**Methods**

*Microbiome sequencing and analysis*

16S rRNA gene library preparation and sequencing was performed by GenomeQuebéc (Canada) with the Illumina MiSeq platform (PE 250bp). We targeted the V4 region with the primers 515f (5’-GTGCCAGCMGCCGCGGTAA) and 806r(5’-GGACTACHVGGGTWTCTAAT) and included PNA clamps to block plant DNA amplification. Low quality ends of the sequences were removed with Trimmomatic v 0.4. Primer sequence removal with Cutadapt, sequence merging and denoising with dada2, and taxonomy assignment with classify-sklearn were all performed in Qiime2 2021.2. We utilized the SILVA 138 SSU database to train the classifier with rescript according standard configurations. ASVs with less than 8 occurrences were discarded. Library sizes were normalized with Comulative Sum Scaling of the “MetagenomeSeq” package for beta diversity analysis, and rarefied to 47.000 reads per sample with the “phyloseq” package for alpha diversity analysis. A PCoA ordination of bray-curtis distances between microbial communities was calculated with the betadisper function of the vegan package. Significantce of community difference was evaluatated with the functions adonis2 from vegan and Adonis.pair from “EcolUtils” package. Fisher diversity index was calculated with the diversity function of the “microbiome” package, significance was evaluated with the functions “aov” from stats package and LSD.test function from the “agricolae” package. Differential abundance analysis was performed with the DESeq2 package. Random forest feature selection was performed on rarefied data with the “Boruta” package, and evaluated in a 5-fold cross validation repeated 200 times with the “caret” package. The full analysis code with raw data is available at <https://github.com/PedroBeschoren/Katherine_thesis>.

**Results**

We obtained 3.76M pair-ended 250bp sequences from 46 samples, with median phred quality score of 37 in the last base of the sequence after primer removal (SUP\_1\_phed\_quality). 3.09M sequences were filtered, denoised, and merged into 2.48M non-chimeric sequences. After removing plastid and chloroplast ASVs, ASVs occurring less than 8 times, and 6 samples with less than 6000 sequences, the library size per sample was 61,070±9,661 reads (SUP\_2\_rarefaction\_curve)

Microbial communities composition differed according to treatment (**1\_Beta\_Dipersion\_PCoA**). Beta dispersion tests indicated homogeneous multivariate variance (F = 1.907, p=0.1187). There were clear effects for treatment (F = 3.528, R² = 0.341, p = 0.001) and all pairwise treatment comparisons (SUP\_pairwise\_adonis\_table1). The most similar communities were in the MW and HC treatments, as can be observed by the proximity of the centroids. The BSF treatment was the most dissimilar from either controls, accentuating the community differences between CHT and C and between OF and MW/HC.

Differential abundance analysis also indicates clear bi-clustering of samples over 62 different ASVs in 25 Orders (**2\_deseq\_order**). ASV cluster 1 separates C and CHT from other treatments, and cluster 2 shows ASVs missing in OF. Cluster 3 shows Paenibacilalles missing in C and CHT and Catenulisporales missing in C and OF. Cluster 4 has ASVs missing in HC, and cluster 5 has a large group of ASVs, spread out in different samples. Cluster 6 is dominated by high-abundance ASVs which are less frequent in BSF and MW. As a general pattern, Pseudomonadales (10 ASVs), are more present in OF and less present in BSF treatments; Paenibacilalles (7 ASVs) are less present in C but more abundant in HC, MW and BSF; Bacillales (5 ASVs) are less frequent in OF and C; and Burkholderiales (5 ASVs) were spread out but slightly more frequent in HC. There is a large group of 29 ASVs from 14 Orders whose presence characterize HC, BSF and MW and is well populated by Paenibacillales and Catenulisporales. This groups shares Kineosporiales, with C and CHT and 9 ASVs from 7 Orders with OF. The higher presence of Catenulisporales in CHT and ASVs from cluster 4 in C best differentiate these treatments. The NSF and MW treatments are slightly differentiate by abundances of ASVS from Cluster 3.

Alpha diversity levels, measured by the Fisher Diversity index, also clearly differed between treatments (F = 8.81, p <0.001). The BSF treatment presented the highest diversity, similar only to MW. CHT treatment presented an intermediate diversity, as HC and C presented less diversity than MW. OF presented the lowest diversity, comparable only to C (**3\_fihser\_diversity**).Fisher Diversity index was used in place of Shannon diversity index due to better homogeneity of variances by the level test (p = 0.986 for Fisher and 0.058 for Shannon).

Random Forest found 94 ASV features as important predictors of treatment with accuracy of 0.951 and Kappa of 0.940. The most represented taxonomic groups are Family Paenibacillaceae (12 ASVs in 3 genera, 9 of them in Genus Paenibacillus) and Class Actinobacteria (27 ASVs in 7 orders, 7 of them in Order Streptomycetales).From the 15 ASVs with highest importance to the model, 9 are in class Bacilli and 5 in Class Actinobacteria, with an ASV from genus Kitasatospora showing the highest importance. Genus Pseudomonas and Family Blastocatellaceae are also well represented, with 5 ASVs each. As can be seen **4\_RF\_features\_heat\_tree**, BSF has the most Paenibacillus and Controls the least. HC and MW are well represented by Actinobacteria while OF has the most Pseudomonas. CHT is the most similar to control, but does not have large groups of clearly different ASVs when compared to other treatments.

We also detected 23 ASVs as RF predictors of number of flowers. While Firmicutes were the most represente phyla (with 8 ASVs), Class Bacilli and Phylum Proteobacteria presented more importance in the model. Notably, Burkholderiales had a much more relevant role as predictors of number of flowers than of treatment. 13 ASVs were also predictors of the different treatments. Boruta could not find any ASV that was imporntat to predict plant biomass

**Tables**

**SUP\_pairwise\_adonis\_table1:** pairwise comparsion of microbial community composition between treatments. OF = Organic fertilizer…..

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Combination | | | SumsOfSqs | MeanSqs | F.Model | R2 | P.value | P.value.adjs |
| BSF | <-> | C | 0.5012 | 0.5012 | 4.9698 | 0.2766 | 0.0020 | 0.0033 |
| BSF | <-> | CHT | 0.2944 | 0.2944 | 3.2914 | 0.2152 | 0.0020 | 0.0033 |
| BSF | <-> | HC | 0.3344 | 0.3344 | 4.7594 | 0.2840 | 0.0020 | 0.0033 |
| BSF | <-> | MW | 0.1960 | 0.1960 | 2.6510 | 0.1942 | 0.0020 | 0.0033 |
| BSF | <-> | OF | 0.6569 | 0.6569 | 6.9115 | 0.4087 | 0.0030 | 0.0041 |
| C | <-> | CHT | 0.2252 | 0.2252 | 2.0067 | 0.1337 | 0.0120 | 0.0120 |
| C | <-> | HC | 0.3434 | 0.3434 | 3.6325 | 0.2184 | 0.0010 | 0.0033 |
| C | <-> | MW | 0.2849 | 0.2849 | 2.8514 | 0.1920 | 0.0040 | 0.0043 |
| C | <-> | OF | 0.3852 | 0.3852 | 3.1702 | 0.2237 | 0.0040 | 0.0043 |
| CHT | <-> | HC | 0.2558 | 0.2558 | 3.0968 | 0.2051 | 0.0010 | 0.0033 |
| CHT | <-> | MW | 0.1876 | 0.1876 | 2.1469 | 0.1633 | 0.0040 | 0.0043 |
| CHT | <-> | OF | 0.4119 | 0.4119 | 3.7496 | 0.2727 | 0.0020 | 0.0033 |
| HC | <-> | MW | 0.1588 | 0.1588 | 2.3895 | 0.1785 | 0.0010 | 0.0033 |
| HC | <-> | OF | 0.3116 | 0.3116 | 3.5876 | 0.2640 | 0.0020 | 0.0033 |
| MW | <-> | OF | 0.3761 | 0.3761 | 4.0374 | 0.3097 | 0.0030 | 0.0041 |

**Legends**

**1\_Beta\_Dipersion\_PCoA:** PCoA ordination of Bray-Curtis distances between microbial communities. Different colors and shapes indicate different treatments, and the treatment label indicates the centroid. OF = Organic fertilizer…..

**2\_deseq\_order:** Bi-cluster heatmap indicating log-transformed the frequency of differentially abundant ASVs (rows) across the different samples (columns). ASVs clusters are numbered and alternating in grey scale to facilitate identification. Asterisks indicate ASVs that were also defined as important to separate treatments by the random forest model. Orders with a single ASV representative are also in grey scale.

**3\_Fisher\_diversity**: Fisher diversity index indicating treatment effect. Letters denote significant pairwise differences under the LSD test. Colors denote different treatment. OF = Organic Fertilizer…

**4\_RF\_features\_heat\_tree:** Matrix of heat trees comparing ASVs that were important according the Boruta RF model across the treatments. The large grey tree to the left shows a key to the legend. Each node represet a taxonomic group, from domain to ASV. Colors indicate log2-transformed relative abundances in pairwise comparsions across the rows and columsn that represent treatments.

**SUP\_1\_phed\_quality:** phred quality scores of forward and reverse reads before (a) and after (b) trimming of low quality ends with Trimmomatic and of primer sequences with Cutadapt.

**SUP\_2\_rarefaction\_curve:** Rarefaction curve showing library size and ASV diversity per sample (black lines). Six samples with less than 6.000 reads were removed from the analysis. Libraries were rarefied to at least 47.124 reads per sample (red dashed line)