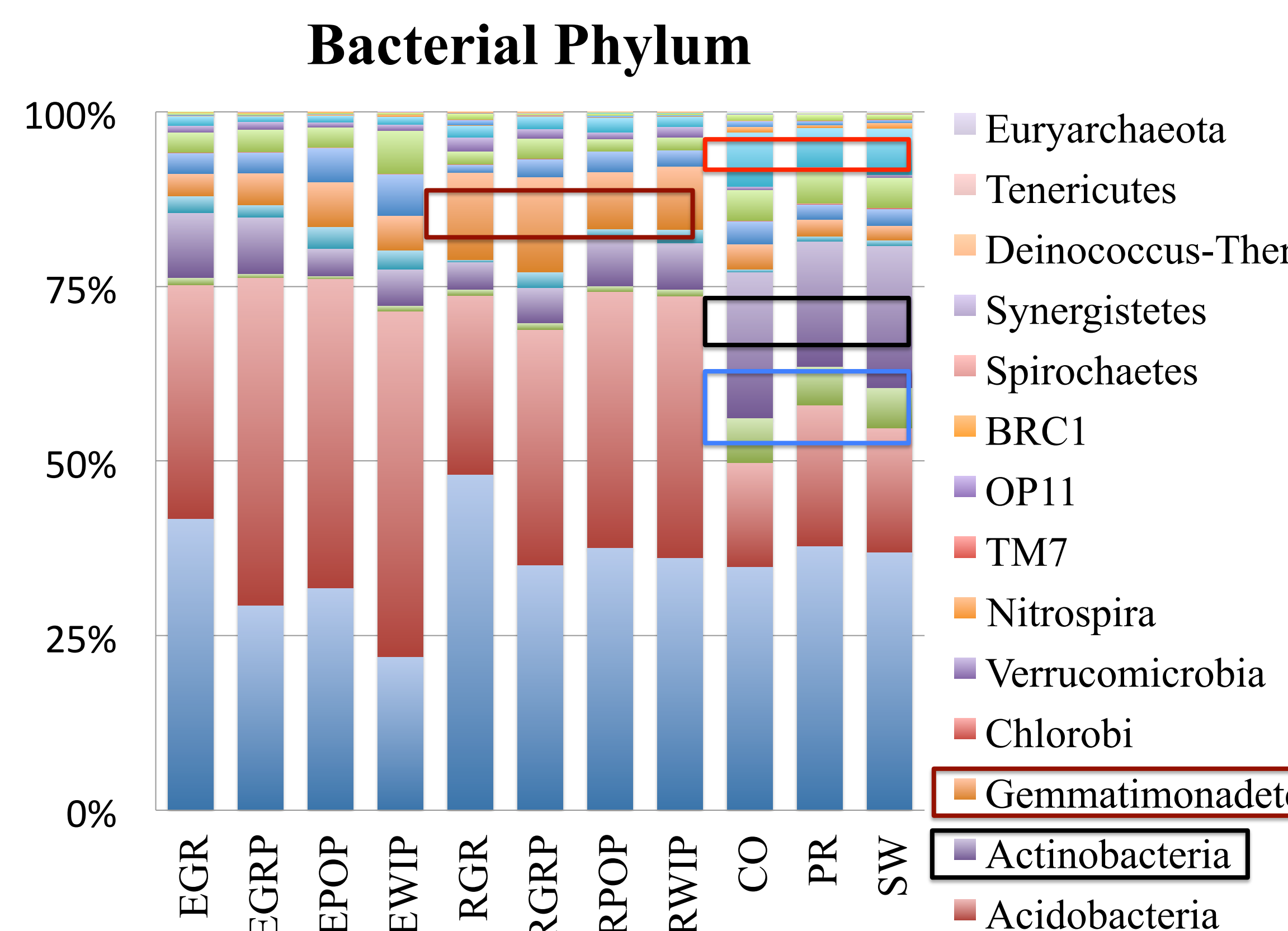
Introduction: Understanding how the cultivation of biofuel crops impacts soil microbial communities is critical to successfully managing the sustainability of these agricultural systems. We evaluated the effects of four typical biofuel crops (corn, switchgrass, poplar, and willow) which could be classified into two groups: grass and trees, on soil microbial communities using pyrosequencing of their rRNA genes. All the woody biofuel crops were sampled in Escanaba, MI (ES) and Rhinelander, WI (RH). And all the grass biofuel samples were collected in southern Michigan and Wisconsin.



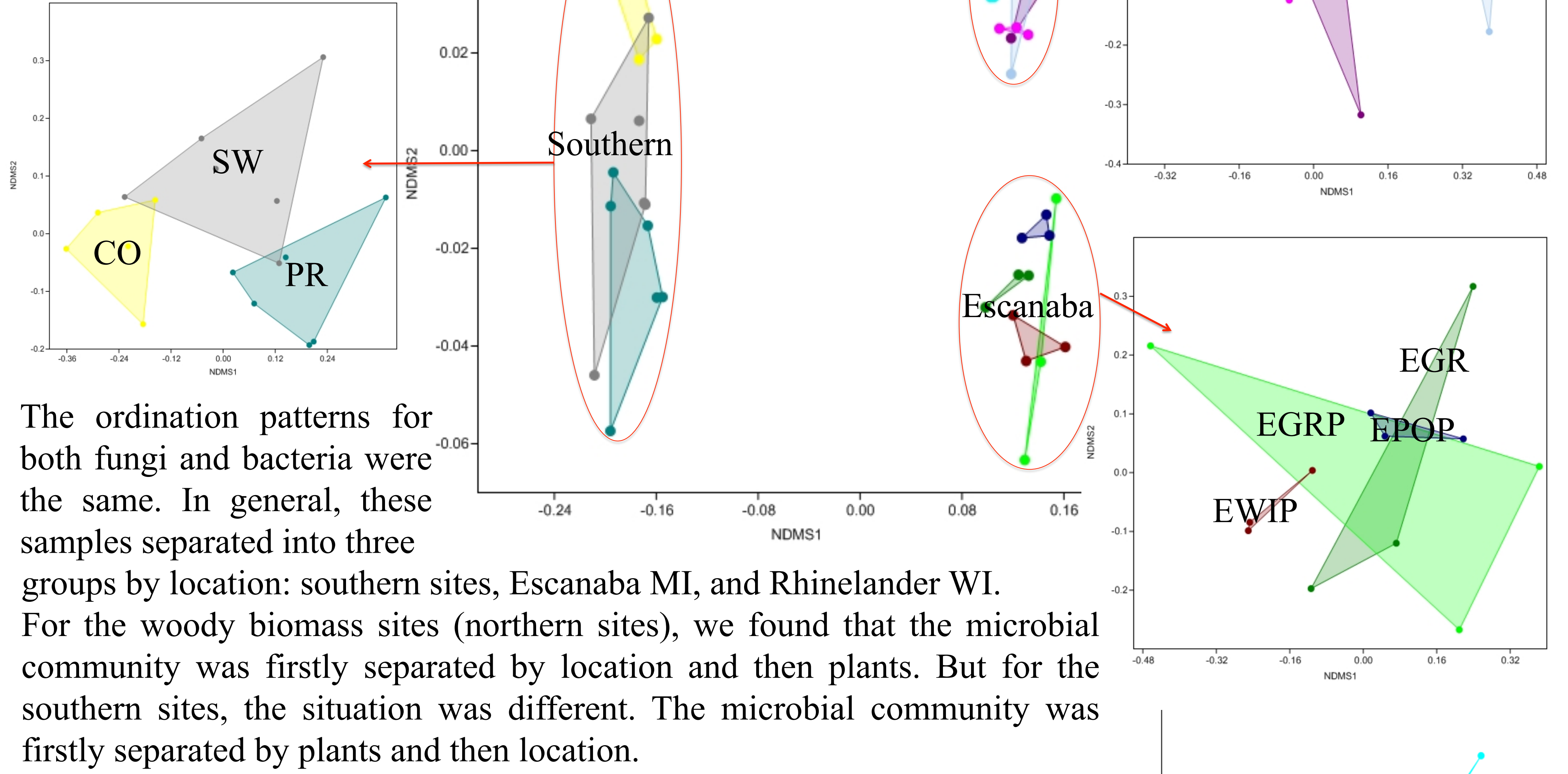
Diversity: The microbial diversity differs by regions. Samples from south had higher microbial diversity than the north. The grass biofuel samples had higher microbial diversity than the trees.



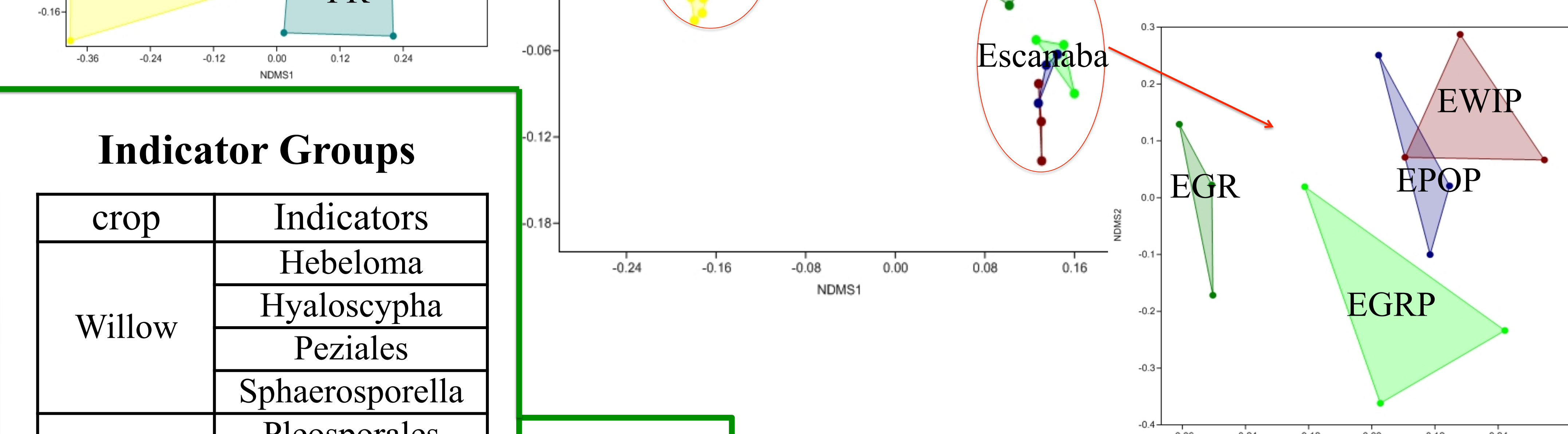
Microbial composition: All the samples had the same microbial component at the phylum level. However, the southern grass samples had higher Bacteroidetes, Actinobacteria, and Chloroflexi than other samples. The RH samples had higher abundance of Gemmatimonadetes. ES and RH samples showed different patterns of fungal community shift.



Ordination: We did the ordination for the whole data. Then according to the ordination pattern, we divided it into three groups (southern grass, Escanaba tree, Rhinelander tree.)



The ordination patterns for both fungi and bacteria were the same. In general, these samples separated into three groups by location: southern sites, Escanaba MI, and Rhinelander WI. For the woody biomass sites (northern sites), we found that the microbial community was firstly separated by location and then plants. But for the southern sites, the situation was different. The microbial community was firstly separated by plants and then location.



Indicator Groups

crop	Indicators
Willow	Hebeloma
	Hyaloscypha
	Peziales
	Sphaerosporella
Poplar	Pleosporales
	Phaeosphaeria
	Phaedothis
	Paraphaesphaeria
Corn	Hypocreales
	Ditopella
	Nohea
	Reddellomyces
Switchgrass	Spencermartinsia
	Sporophagomyces
	Stephanonectria
	Pyrenomyxa
Switchgrass	Pseudocercospora
	Harposporium
	Cytospora
	Chromendothia
	Chalastospora
	Asterodon
	Ascitendus

Summary

In general, the patterns of soil fungal and bacterial diversity and ordination were the same for all the samples. The fungi showed a more distinguishing pattern than bacteria. The southern grass biofuel sites had higher soil microbial diversity than the northern woody biomass sites. The soil microbial communities of woody biomass sites were separated into two groups by location. In the same location, they were separated by crop. The soil microbial communities of southern grass biofuel samples grouped by crop. Both grass biofuel plants and woody biomass crops shaped soil microbial communities.

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