Figure explanations and background

Before: Swabbed in June before attachment to transplant platform

After: Swabbed in August upon collection

Ambient: Collected from next to transplant in August upon collection

Present: Smithora growing on blade

Absent: No Smithora growing on blade

Smithora: Smithora blades themselves

Figure: Taxonomic Comp Phylum

These are the relative abundances of bacteria from each phylum in each treatment group. I have an uneven sample size and some swabs have more reads than others which is why the heights are uneven. This is just to show the main phylums that showed up at a relative abundance greater than 0.02% in each sample. I then grouped them together based on if they were swabs from before or after or if they were an ambient swab from when the transplant was collected. Since we are interested in the effect time could have in these figures compare ambients and before. To see a time affect unaffected by the action of transplanting.

Figure: Taxonomic Comp Class

You can start to see differences among treatments now. Anything that had an abundance lower than 0.02 percent was removed. So these aren't all classes just the main ones that are visible on the graph.

Figure: Taxonomic Comp Family

The most notable thing here is that shoots that were in the before & absent group have certain unique bacterial families that also showed up once they were in the after group and colonized by Smithora. It could be that they kept some of their original bacteria. Maybe they weren't just wiped clean and at the mercy of their environment after transplant (if this is a huge leap in logic please let me know).

Figure: PCOA

The ambients that were taken after the transplants seem to cluster with samples taken after the transplant so you can see that time is having an effect. But within the ambients and within the before communities you can see strong clustering based on smithora presence. After the transplant everything is less distinct. Ambient shoots that are never transplanted show some distance between those with/without smithora.

After shoots that have been transplanted show more overlap than non transplanted shoots. This could be because killing a shoot compromises its ability to maintain its own community. Unifrac was used as a distance measure.

Figure: NMDS

Similar clustering pattern to PCOA. Also notice that shoots with smithora are more spread out than those without. Unifrac was used as a distance measure.

Figure: different diversities

Phyloseq has this really nice feature where they calculate diversity for you using a variety of metrics and allow you to compare.

Figure: Random sample rarefy

I thought this was an interesting method that one blogger used. He created a loop that uses rarefy on 100 random samples and then calculates diversity and richness for them and then takes the mean. The random sample size is the minimum number of reads, It makes for a neater data set, and it makes sense to me. I like this method but if you have objections let me know.

Figure: Constrained PCA

I struggled with this one, and it’s still a work in progress. I wanted to use the orthogonal arrows to show that the effects of transplant (confounded with time unfortunately) are independent of each other. The only arrows that overlap are presence/absence of smithora. I think this is because shoots kept some of their original bacteria after they were colonized by bacteria and time and the action of transplanting affected shoots in a similar way regardless of whether or not they were colonized by smithora. Unifrac was used as a distance measure.