Panicum virgatum microbial community and soil chemistry responses to conservation agriculture management

by

Anna Kazarina

B.S., Alcorn State University, 2017

A THESIS

submitted in partial fulfillment of the requirements for the degree

MASTER OF SCIENCE

Division of Biology
College of Arts and Sciences

KANSAS STATE UNIVERSITY
Manhattan, Kansas

2021

Approved by:

Major Professor
Ari Jumpponen

Copyright

Abstract

The holobiont concept of plants treats plants with their associated microbiomes that mostly consist of the fungi and bacteria as a single unit. Previous studies have shown the central role of microbiomes for plant health and performance, while also highlighting that the dynamic nature of the microbiomes can be affected by various biotic and abiotic factors that can rapidly change microbiome functionality. In the past two decades, development of novel technologies has substantially advanced research methods used to study plant and microbiome interactions – thus allowing for better identification of factors that shape microbiomes. Although effects of agricultural and production management on the plant, plant microbiomes and plant-associated soils are relatively well understood, effects of practical tools commonly employed in conservation agriculture remain largely unknown. Conservation agriculture management aims to achieve sustainable plant growth and productivity while minimizing active management such as fertilization, tillage, and soil movement. As a result of this lack of active management, conservation agriculture regimes promote the use of practical tools such as variety and planting density choices to achieve sustainable conservation goals The research described in this thesis aims to evaluate effects of conservation agriculture management on bacterial and fungal communities associated with soil and roots of four varieties of the native warm-season perennial grass Panicum virgatum L. (a.k.a. switchgass) initially planted at two different densities and growing under conservation agriculture conditions in southeastern Mississippi. To also assess the temporal dynamics, we repeatedly sampled switchgrass roots and associated soils approximating a log2 time series for a total of six times during one growing season, starting from within a week from the first leaf emergence in early spring to pre-frost in late fall. A small-scale pilot study comparing DNA isolation kits (Phire Plant Direct PCR vs. PowerSoil DNA Isolation kits)

confirmed that, although the direct extraction and amplification kits provide a cost-effective and expedient alternative to the more commonly used PowerSoil kits, the direct kits do not produce comparable community views from all plant tissues. Our studies of switchgrass microbiomes highlight that, while bacterial and fungal communities in roots and soils are temporally dynamic and shift compositionally during the growing season, planting densities have no strong overall effect on microbiome richness, diversity, or composition, and that if microbiomes associated with four switchgrass varieties differed among switchgrass varieties, they did so only in the beginning of the growing season. Indicator taxon analyses identified many bacterial and fungal taxa in soil and roots that represent potential variety specific taxa in the early season and temporally dynamic taxa. Similar to the biotic attributes, the soil chemistry was minimally affected by switchgrass variety choice or planting density, although some temporal dynamics were observed. These findings indicate that in the hierarchy of tested factors, seasonal dynamics are the strongest driver of switchgrass microbiomes and soil chemistry. The seasonal dynamics overwhelm the effects of conservation agriculture management choices, as shown here for choice of switchgrass variety and planting density. Notwithstanding and based on our indicator taxon analyses that identified putative plant symbionts and pathogens or soil-inhabiting nitrogen fixing taxa, careful variety choices can potentially facilitate mindful microbiome manipulations to support the sustainable switchgrass productivity.

Table of Contents

List of Figures

List of Tables

Acknowledgements

I had an amazing journey as a Master of Science (M.Sc.) student at Kansas State University. None of this would be possible without my academic support team. I am very thankful for my wonderful mentor, Ari Jumpponen, for his guidance and support every step of the way. His optimism and professionalism always inspired me, and I have been very lucky to learn from him. I also would like to thank my undergraduate mentor and the member of my M.Sc. committee, Keerthi Mandyam, for believing in me, and always seeing more in me than I could. She is a role model who has combined both being a loving mother and a woman of science. I am very thankful for Ananda Nanjundaswamy for giving me my first job in the science laboratory where my journey in science began. I would like to thank Lydia Zeglin for serving as a member of my M.Sc. committee as well as for giving me insightful advice and guidance in my research. I also would like to thank members of Jumpponen lab to include Hannah Dea, Samantha Fox, and Kyle Ismert for their willingness to help with my research and data analysis. My journey at the Kansas State University would have been very different without these people.

I would also like to thank people and organizations who have made this research possible. I would like to thank NSF-DEB award #1457309, NSF-EPSCoR award #1656006 and USDA AFRI award #2017-67014-26265 for providing funding source to conduct my research. I would like to thank Girish Panicker, Professor and Director of Conservation Research for establishing and maintaining the switchgrass site at Alcorn State University where sampling for my research took place. I would like to thank the Alcorn crew and in particular Joseph Bridges for their help and support during the field work. I would like to thank Heather Tyler for giving me an amazing opportunity to work in her lab to generate some of my data and teaching me

extraction techniques. I also would like to thank Alina Akhunova, the director of the Integrated Genomics Facility at Kansas State University for her hard work and delivering sequencing data in very short periods of time.

Finally, I would like to thank my amazing family and friends. I would like to thank Jeff Shehan for being my true friend, always being there for me and making my Manhattan journey so much better. I am very grateful for Hannah Dea for always being on my team and cheering me on during this process. I also would like to thank my partner Richard Blakesleay for the love, support, and reminding me of my big picture goals when I was stuck on little things. And lastly, I cannot express how thankful I am for my loving parents Oleg and Elena. I am very grateful for their love and encouragement throughout my life, always giving me advice, looking out for my best interest, and watching me grow and develop into the woman I am today.

Dedication

I dedicate my work to my parents Oleg and Elena Kazariny

Chapter 1 - Introduction

Plants are no longer considered as single organisms, but as a holobiont system of the plant host and its associated microbial communities that together form and function as a discrete ecological unit. Microbial communities associated with the plant, also called plant microbiome mostly consist of fungi and bacteria that play a vital role in plant development and fitness (Mendes et al 2013; Vandenkoornhuyse et al. 2015). Many scientists have focused on understating the plant-microbiome interactions, dynamics, and functionality for the potential informed system management to improve overall plant health, performance, and sustainable productivity (Kim et al. 2012; Ray et al. 2015). With the continued technological improvements, many tools have been developed to study plant-microbiome. Currently, one of the common tools to dissect the plant-associated microbial communities is the use Next Generation Sequencing (NGS) (e.g., Cai et al. 2017, Fuentes et al. 2020, Rodrigues et al. 2017, Wand & Sugyama 2020). NGS technologies have allowed for generation of microbial sequence data from plant tissues and plant-associated soils and have therefore revolutionized our way of studying microbial diversity, richness, and community composition. Although these NGS tools are expedient and cost-efficient, the nucleic acid isolation still represents a bottleneck and usually requires substantial monetary and time investments. While many tools have become available to acquire microbial DNA, the data produced using different materials, protocols, and reagents are less studied and may come with a range of potential biases or result in incongruent conclusions (Zinger et al. 2019). For plant microbiome studies, NGS library preparation biases have been described for example for rhizosphere bacteria (Haro et al. 2021). Although studies that compare sequence library preparation tools for bacterial data, there is a lack of knowledge on how different DNA extraction methods may affect fungal community data characterizing communities in different plant tissues.

Direct microbial DNA extraction and amplification tools designed for plant tissues are cost-efficient and expedient alternatives to the commonly used nucleic acid isolation systems. In Chapter 1, we test if direct extraction and amplification kits (e.g., Phire Plant Direct PCR – ThermoFisher Scientific) can perform comparably in generating fungal MiSeq metabarcode data to the more common conventional DNA isolation kit (PowerSoil DNA Isolation Kit – Qiagen, Hilden, Germany) from different plant tissues.

In Chapter 3, we dissected the microbiomes of the *Panicum virgatum* L. (switchgrass) growing under conservation agriculture management conditions. Plant microbiomes are dynamic, and a range of abiotic and biotic factors can change the composition and functionality of the microbial community in very short periods of time. A better understanding of the switchgrass microbiome dynamics can help in finding ways for informed microbiome management to achieve desired sustainable conservation goals. Conservation agriculture management aims to achieve sustainable plant growth and biomass production while minimizing active management such as fertilization and tillage. Because of the lack of active management guided by the conservation agriculture principles, some practical tools are commonly employed in conservation agriculture management including choice of crop cultivar or planting density – potential factors that shape the plan microbiome. However, the effect of those factors on the plant microbiome is understudied and poorly understood. In addition, only limited data are available to characterize the switchgrass microbiome seasonal dynamics in the course of the growing season. The second chapter of this thesis aimed to evaluate effects of switchgrass variety and planting density on the chemistry of soils underneath switchgrass grown under conservation agriculture management as well as on bacterial and fungal communities in roots and soil. Additionally, samples collected six times over the course of a growing season permitted characterization of the temporal dynamics of soil chemistry as well as of microbiomes in soils and switchgrass roots.

Ongoing technological progress keeps opening horizons of methods that can be used to study plant-microbiome interactions and dynamics. These studies further our understanding of the effects of factors affecting plant associated microbial communities and soil environment.

References

Cai, F., Pang, G., Miao, Y., Li, R., Li, R., Shen, Q., et al. (2017). The nutrient preference of plants influences their rhizosphere microbiome. Applied Soil Ecology, 110, 146-150.

Fuentes, A., Herrera, H., Charles, T. C., & Arriagada, C. (2020). Fungal and Bacterial Microbiome Associated with the Rhizosphere of Native Plants from the Atacama Desert. Microorganisms, 8(2). https://doi.org/10.3390/microorganisms8020209

Haro, C., Anguita-Maeso, M., Metsis, M., Navas-Cortés, J. A., & Landa, B. B. (2021). Evaluation of Established Methods for DNA Extraction and Primer Pairs Targeting 16S rRNA Gene for Bacterial Microbiota Profiling of Olive Xylem Sap [10.3389/fpls.2021.640829]. Frontiers in Plant Science, 12, 296.

Kim, S., Lowman, S., Hou, G., Nowak, J., Flinn, B., & Mei, C. (2012). Growth promotion and colonization of switchgrass (Panicum virgatum) cv. Alamo by bacterial endophyte Burkholderia phytofirmans strain PsJN. Biotechnol Biofuels, 5(1), 37. https://doi.org/10.1186/1754-6834-5-37

Mendes, R., Garbeva, P., & Raaijmakers, J. M. (2013). The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms. FEMS Microbiol Rev, 37(5), 634-663. https://doi.org/10.1111/1574-6976.12028

Ray, P., Ishiga, T., Decker, S., Turner, G., & Craven, K. (2015). A Novel Delivery System for the Root Symbiotic Fungus, Sebacina vermifera, and Consequent Biomass Enhancement of Low Lignin COMT Switchgrass Lines. BioEnergy Research, 8. https://doi.org/10.1007/s12155-015-9636-8

Rodrigues, R. R., Moon, J., Zhao, B., & Williams, M. A. (2017). Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. Global Change Biology Bioenergy, 9(6), 1057-1070. https://doi.org/10.1111/gcbb.12396

Vandenkoornhuyse, P., Quaiser, A., Duhamel, M., Le Van, A., & Dufresne, A. (2015). The importance of the microbiome of the plant holobiont [https://doi.org/10.1111/nph.13312]. New Phytologist, 206(4), 1196-1206. https://doi.org/https://doi.org/10.1111/nph.13312

Wang, B., & Sugiyama, S. (2020). Phylogenetic signal of host plants in the bacterial and fungal root microbiomes of cultivated angiosperms. Plant J, 104(2), 522-531. https://doi.org/10.1111/tpj.14943

Zinger, L., Bonin, A., Alsos, I. G., Bálint, M., Bik, H., Boyer, F., . . . Taberlet, P. (2019). DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions [https://doi.org/10.1111/mec.15060]. Molecular Ecology, 28(8), 1857-1862. https://doi.org/https://doi.org/10.1111/mec.15060

Chapter 2 - Performance comparison of direct DNA extraction and amplify kits: promising tool to analyze fungal communities

Abstract

Next-generation sequencing (NGS) of fungal DNA metabarcode amplicons has revolutionized our abilities to study fungal communities in a wide range of habitats including plant tissues. Although these NGS tools are expedient and cost-efficient, the nucleic acid isolation usually requires substantial monetary and time investment. With the growing interest in NGS, many tools have become available on the market for acquiring microbial DNA. However, the effect of these approaches on the evaluation of fungal communities remains unexplored and can result in a range of potential biases. We aimed to compare so called direct microbial DNA extraction and amplification tools designed for plant tissues with those more commonly used for DNA extraction from plant tissues. We sampled leaves and roots from a common prairie plant, *Schizachyrium scoparium* (Michx.) Nash (little bluestem), from four grassland plots at two different times for a total of eight samples and compared direct extraction and amplification kits (Phire Plant Direct PCR – ThermoFisher Scientific, Wilmington, Delaware; E.Z.N.A. Plant Direct – Omega Bio-tek, Narcoss, Georgia; Extract-N-Amp – Invitrogen, Carlsbad, California) with a conventional DNA isolation kit (PowerSoil DNA Isolation Kit – Qiagen, Hilden, Germany). Pilot experiments indicated that all four systems permitted PCR amplification of the ITS2 region using fITS7 and ITS4 primers, but Phire system seemed to produce amplicons most consistently. Therefore, we selected the Phire Plant Direct PCR kit for the further comparisons with the commonly used MoBio Extraction kit. We analyzed pairs of ITS2 MiSeq libraries generated with the two systems and amplified with identical reagents under identical reaction conditions. Both systems produced amplicons for fungal metabarcode analyses and provided comparable community data for root samples but not for leaf samples. We conclude that direct extract and amplification systems can provide a user-friendly alternative to the commonly used systems lowering the cost and expediting the sample processing. However, further protocol modifications might be necessary to achieve comparable richness/diversity metrics from different plant tissues and, consequently, comparable ecological conclusions. Although fungal DNA extracted from the same plant roots and leaves using direct extraction and amplify kits may differ in DNA yield, community coverage, and composition, this study suggests that these tools bear a promise for expedient amplicon generation from plant tissues whilst also highlighting the importance of the consistency in the research methods and the awareness of potential biases among various studies.

Introduction

Over the past decade, the number of studies on plant-associated bacteria and fungi (collectively called plant microbiomes) has dramatically increased. Similar to the human microbiome, plant microbiomes are compositionally and functionally diverse impacting the health of the host (Sánchez-Cañizares et al. 2017). For example, while some members of the plant microbiome can improve growth and increase plant stress tolerance, others can cause disease (reviewed in White et al. 2019). Understanding the important roles microbiomes play in plant performance is essential for developing new management strategies for effective microbiome manipulation to support sustainable agriculture (Busby et al. 2017). The interest in plant microbiomes has concurrently accelerated the development of tools for studying microbiomes as well as development of marketable products to meet the increasing demand for microbiome applications or microbial biofertilizers.

MiSeq, Illumina’s integrated next generation sequencing (NGS) platform, is a commonly used tool to analyze microbiomes that inhabit plant tissues (e.g., Cai et al. 2017; Fuentes et al. 2020; Rodrigues et al. 2017; Wand & Sugyama 2020). Like some other NGS tools, MiSeq technology is expedient, cost-efficient, and easy to implement. It is the most widely used NGS tool to study plant microbiomes, partly as a result of the length of paired-end reads that conveniently cover bacterial and fungal metabarcode markers. However, steps that precede sequencing can be complex and introduce biases that may alter either coverage, diversity or composition of the sequence data used to characterize the target communities. Among these steps is nucleic acid extraction, for which many tools are available on today’s market. Commercially available kits can vary substantially in user convenience, cost, and time needed for sample processing. For example, a variety of so-called direct extraction kits (*e.g*., Phire Plant Direct PCR Kit – ThermoFisher Scientific, Wilmington, DE; Extract-N-Amp Plant PCR Kit – Sigma-Aldrich, St. Louis, MO; or, Tissue Direct PCR Kit – Omega Bio-Tek, Norcross, GA) designed for direct PCR amplification of DNA from plant tissues, provide an attractive alternative to more commonly used extraction systems (e.g., MoBio PowerSoil DNA Isolation Kit – MoBio Laboratories, Carlsbad, CA or E.Z.N.A. Plant/Soil DNA Kits – Omega Bio-Tek, Norcross, GA). Unfortunately, variability of the DNA isolation kits and lack of method standardization can become an issue for the acquired sequence data – particularly their comparability (Zinger et al. 2019). For plant microbiome studies, NGS library preparation biases have been described for rhizospehere bacteria (Haro et al. 2021). Although studies that compare sequence library preparation tools for bacterial data, there is a lack of knowledge on how different DNA extraction methods may affect fungal community data associated with different plant tissues. As a result, there is a need to compare data acquired after using different DNA isolation kits, especially for different plant compartments.

Given the substantial promise of expedience and cost-efficiency that direct tissue PCR tools offer, we aimed to systematically evaluate how different DNA extraction methods compare when used to dissect fungal communities inhabiting plant tissues. To our knowledge, no study has compared fungal data generated using different extraction kits in a side-by-side experiment. Our primary objectives were to (1) evaluate compatibility direct PCR kits for generating fungal MiSeq data; (2) compare the performance of one such direct PCR kit to a more commonly employed DNA isolation kit; and, (3) examine the effect of the plant tissue on how the different DNA extraction kits perform. Better understanding of how available cost-effective and expedient DNA isolation and amplicon generation tools is critical to ensure compatible data generation and key to successful exploration of the plant microbiome systems.

Materials and methods

Study sites and sampling

We sampled *Schizachyrium scoparium* (Michx.) Nash (little bluestem) leaf and root tissues at two prairie sites in Northeastern Kansas, USA in the summer of 2018 during early and late in the growing season. We selected one prairie site in eastern Kansas (Anderson County Prairies near Welda, KS; EKS: 38° 10' - 95° 16') and one in north central Kansas (Konza Prairie Biological Station; KPBS: 39° 6' - 96° 36'). The two sites differ in their mean annual precipitation: EKS receives an annual average of 1016 mm and KPBS an annual average of 838mm. At each site, we located two adjacent plots measuring 20m x 50m for a total of four whole plots. At each corner of each whole plot, we located the *S. scoparium* plant closest to the corner and excavated the whole plant with a transplant shovel. The four plants sampled from each whole plot were considered subsamples and, thus, the whole plot is the experimental unit. To avoid soil contamination on the foliar tissues, we first sampled several leaves with dissecting scissors, placed the sampled leaves in a Ziploc bag and stored them in a cooler with ice. To ensure that only *S. scoparium* roots were sampled, only roots attached to identifiable tillers were excised with dissecting scissors, cleaned from loose soil, and placed in a Ziploc bag and stored in a cooler with ice. All sampled plant tissues were stored on ice until transfer within eight hours to a -20°C freezer where stored until further processing. The tissues were sampled once early (May/June) and once late (September) in the growing season. KPBS plots were sampled on May 15th and on September 20th; EKS plots on June 1st and again September 19th. This resulted in 32 total pairs of leaf and root samples from four whole plots sampled twice.

Pilot experiment

Several kits were tested for the direct amplification of the fungal metabarcodes from the plant tissues. *Schizachyrium scoparium* root and leaf samples were selected for the experiment. One fine root and one leaf were randomly selected from each 32 plants and a total of six 3mm leaf disks and six 5mm root segments were randomly excised with the sterile Ted Pella Biopsy Punches (Ted Pella Inc., Redding, CA). Two leaf disks and two root segments were randomly assigned to one of the three direct extract and amplify systems: 1) Phire Plant Direct PCR – ThermoFisher Scientific, Wilmington, Delaware; 2) E.Z.N.A. Plant Direct – Omega Bio-tek, Narcoss, Georgia; and, 3) Extract-N-Amp – Invitrogen, Carlsbad, California. The DNA from each plant tissue was extracted following the manufactures' protocols, followed by the PCR amplification of the ITS2 region using fITS7 and ITS4 primers with identical conditions (see below for the reaction conditions). All three systems produced visible amplicons, although Phire seemed to produce amplicons most consistently. As a result, we chose Phire Plant Direct PCR system for the direct comparison with the commonly used MoBio PowerSoil DNA Isolation Kit (MoBio Laboratories, Inc., Carlsbad, CA, USA).

DNA extraction, PCR amplification, and sequencing

Schizachyrium scoparium root and leaf samples were thawed and prepared for PCR amplicon generation. A total of six 3mm leaf disks and six 5 mm root segments were excised with sterile Ted Pella Biopsy Punch and three of each randomly assigned to one of the two extraction systems: either MoBio PowerSoil DNA Isolation Kit or Phire Plant Direct PCR Kit resulting in pairs of leaf samples extracted by either of the two methods. Total DNA was extracted following the manufacturers' protocols for either extraction system. The final MoBio extracts were eluted in a total of 100µl of elution buffer, DNA yields were low and left unnormalized for metabarcode amplicon generation. The Phire extractions were conducted in 50µl volumes of dilution buffer and tissues crushed with sterile fine point forceps as instructed in the manufacturer's protocol. DNA from the subplot-level samples was pooled to one representing the whole plot, for a total of eight leaf and root samples extracted using one of the two extraction systems for a total of 16 individual extracts for each of leaves and roots. The extracted DNAs were 10-fold diluted (10^0-10^{-2}) in sterile molecular grade water and the dilutions consistently producing amplicons (10^{-2}) in pilot reactions were selected for production of metabarcode amplicons for sequencing. Positive and negative controls were included for yield and contamination checks. Molecular grade RNA- and DNA-free H_2O was used as the negative control. *Saccharomyces cerevisiae* was used as a positive control.

We chose the Internal Transcribed Spacer (ITS) of the ribosomal RNA gene – the proposed universal fungal barcode (Schoch et al. 2012) – for our analyses. We used the fITS7 (Ihrmark et al. 2012) and ITS4 (White et al. 1990) primers with unique 12bp barcodes in each 5'-end in 50 µl PCR reactions. The volumes and final concentrations of reagents were as follows: 10 µl forward and reverse primer (1 µM), 10 µL template DNA, 5 µl dNTP (200 µM), and 0.25 µL (1/2 unit) Phire Green Hot Start II DNA polymerase (ThermoFisher Scientific, Waltham, MA), 10 µL of Phire 5X HF Buffer with 7.5 mM $MgCl_2$, and 14.5 µL molecular grade water. The PCR reactions began with an initial denaturing step for 30 s (98°C) and were followed by 30 cycles (root samples) or 35 cycles (leaf samples) of 10 s of denaturing (98°C); 30 s of annealing (54°C); 1 min of extension (72°C); and concluding with a 10 min final extension (72°C). Amplification of PCR contaminants was determined by a negative PCR control in which templates were replaced with ddH_2O. Each sample was PCR-amplified in triplicate and 20 µL of each amplicon was combined into one per experimental unit. The pooled 60 µl amplicons were purified using the Mag-Bind RXNPure Clean-up system (Omega Bio-Tek Inc., NorCross, GA) following a modified manufacturer protocol except for a 1:1 ratio of PCR product to magnetic bead solution and two rinse steps with 80% ethanol. Following cleanup, a total of 250 ng of amplified DNA per sample was pooled into one. Because the negative controls yielded DNA quantity measurements similar to the elution buffer alone, the entire elution volume from the cleanup (40µl) was included. Illumina adapters and indices were added using four PCR cycles, KAPA Hyper Prep Kit (Roche, Pleasenton, CA USA), and 0.5µg starting DNA. The library was sequenced (2 x 300 cycles) using the Illumina MiSeq Personal Sequencing System at the Integrated Genomics Facility (Kansas State University, Manhattan KS USA). The sequence data are available through the Sequence Read Archive under BioProject PRJNA714089; BioSamples SAMN18287690-SAMN18287815.

Sequence data processing

The sequence data were processed using the mothur pipeline (v. 1.44.3; Schloss et al. 2009) following the MiSeq standard operating protocol to generate ASV (Amplified Sequence Variant) data. In brief, the sequence data were extracted from the paired-end .fastq files and contiged. Sequences with more than 1 bp difference with the primers, without an exact match to the sample-specific identifiers, or with long homopolymers (maxhomop=9) were omitted. The sequences were truncated to the length equal of the shortest high-quality read (237 bp excluding primers and sample-specific identifiers), pre-clustered (Huse et al. 2008), and potential chimeras identified (UCHIME; Edgar et al. 2011) and removed. The remaining sequences were assigned to taxon affinities using the Naïve Bayesian Classifier (Wang et al. 2007) and the UNITE taxonomy reference (http://unite.ut.ee/repository.php; Köljalg et al. 2013). Non-target reads (those with no match in the UNITE-curated INSD or assigned to Protista and Plantae) were removed from further analyses. The quality-screened sequences were assigned to ASVs. Rare ASVs represented by fewer than ten reads were removed (a total of 94,573 sequences or 7.0% of the total yield and 68,246 ASVs or 94.5% of the total number of ASVs) as potential artifacts (Brown et al. 2015; Oliver et al. 2015). To estimate richness and diversity, we iteratively (100 iterations) calculated observed (S_{Obs}) and extrapolated (Chao1) OTU richness, diversity (Shannon's diversity; H' = - $\sum p_i \, ln \, p_i$), and evenness (Shannon's equitability; $EH = H'/ln \, S_{Obs}$) with the data subsampled to 12,500 sequences per sample, as recommended in Gihring et al. (2011) to avoid biased comparisons of diversity and richness estimators in samples with unequal sequence yields.

Data analysis

The leaf (N = 16) and root (N = 16) disks for MoBio and Phire extractions were excised from the same tissues and are thus inherently paired. As a result, the richness and diversity estimators from samples extracted with the two systems were compared using the non-parametric, paired Wilcoxon tests that are based on simple signed rank scores; in case of ties, average ranks were used. To visualize and infer compositional differences in the fungal community composition, we estimated pairwise Bray-Curtis distances and visualized these data Principal Coordinates Analyses (PCoA). The community data across the extraction systems were compared using a nonparametric permutational analog of traditional analysis of variance (PERMANOVA). We also tested whether the variability in the fungal communities from the two extraction systems was homogeneous using betadispr. All data analyses were conducted using packages in R: vegan (Oskanen et al. 2020), indicspecies (De Caceres & Legendre 2009), ape (Paradis & Schliep 2019), lme4 (Bates et al. 2015),R studio (v 4.0.2 R Core Team; 2020)

Results

General data description

We analyzed a total of 1,254,848 high quality sequences assigned to a total of 3,958 ASVs. MoBio extractions yielded a total of 503,874 sequences – 242,432 from leaves (30,304 ± 9,984; mean ±st.dev per sample) and 261,441 from roots (32,680 ±13,934), whereas the Phire extractions yielded a total of 750,974 sequences – 423,607 from leaves (52,951 ±27,793) and 327,367 from roots (40,920 ±22,124). The MoBio extracted sequence data were assigned to total of 2,165 ASVs from leaves (695 ±74; mean ±st. dev.) and 2,180 ASVs from roots (663 ±70) and the Phire extracted sequence data were assigned to 2,298 ASVs from leaves (604 ±133) and 2,194 ASVs from roots (575 ±133). Overall, despite the greater sequence yields from Phire extracted samples, the number of ASVs was marginally higher in leaf samples extracted with MoBio than with Phire (Wilcoxon Signed Rank Test W = -13.0, P = 0.0703). In contrast, the number of ASVs recorded from root samples did not differ between the two systems (Wilcoxon Signed Rank Test W = -11.0, P = 0.1484).

The sequence data were strongly dominated by the Phylum Ascomycota in both leaves (451,384 sequences or 67.7%; 1,786 or 21.9% of leaf ASVs) and roots (382,111 or 64.9%; 1,743 ASVs and 61.2% of root ASVs), followed by the Phylum Basidiomycota (203,541 or 30.6% sequences and 859 or 30.0% ASVs in leaves and 195,330 or 33.2% sequences and 845 or 30.0% in roots). Other phyla were infrequent accounting for less than 1.6% of all sequence data, although contributing a substantial number of ASV (326 ASVs and 8.2%). A small proportion of sequences remained unclassified (3,276 or 0.26% sequences; 36 or <1% ASVs). The leaf and root sequence data were distributed across 408 and 401 fungal genera, respectively. Genera in Mycosphaerellaceae (Dissoconium 50,636 sequences or 7.6% and Ramicloridium 50,229 sequences or 7.5%) and Bionectriaceae (Ijuhya 41,775 sequences or 6.2%) dominated the leaf communities, whereas Mycosphaerellaceae (Dissoconium 41,039 sequences or 7.0%), Bionectriaceae (Ijuhya 40,937 sequences or 7.0%) and Xylariaceae (Anthostomella 38,515 sequences or 6.5%) dominated root communities.

The two methods resulted in some different richness and diversity estimates in leaves (Figure 2.1). Extrapolated Chao 1 richness was higher in leaf samples extracted with MoBio (W = – 18; P = 0.0078), whereas the observed (S_{Obs}) richness was only marginally higher (W = – 14; P = 0.0547) in those samples. Neither diversity (H') (W = – 1; P = 0.9453) nor evenness (E_H) (W = 2; P = 0.8438) differed between the leaf samples processed through the two protocols. The richness and diversity estimators for the root samples seemed less sensitive to the processing protocols. Only extrapolative Chao1 richness differed between the two protocols and was higher in samples processed with MoBio (W = -15; P = 0.0391), whereas others did not differ (W < 11; P > 0.1484).

Consistent with the richness and diversity analyses, ASV-inferred communities in leaves appeared more sensitive to sample processing protocols than those in roots (Figure. 2.2). The two sample processing protocols resulted in distinct communities in leaves ($F_{1,14}$ = 1.85; P = 0.003; R^2 = 0.12), but not in roots ($F_{1,14}$ = 1.15; P = 0.255; R^2 = 0.08). Further, there was no difference between the community dispersion as inferred from the median distance from the estimated community centroid (betadispr: P > 0.05).

Discussion

Metabarcode analyses of fungal communities using NGS tools is a cost-effective, fast, and easy to implement tool to estimate fungal diversity across a wide range of ecosystems and habitats (Song at al. 2015). Though generating fungal metabarcode data is rather straightforward, it involves many steps that can introduce bias (Zinger et al. 2019). In this study, we compared a direct extract and amplify kit with a more commonly used and more elaborate DNA isolation kits. A wide range of the DNA extraction kits and protocols exist and can become a source of bias, compromising the quality of acquired NGS data and leading to variability in ecological conclusions. For example, several studies have described the effect of the DNA extraction method on generated fungal sequence data from soils (Song et al. 2015, Woodhall et al. 2012), fungal tissues in pure culture (Jang et al. 2010, Fredricks et al. 2005), blood (Menu et al. 2021) or environmental samples (Hermans et al. 2018). However, the effect of the choice of DNA acquisition tool on the characterization of fungal communities from different plant tissues has remained poorly understood.

To our knowledge, our study is the first to compare the Prire Plant Direct PCR system with the more commonly used PowerSoil® DNA Isolation kit and subsequent fungal metabarcode marker amplification from different plant compartments. Overall, both Phire and MoBio DNA systems produced DNA that could be used for metabarcode analysis. However, our analyses indicated that MoBio captured greater fungal richness, but not diversity, in plant roots and leaves. Further, analyses of the community composition indicated that fungal communities in roots were similar between the extraction systems, whereas the fungal communities associated with plant leaves differed.

The tissue issue

Though Phire and MoBio DNA extraction systems produced DNA that could be used for metabarcode analysis, the sample tissue of different plant compartments greatly influenced the generated data. We can only speculate on the causes of the observed differences, and we hypothesize that the minimal plant tissue homogenization using the Phire Plant Direct PCR kit is likely the primary source of the lower fungal ASV richness in roots and leaves as well as differences in the composition of foliar fungal communities. The DNA extraction using Phire kit is quick and only requires mechanical cell lysis through crushing the tissues with sterile fine point forceps. In contrast, cell lysis with MoBio includes both chemical cell lysis using negatively charged detergent sodium dodecyl sulfate (SDS) combined with rigorous mechanical homogenization using a vortex at maximum speed for 10 minutes. While leaf samples processed with MoBio kit were uniformly homogenized, we found it challenging to achieve the same consistency and level of tissue homogenization using the Phire kit protocol. It is likely that MoBio disrupts the loosely adhering particles and small fungal colonies in leaves better, whereas plant tissues processed with Phire were poorly homogenized following the manufacturer's instructions. As a result, the small colonies of foliar endophytes or pathogens that may be confined to a single host cell may have remained undetected using the Phire system.

Previous studies have demonstrated the necessity of tissue homogenization by bead beating due to its ability to break down the plant material and therein associated fungi with thick chitinous cell walls — resulting in higher fungal DNA quantities and greater fungal diversity and richness following rigorous homogenization (Cheng et al. 2016, Griffiths et al. 2006). As a result, we recommend including a bead beating step to the DNA extraction process to achieve even plant tissue homogenization as well as better break down and release of fungal nucleic acids. Users should, however, be aware that extended bead beating protocols, while improving tissue homogenization, also tend to fragment DNA and may compromise the use of acquired DNA for some platforms that require long templates (e.g., NanoPore, PacBio).

Differences in procedures and resources required

Metabarcode amplicon generation using tissues processed through MoBio PowerSoil or Phire Plant Direct PCR systems differ substantially in procedures, cost, and time required. Although DNA isolation with PowerSoil has a reputation of generating high quality DNA from challenging samples, it is rather costly and requires substantially more time than Phire. The Phire kit is quick and only requires aliquoting buffer solution and tissue crushing with forceps. However, following the Phire protocol, manual homogenization of plant tissues allows processing only one sample at the time, a substantial time investment if the experiment includes a large number of samples. Processing a large number of samples this way may also decrease consistency between samples. In contrast, the number of samples that can be homogenized simultaneously using the MoBio kit depends on the vortex microtube accessory, permitting up to 24 samples at the time, and tissue homogenization tends to be consistent across all the samples. Note that 96-well homogenization tools are also available for MoBio systems. Following the cell lysis, MoBio sample processing protocol requires an additional five steps to acquire, isolate and purify nucleic acids, whereas Phire samples only required dilution prior to the PCR-amplification. In addition, compared to MoBio PowerSoil kit, the Phire kit requires purchase of no additional polymerase, greatly decreasing the cumulative expenses, especially in studies with large numbers of samples.

Our comparison of a direct DNA extraction and amplification kit with the more commonly used MoBio DNA extraction kit suggests that the direct kit is a promising tool for generating metabarcode data for fungal communities from plant root tissues and can be a user friendly alternative due to its low cost and expedience in sample processing. However, we recommend that users consider the aims of their studies. Modifications and adjustment in the extraction protocols might be necessary to generate data that are comparable in richness/diversity metrics among different plant tissues and result in sound ecological conclusions. We propose including mechanical a bead beating cell lysis in the Phire sample processing protocol to improve tissue homogenization and therefore improve the comparability of fungal community richness/diversity metrics as well as community composition in plant leaves.

Acknowledgments

This research was funded in part by NSF-DEB award # 1457309 “COLLABORATIVE RESEARCH: Parsing the effects of host specificity and geography on plant-fungal symbioses under climate change” and NSF-EPSCoR award # 1656006 “Microbiomes of Aquatic, Plant and Soil Systems across Kansas (MAPS).” We are grateful to technical assistance by Alina Akhunova, Monica Fernandez De Soto, and Jie Ren at the Integrated Genomic Facility at Kansas State University (https://www.k-state.edu/igenomics/).

References

Brown, C. T., Hug, L. A., Thomas, B. C., Sharon, I., Castelle, C. J., Singh, A., . . . Banfield, J. F. (2015). Unusual biology across a group comprising more than 15% of domain Bacteria. Nature, 523(7559), 208-211. https://doi.org/10.1038/nature14486

Busby, P. E., Soman, C., Wagner, M. R., Friesen, M. L., Kremer, J., Bennett, A., . . . Dangl, J. L. (2017). Research priorities for harnessing plant microbiomes in sustainable agriculture. PLOS BIOLOGY, 15(3). https://doi.org/10.1371/journal.pbio.2001793

Bates, D. Maechler M., Bolker B., Walker S. (2015). Fitting Linear Mixed-Effects Models Using lme4. Journal of Statistical Software, 67(1), 1-48. doi:10.18637/jss.v067.i01.

Cheng, F., Hou, L., Woeste, K., Shang, Z., Peng, X., Zhao, P., & Zhang, S. (2016). Soil pretreatment and fast cell lysis for direct polymerase chain reaction from forest soils for terminal restriction fragment length polymorphism analysis of fungal communities. Brazilian Journal of Microbiology, 47(4), 817-827. https://doi.org/https://doi.org/10.1016/j.bjm.2016.06.007

De Caceres, M., Legendre, P. (2009). Associations between species andgroups of sites: indices and statistical inference. Ecology, URL http://sites.google.com/site/miqueldecaceres/

Fredricks, D. N., Smith, C., & Meier, A. (2005). Comparison of six DNA extraction methods for recovery of fungal DNA as assessed by quantitative PCR. J Clin Microbiol, 43(10), 5122-5128. https://doi.org/10.1128/jcm.43.10.5122-5128.2005

Griffiths, L. J., Anyim, M., Doffman, S. R., Wilks, M., Millar, M. R., & Agrawal, S. G. (2006). Comparison of DNA extraction methods for Aspergillus fumigatus using real-time PCR. J Med Microbiol, 55(Pt 9), 1187-1191. https://doi.org/10.1099/jmm.0.46510-0

Haro, C., Anguita-Maeso, M., Metsis, M., Navas-Cortés, J. A., & Landa, B. B. (2021). Evaluation of Established Methods for DNA Extraction and Primer Pairs Targeting 16S rRNA Gene for Bacterial Microbiota Profiling of Olive Xylem Sap [10.3389/fpls.2021.640829]. Frontiers in Plant Science, 12, 296.

Hermans, S. M., Buckley, H. L., & Lear, G. (2018). Optimal extraction methods for the simultaneous analysis of DNA from diverse organisms and sample types. Mol Ecol Resour, 18(3), 557-569. https://doi.org/10.1111/1755-0998.12762

Huse, S. M., Dethlefsen, L., Huber, J. A., Welch, D. M., Relman, D. A., & Sogin, M. L. (2008). Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag Sequencing. Plos Genetics, 4(11), Article e1000255. https://doi.org/10.1371/journal.pgen.1000255

Ihrmark, K., Bodeker, I. T. M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., . . . Lindahl, B. D. (2012). New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. Fems Microbiology Ecology, 82(3), 666-677. https://doi.org/10.1111/j.1574-6941.2012.01437.x

Jang, C. S., Lim, J. H., Seo, M. W., Song, J. Y., & Kim, H. G. (2010). Direct Detection of Cylindrocarpon destructans, Root Rot Pathogen of Ginseng by Nested PCR from Soil Samples. Mycobiology, 38(1), 33-38. https://doi.org/10.4489/MYCO.2010.38.1.033

Koljalg, U., Nilsson, R. H., Abarenkov, K., Tedersoo, L., Taylor, A. F. S., Bahram, M., . . . Larsson, K. H. (2013). Towards a unified paradigm for sequence-based identification of fungi. Molecular Ecology, 22(21), 5271-5277. https://doi.org/10.1111/mec.12481

Menu, E., Landier, J., Prudent, E., Ranque, S., & L'Ollivier, C. (2021). Evaluation of 11 DNA Automated Extraction Protocols for the Detection of the 5 Mains Candida Species from Artificially Spiked Blood. Journal of fungi (Basel, Switzerland), 7(3), 228. https://doi.org/10.3390/jof7030228

Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner (2020). vegan: Community Ecology Package. R package version 2.5-7. https://CRAN.R-project.org/package=vegan

Oliver, T. H., Isaac, N. J. B., August, T. A., Woodcock, B. A., Roy, D. B., & Bullock, J. M. (2015). Declining resilience of ecosystem functions under biodiversity loss. Nature Communications, 6(1), 10122. https://doi.org/10.1038/ncomms10122

Paradis E. & Schliep K. 2019. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. Bioinformatics 35: 526-528.

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/

Rodrigues, R. R., Moon, J., Zhao, B., & Williams, M. A. (2017). Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. Global Change Biology Bioenergy, 9(6), 1057-1070. https://doi.org/10.1111/gcbb.12396

Sánchez-Cañizares, C., Jorrín, B., Poole, P. S., & Tkacz, A. (2017). Understanding the holobiont: the interdependence of plants and their microbiome. Current Opinion in Microbiology, 38, 188-196

Schloss Patrick, D., Westcott Sarah, L., Ryabin, T., Hall Justine, R., Hartmann, M., Hollister Emily, B., . . . Weber Carolyn, F. (2009). Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 75(23), 7537-7541. https://doi.org/10.1128/AEM.01541-09

Schoch, C. L., Seifert, K. A., Huhndorf, S., Robert, V., Spouge, J. L., Levesque, C. A., & Chen, W. (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proc Natl Acad Sci U S A, 109(16), 6241-6246. https://doi.org/10.1073/pnas.1117018109

Song, Z., Schlatter, D., Kennedy, P., Kinkel, L. L., Kistler, H. C., Nguyen, N., & Bates, S. T. (2015). Effort versus Reward: Preparing Samples for Fungal Community Characterization in High-Throughput Sequencing Surveys of Soils. PloS one, 10(5), e0127234-e0127234. https://doi.org/10.1371/journal.pone.0127234

Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Applied and Environmental Microbiology, 73(16), 5261-5267. https://doi.org/10.1128/aem.00062-07

White, J. F., Kingsley, K. L., Zhang, Q., Verma, R., Obi, N., Dvinskikh, S., . . . Kowalski, K. P. (2019). Review: Endophytic microbes and their potential applications in crop management [https://doi.org/10.1002/ps.5527]. Pest Management Science, 75(10), 2558-2565. https://doi.org/https://doi.org/10.1002/ps.5527

White, T., Bruns, T., Lee, S., Taylor, J., Innis, M., Gelfand, D., & Sninsky, J. (1990). Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In (Vol. 31, pp. 315-322).

Woodhall, J. W., Adams, I. P., Peters, J. C., Harper, G., & Boonham, N. (2013). A new quantitative real-time PCR assay for Rhizoctonia solani AG3-PT and the detection of AGs of Rhizoctonia solani associated with potato in soil and tuber samples in Great Britain. European Journal of Plant Pathology, 136(2), 273-280. https://doi.org/10.1007/s10658-012-0161-8

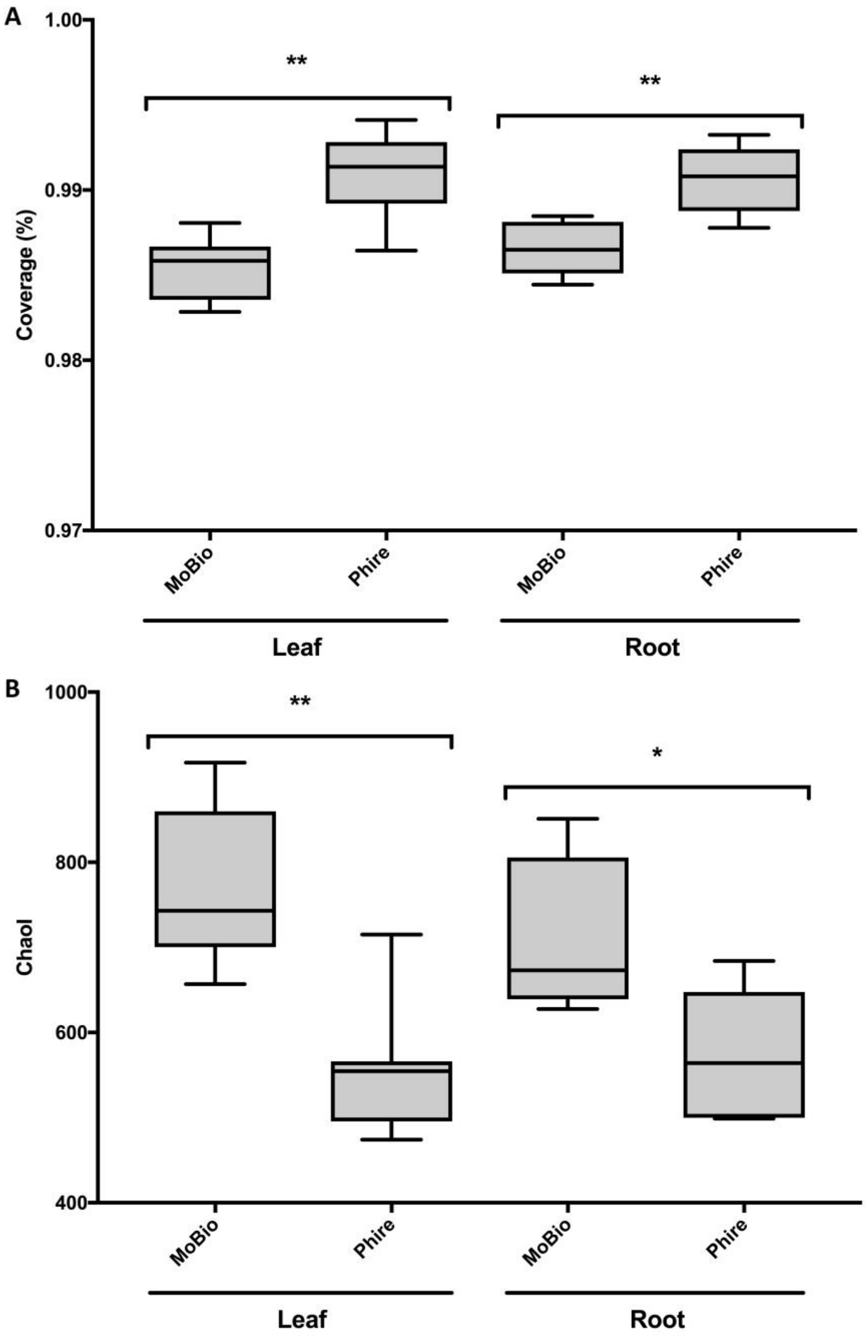
Zinger, L., Bonin, A., Alsos, I. G., Bálint, M., Bik, H., Boyer, F., . . . Taberlet, P. (2019). DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions [https://doi.org/10.1111/mec.15060]. Molecular Ecology, 28(8), 1857-1862. https://doi.org/https://doi.org/10.1111/mec.15060

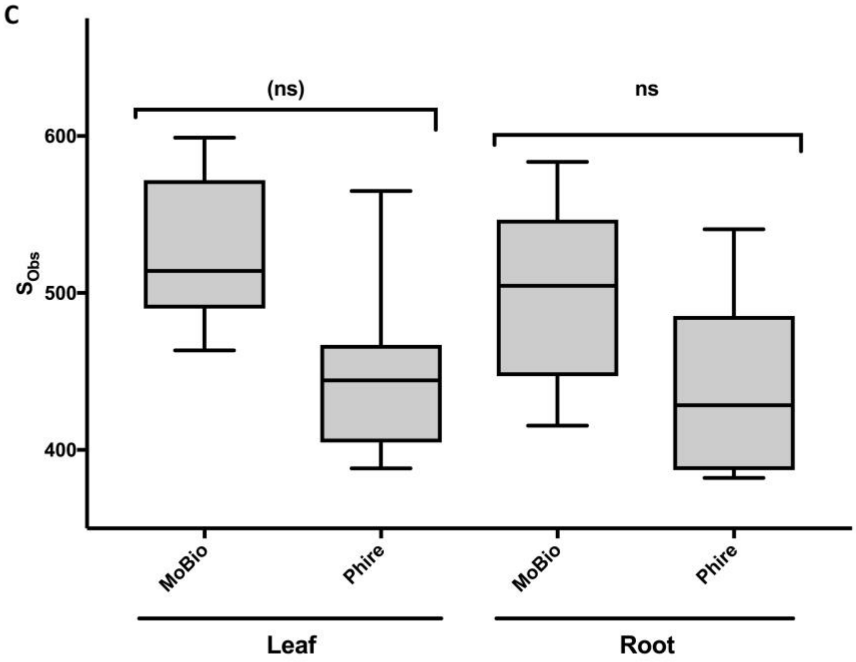
Tables and figures

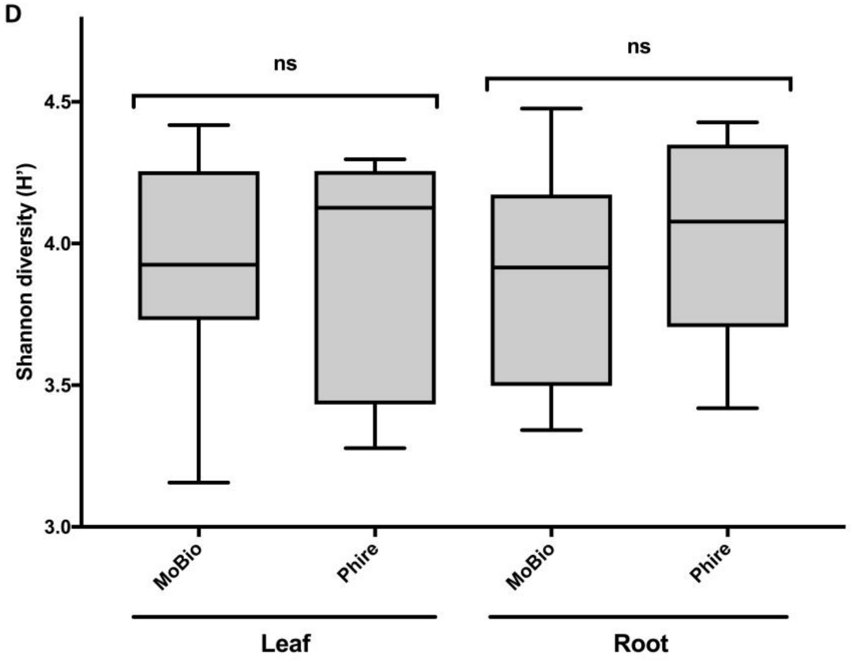
Figure 2.1.

MoBio and Phire Fungal Alpha Diversity Metrics across Leaves and Roots

ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$




C
(ns)
ns
600
500
400
S_{Obs}
MoBio
Phire
MoBio
Phire
Leaf
Root


D
ns
ns
4.5
4.0
3.5
3.0
Shannon diversity (H')
MoBio
Phire
MoBio
Phire
Leaf
Root

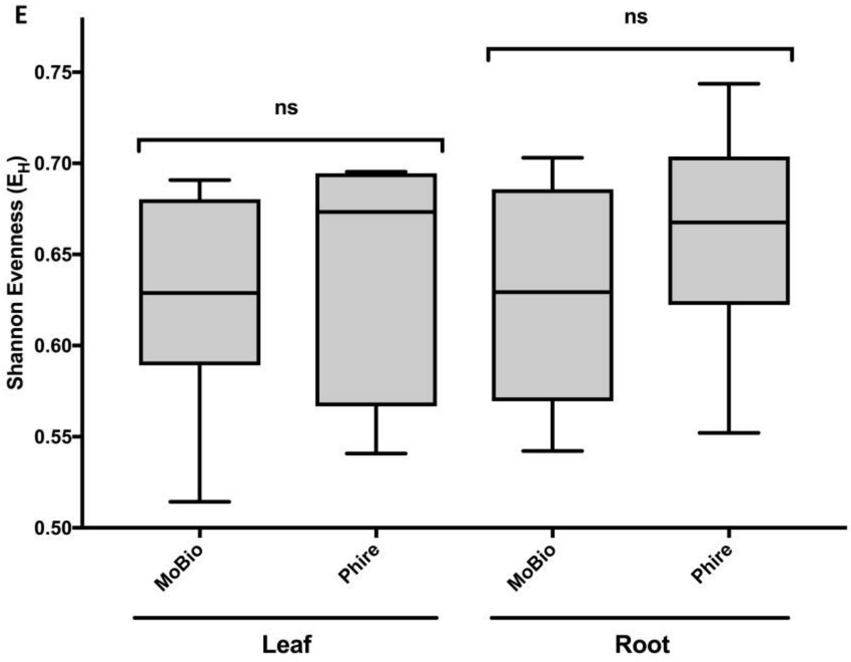
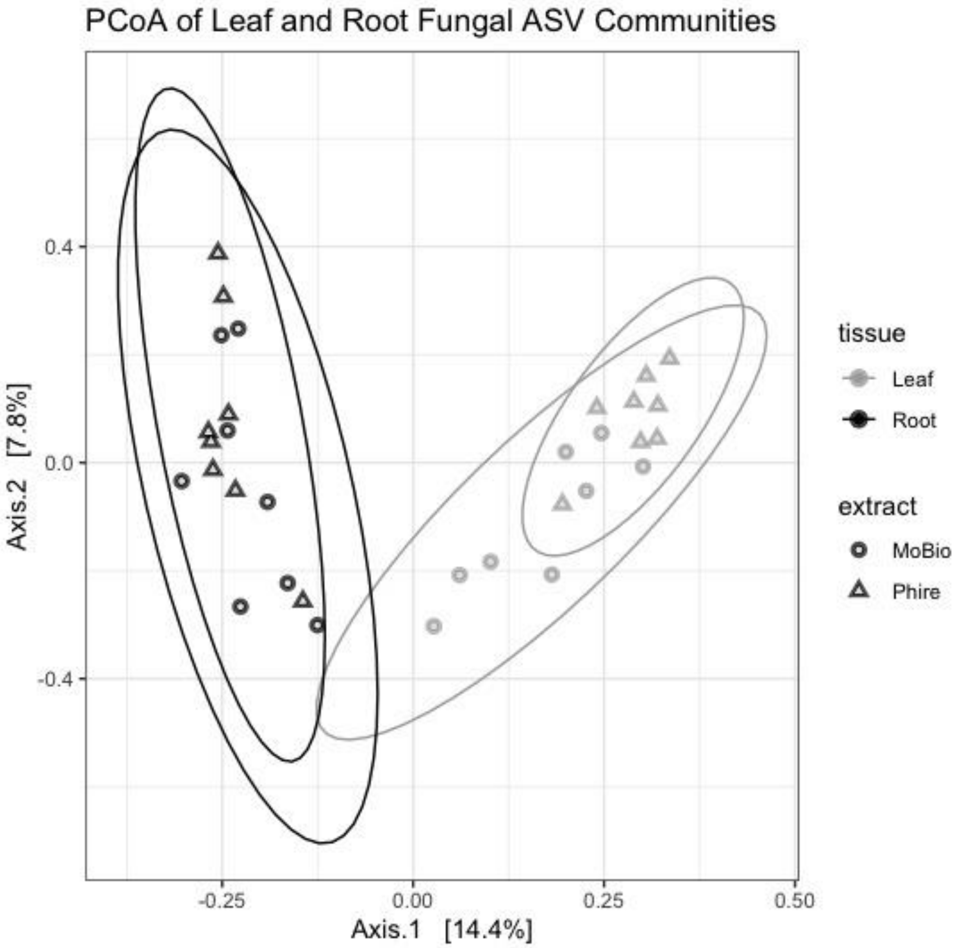

E
ns
ns
Shannon Evenness (E_H)
0.75
0.70
0.65
0.60
0.55
0.50
MoBio
Phire
MoBio
Phire
Leaf
Root

Figure 2.2.

PCoA of Leaf and Root Fungal ASV Communities

Principle Coordinate Analysis (PCoA) ordination across Axis 1 (14.4% variance) and Axis 2 (7.8% variance) of the two MiSeq libraries generated with the Phire and MoBio extraction kits. The two sample processing protocols resulted in distinct communities in leaves ($F_{1,14}$ = 1.85; P = 0.003; R^2 = 0.12), but not in roots ($F_{1,14}$ = 1.15; P = 0.255; R^2 = 0.08).



Chapter 3 - Seasonal dynamics of Panicum virgatum associated bacterial and fungal communities trump variety and planting density effects.

Abstract

Conservation agriculture management aims to achieve sustainable plant growth and productivity while minimizing active management such as fertilization, tillage, and soil movement. We analyzed bacterial and fungal communities associated with soil and roots of four varieties of the native warm-season perennial grass *Panicum virgatum* L. (a.k.a. switchgass) initially planted at two different densities and growing under conservation agriculture conditions in southeast Mississippi. Switchgrass has been championed for conservation agriculture because of its broad geographical distribution and its high performance on marginal or low-productivity agricultural lands. Because of this potential, there is an increasing interest in understanding how to exploit switchgrass microbiome to improve the crop performance. The microbiome – including bacteria and fungi inhibiting soil and plant tissues – is important for switchgrass health and performance. However, the microbiome is dynamic and can be affected by various biotic and abiotic factors that can rapidly change its functionality. Thus far, only limited data are available on the microbiome seasonal dynamics during the growing season and plant development. Here, we aimed to evaluate the effects of four switchgrass varieties and their planting densities on the soil chemistry and microbiomes in a common garden experiment that minimizes the environmental variation and its impacts on microbiome. To also assess the temporal dynamics, we repeatedly sampled switchgrass roots and associated soils approximating a $\log^2$ time series for a total of six times during one growing season, starting from within a week from the first leaf emergence in early spring to pre-frost in late fall. We extracted the total DNA and MiSeq-analyzed bacterial (v4 of the 16S ribosomal RNA gene) and fungal (Internal Transcribed Spacer 2 (ITS2) of the ribosomal RNA repeat) metabarcode markers. We tested for variety, planting density, and temporal effects on switchgrass associated soil chemistry as well as on bacterial and fungal communities in roots and soil. In general, our data indicated that bacterial and fungal communities were temporally dynamic and shifted during the growing season, whereas the switchgrass varieties and their planting densities minimally affected the associated bacterial or fungal community richness and their community composition. If any variety effects were present, they occurred mainly early in the growing season - within the first few weeks since leaf emergence. Indicator taxon analyses aiming to identify taxa underlying the early season compositional differences among the varieties identified putative pathogens and potential beneficial members of the microbiome among others, suggesting that varieties may differ in their disease susceptibility and ability to attract beneficial commensals or mutualists during the early growing season. Similar to the biotic attributes, the soil chemistry was minimally affected by switchgrass variety or planting density, although some temporal dynamics could be observed there as well. These data suggest that variety choices may enable optimization of microbiomes with minimal disease susceptibility and select microbiome components that support the sustainable switchgrass productivity. These data contribute towards a better understanding of interactions among plants and their associated microbiomes as well as their seasonal dynamics.

Introduction

Panicum virgatum L. (switchgrass) is a perennial warm-season grass adapted to a variety of habitats and climates. It is native to North America and distributed throughout the contiguous United States except west of the Rocky Mountains and north of 55° N latitude. Switchgrass grows in natural systems such as prairies and steppes but is also grown in managed systems in pastures or for hay production and as an ornamental. Because of its perennial lifecycle, high tolerance to biotic and abiotic stress, and adaptation to an extensive geographical range, switchgrass is broadly used for conservation agriculture and grown to provision a range of ecosystem services. These ecosystem services include – but are not limited to – soil, water and wildlife conservation, carbon sequestration and restoration of nutrient- and water-limited marginal lands (Follett et al. 2012; Skinner 2012; Werling et al. 2014). Additionally, switchgrass is used as a cellulosic feedstock for bioenergy production due to its high yield quality and potential, particularly on marginal lands (Vogel et al. 2002; Mitchell et al. 2008; Liebig et al. 2008).

Wide geographical range of the switchgrass in North America has resulted into two phenotypically and genotypically distinct ecotypes, whose genotypic diversity has facilitated switchgrass breeding (Caster 2012; Zalapa et al. 2011; Zhang et al. 2011). North American upland ecotype varieties are more adapted to the northern geographical ranges, whereas the lowland ecotypes are more common in southern regions. Due to the genetic diversity and the variety of valuable economic and agriculture switchgrass functions, switchgrass breeding programs have developed a number of varieties with different strengths for productivity available on today’s market.

Switchgrass varieties differ in growth habit, climate range tolerance, biomass yield and potential disease tolerance (Lowry et al. 2014; Rodrigues et al. 2017; Zalapa et al. 2011; Zhang et al. 2011). Furthermore, some evidence exists for differences in the nutrient use among switchgrass varieties, a trait particularly important in nutrient limited environments typical of the marginal lands (Sawyer et al. 2019). In addition to exploring the phenotypic and genotypic variation among switchgrass varieties, the interest in interactions between the switchgrass host and its microbiome – the switchgrass holobiont system – has increased and been a topic of interest for many scientists (Jesus et al. 2010, 2016; Kleczewski et al. 2012; Mao et al. 2011, 2013, 2014; Mendes et al. 2013; Chaudhary et al. 2012; Hargreaves et al. 2015; Rodrigues et al. 2017; Wright & Turhollow 2010). Plant holobiont is a complex symbiotic relationship between the plant-host and its microbiota – mostly bacteria and fungi, whose cells outnumber the number of plant cells (Mendes et al. 2013). Plant microbiomes are involved in many processes vital to the plant and range from beneficial to pathogenic in their nature (Rodrigues et al. 2017; Vacher et al. 2016). However, plant microbiome is dynamic and can be affected by a variety of biotic and abiotic factors that can rapidly change its composition, diversity, and functionality (Chen et al 2019; Grady et al. 2019; Ghimire et al. 2011; Rodrigues et al. 2017). Several studies have explored switchgrass-microbiome interactions in efforts to find factors potentially driving the microbial community assembly (reviewed in Hestrin et al. 2021). These studies often conclude that mindful switchgrass microbiome manipulation has the potential to enhance plant growth and productivity (Kim et al. 2012; Ray et al. 2015), reduce the plant abiotic stress (Wang et al. 2016), facilitate nutrient intake (Clark et al. 2005), improve disease resistance and pest suppression (Emery et al. 2017) and even provide ecosystem services essential to conservation such as carbon sequestration and maintenance of soil biodiversity (Chamberlain & Miller 2012). Although host genotypes may control the microbiome assembly and its composition (Rodrigues et al. 2017), to date the effect of conspecific varieties is mostly considered minor and not a primary factor in shaping the microbial communities. Rather, it is the environmental variation attributable to differences among sites that has been highlighted as the foremost control of the microbiome composition. For example, Brodsky et al. (2019), Hargreaves et al. (2015), Jesus et al. (2016), Whitaker et al. (2018) observed that switchgrass microbiome composition is more strongly controlled by abiotic soil characteristics that overwhelmingly mask the plant species or genotype effects. Although the site characteristics appear to be the primary drivers of the switchgrass microbiome assembly and composition, it has remained unclear whether and how switchgrass varieties may affect the plant microbiome. Therefore, we compared four switchgrass varieties in a side-by-side common garden field experiment to elucidate how the varieties may affect the switchgrass-associated microbiomes.

In addition to plant varieties or genotypes, agricultural management choices can substantially influence physical and chemical soil properties as well as microbial activity and community composition. As a perennial crop thriving with minimal inputs on marginal lands, switchgrass is often grown under conservation agriculture management regimes. The core concept of conservation agriculture is to enhance sustainable plant productivity, whilst minimizing active management including no-tillage regimes, using crop residue as the winter soil cover after the annual harvest, and omission of any inorganic NPK fertilization (Hoorman et al 2009). While there is some research effort to determine the management effects on switchgrass microbiomes (see Grady et al. 2019; Jach-Smith & Jackson 2018, 2020; Oates et al. 2016), some practical tools - particularly those commonly employed in conservation agriculture - have remained unexplored. Planting density is one tool to promote sustainable conservation agriculture with potential impacts on microbiomes and their management (Li & Du 2011; Malmberg & Smith 1982; Marquard et al. 2009; Samih et al. 2008; Stachová 2013). Plants growing in different densities are exposed to the different levels of UV stress, soil, and leaf wetness level as well as different levels of intraspecific competition for nutrients, light, and space. The within-stand environment or changes in plant physiology resulting from different stand densities may directly or indirectly shape microbial communities. Considering the planting density as a management tool is a potential key to a successful conservation agriculture practice. Unfortunately, only few studies have focused on the effects of this management practice on the plant microbiome (*e.g.*, Cavaliery et al. 2020; Harker et al. 2003; Lay et al. 2018).

Minimal soil disturbance and omission of any inorganic NPK fertilizers are among the main principles of conservation agriculture management. Because of the minimal active management, natural processes and temporal dynamics can drive the microbiome assembly and compositional shifts over time. Seasonal variability in environmental factors such as changes in mean temperature or soil moisture as well as coinciding changes in host physiology during its development may alter plant C inputs into the soil system and can shape microbial communities (Chen et al. 2019; DeBruyn et al. 2017; Kramer et al. 2013; Lewandowski et al. 2015; Lauber et al. 2013). Although some studies have emphasized the importance of a seasonality on switchgrass microbiome composition (Chen et al. 2019; Rodrigues et al. 2017), comprehensive analyses of temporal dynamics of biotic and abiotic factors associated with field-grown switchgrass are largely lacking. To fill this knowledge gap, we sampled switchgrass roots and associated soils six times over one growing season; within one week from the first leaf emergence in the spring to pre-frost in late fall to elucidate both the effects of variety choices as well as their planting densities and temporal dynamics of soil chemistry and switchgrass-associated microbiomes.

A better understanding of plant microbiome dynamics in the plant rhizosphere is critical for sustainable conservation agriculture and sustainable crop production. We present a unique broad investigation of switchgrass root and rhizosphere microbiomes combining an investigation of temporal dynamics and assessing the effects of varieties as well as the densities in which they were initially planted. Further, we investigated the soil chemistry and its dynamics during one growing season and compared how switchgrass varieties and their planting densities may affect the dynamics of the soil chemistry. Our three primary objectives were to (1) evaluate differences in soil characteristics plus in the composition and diversity of bacterial and fungal communities in soil or rhizospheres associated with four switchgrass varieties; (2) explore how high- and low-density plantings may impact switchgrass microbiomes and soil chemistry; and (3) examine the seasonal dynamics of the soil chemistry and switchgrass-associated microbiomes below ground. We hypothesized that switchgrass variety choices, planting density and seasonal dynamics would shape fungal and bacterial communities as well as impact soil chemistry characteristics. Given the important role of the plant-associated microbiomes in the plant performance and soil nutrient cycling, our research offers an insight into plant-microbiome interactions, an understanding of factors that drive switchgrass microbiomes, and how these relationships are influenced by time

Materials and methods

Site description

We utilized an established conservation agriculture experiment located at the Center for Conservation Research, Alcorn State University, Lorman, MS (31°90′01″N – 91°15′30″W). The soil at the site is Memphis Silt Loam - composed of thermic silt and clay, and the climate is within the humid subtropical zone with mean annual precipitation of 1,473mm almost evenly distributed through the year and mean annual temperature of 18.4°C. The climate is characterized by the absence of the severe winter (November – February) with a minimal chance of snow and hot long summers (May –September) with average temperatures 14°C and 31°C, respectively. The growing season typically extends from the late February to late November with a mid-July peak.

The switchgrass experiment was established in 2012 at the Alcorn State University's Conservation Research Station in Lorman, MS. Since its establishment, the experiment has been continuously managed under conservation agriculture conditions. The management regime mimics natural systems through cultivating a switchgrass cover crop continuously, minimizing soil disturbance, omitting any inorganic NPK fertilization and using the crop residue as the winter soil cover after annual harvest (Hoorman et al 2009).

Switchgrass varieties

A total of four switchgrass varieties have been maintained under the conservation agriculture management since 2012. The varieties were selected from more than a dozen based on high and reliable germination as well as performance at the experimental site. All four varieties in our experiment are lowland ecotypes. The variety 'Alamo' was released in 1978 by the Plant Materials Center of the United States Department of Agriculture Natural Resources

Conservation Center (USDA-NRCS) in Knox City, Texas. It is adapted throughout most of the U.S. and primarily used for livestock feed, soil stabilization, wildlife conservation and biofuel source (USDA-NRCS, 2012). Varieties ‘BoMaster’ and ‘Colony’ were cooperatively developed by the USDA Agricultural Research Service (USDA-ARS) and the North Carolina Agricultural Research Service, North Carolina State University, and released in 2006 and 2009, respectively (Burns et al 2008; Burns et al 2010). ‘BoMaster’ and ‘Colony’ were selected for their high biomass and dry matter yield. Variety ‘Kanlow’ was developed collaboratively by the USDA-NRCS, Kansas Agricultural Experiment Station and USDA-ARS and released in 1963. ‘Kanlow’ is commonly used for erosion control, as livestock feed, and in wildlife conservation as well as for biofuel (USDA-NRCS 2011). During the growing season, these switchgrass varieties can reach up to 3m in height, and much of the root biomass resides in the top 30cm in soil. The biomass production depends on the grass variety. For example, among the four varieties selected for this experiment, Alamo and Colony can produce the greatest biomass with Alamo yielding 26.67 tons of dry matter ha^{-1} a^{-1} and Colony yielding up to 30.22 tons ha^{-1} a^{-1}. The other two varieties tend to yield less: BoMaster 23.99 tons ha^{-1} a^{-1} and Kanlow 25.54 tons ha^{-1} a^{-1} of dry biomass (Vance 2015).

Experimental design

Our experimental design consists of four replicate blocks in a randomized complete block split-plot design with four full plots split into two subplots. Each full plot within a block includes one of four switchgrass lowland varieties (Alamo, Bo Master, Colony, or Kanlow) initially planted in two densities (HDP – high density planting or LDP – low density planting with 12.7 and 10.2 cm between plants, respectively) – with each subplots measuring 4.6 m long and 0.46m wide. As per this design, each experimental block includes eight treatment combinations (4 varieties × 2 densities) with four replicate blocks for a total of 32 experimental units (Figure 2.1).

Soil and root sampling and soil properties (soil chemistry analysis)

The soils and roots were sampled six times during the 2018 growing season (March to November). The first sampling (Week 1; March 14th) was scheduled within a week after the first leaf emerge of all the grass varieties in the spring. One of the varieties (BoMaster) was delayed compared to other varieties it was just starting to emerge at the first sampling. Sampling was repeated based approximately on a log2 schedule: Week 2 (March 23); Week 4 (April 5th); Week 8 (April 30th); Week 16 – the mid-season (June 24th); and week 38 (November 29th). The last sampling (Week 38) was scheduled one week before the average pre-frost time. Across the six sampling events, we collected 192 root and 192 soil samples for a total of 384 samples (32 experimental units * 6 times * 2 plant compartments (soil and roots)).

We sampled three 15 cm x 5 cm soil cores adjacent to a plant within each subplot. The three soil cores were composited into one and manually mixed. Roots were manually separated from the homogenized samples and washed in water immediately after collecting. Root and soil samples were placed in plastic zip-lock bags and transported on ice to the laboratory at Alcorn State University, where they were placed in a 4°C refrigerator until the next day (~15 hours). During the following day, the root samples were divided into two aliquots: 1) for storage as a frozen archive in -20°C at Alcorn State University and 2) for shipping on dry ice to Kansas State University for microbial community analyses. The soil samples were divided into five aliquots: 1) for analyses of soil chemistry; 2) for phospholipid fatty acid (PLFA) assays to estimate microbial biomass; 3) for extracellular enzyme activity (EEA) assays; 4) for a frozen archive stored in -20°C at Alcorn State University; and 5) for shipping on dry ice to Kansas State University for microbial community analyses

Soil properties

The aliquot reserved for soil chemistry analyses for was divided to two. One aliquot was sent to Kansas State University Soil Testing Laboratory (www.agronomy.k-state.edu/services/soiltesting/) where it was further divided for analyses of total N% and total C%, and NH4+. Total N% and total C% were measured by dry combustion method using a LECO TruSpec CN combustion analyzer (LECO, St. Joseph, MI) on weight percent basis from a 0.15g of prepared soil. NH4+ was extracted by single KCl method using 2g of soil. Another aliquot was shipped to Waypoint Analytical (Memphis, TN) where it was further divided for analysis of soil pH, P, K, Mg, Ca, OM, CEC, % cation saturations and NO3-. Soil pH was measured using saturation paste method using 1:1 soil and water ratio. P, K, Ca, and Mg were determined using modified Mehlich method (Mehlich 1984). Cadmium reduction was used for nitrate procedure (Gelderman and Beegle 1998) and run-in separate channel in flow analyzer to measure these ions simultaneously. One gram of dry soil was used to estimate OM content through loss on ignition as described in Combs and Nathan (1998). The four cations Ca 2+ , Mg 2+ , K + , Na + were extracted with 1 M ammonium acetate, pH 7.0 measured by ICP Spectrometry using 2g of soil. % Cation saturations were calculated using (meq of cation/CEC) x 100 formula.

Phospholipid Fatty Acid (PLFA) analyses

One soil aliquot was used for to estimate PLFAs biomarkers. A total of 5g of freeze dried soil per sample were incubated in a mixture of methanol:chloroform:citrate buffer with the ratio 2:10.67 (Bligh & Dyer 1959; Frostega˚rd & Ba˚a˚th 1993). Using 3µm Supelco Supelcosil LC-

S21 SPE columns (Sigma-Aldrich, St. Louis, Missouri, USA) we isolated phospholipids based on the polarity of the compound from the chloroform phase. Samples were then saponified and sulfuric acid added to incorporate a methyl group to biomarkers. Fatty acid methyl esters (FAMEs) were then analyzed using Gas Chromatograph (GC) - Thermo Scientific Trace GC-ISQ mass spectrometer (Thermo Fisher Scientific, Waltham, Massachusetts, USA) with a DB5-MS column gas chromatograph. The Bacterial acid methyl ester mix (BAME, Matreya 1114; Matreya LLC, Pleasant Gap, Pennsylvania, USA) and the internal methyl nonadecanoate standard were used to identify soil extract FAME peaks and quantify the amount of C in each peak. Select soil PLFAs were classified as described previously (Ba˚a˚th & Anderson 2003; Brant et al. 2006): bacteria (16:1x9, 16:1x5, 17:1x9, i17:0, a17:0, cy17:0, 18:1x7, and cy19:0), Gram– bacteria (cy17:0, 16:1x9c, 17:1x9c, 18:1x7c, and cy19:0), Gram+ bacteria (i14:0, i15:0, a15:0, i16:0, i17:0, and a17:0), or actinobacteria (10Me16:0, 10Me17:0, and 10Me18:0) and fungi (18:2x6,9), arbuscular mycorrhizal (AM) fungi (16:1x5) and non-arbuscular mycorrhizal, i.e., other fungi (difference between fungi and arbuscular mycorrhizal fungi).

Extracellular Enzyme Activity assays (EEAs)

One soil aliquot was used to estimate soil EEAs. A 1 ml subsample was dried at 75°C for 48 hours to determine soil dry weight. For EEAs, we used four different para-nitrophenol (pNP)-linked assays to measure the activities of phosphatase (Phos), β-glucosidase (βG), N-acetylglucosaminadase (NAG) and cellobiohydrolase (CBH) enzymes as described in Jackson et al. (2013). In short, the soil aliquot was passed thought a 2 mm sieve. A total of 8g of soil was vortexed with 8mL of 50 mM acetate buffer (pH 5.0 – 5.5) in a sterile 15 mL centrifuge tube. A total of 150μl of each homogenized soil slurry was immediately transferred into six wells in a row per sample of the 96-deepwell plate. One controls were added at the end of each row for a total of two controls per row. Two plates with 12 samples per plate were required for each enzyme assay for each of the six sampling events.

pNP-linked substrate was prepared individually for each enzyme. We used 5mM pNP-phosphate, 5mM pNP- β- glucopyranoside, 2mM pNP- β-N-acetylglucosaminide and 2mM pNP-cellobioside in 50 mM acetate buffer mixed in 15 mL sterile centrifuge tubes. A total of 150µl of pNP substrate or 150µl acetate buffer – the sample control – were transferred into the substrate and control wells for each sample. Enzyme plates then were placed at 24°C for the substance incubation: Phos for 30 minutes, βG for 60 minutes, NAG for 120 minutes and CBH for 180 minutes. The incubated substrates were centrifuged at 5,000 x g for 5 min in the room temperature. To stop the extraction reactions a total 100µl of the supernatant from each well were transferred to a 96-well microplate with 10 µl 1M NaOH and 190µl of distilled water. NaOH increases the pH, thus inhibiting the reaction and enhancing the color of the pNP released during the reaction. The EEAs were recorded on a microplate reader (Synergy HT Microplate Reader; BioTek Instruments, Winooski, VT) at 410nm. The final absorbance was determined as a difference between the absorbances of the sample assay and the mean of two controls To determine the conversion factor of absorbance to µmole of pNP in each enzyme, we used pNP-linked reference substrates in 50mM acetate buffer with three concentrations ranging from 0.025 mM to 1 mM; pNP concentration in the 300µL was estimated based on the concentrations in the standard curve and multiplied by 0.3. The conversion factor represents a slope in the curve between the absorbance and pNP concentration (µmole) in each enzyme reaction. The enzyme activity was determined by dividing the final absorbance with the incubation time, sample dry mass and the conversion factor.

DNA extraction and Next generation sequencing

For microbial community analyses, aliquots of the sampled roots and soils were shipped to Kansas State University on dry ice and stored at -20°C until processed further. Root samples were ground by hand in liquid nitrogen using autoclave-sterilized mortars and pestles. Mortars and pestles were re-sterilized in autoclave for 20 min at 121°C between samples. DNA was extracted from ~0.25g of ground roots or from ~0.25g of thawed and homogenized soil using a MoBio PowerSoil DNA Isolation Kit (MoBio Laboratories, Inc., Carlsbad, CA, USA) as per the manufacturer's protocol and eluted in a total of 100µl of the kit elution buffer. The DNA yield was measured using a Nanodrop ND2000 spectrophotometer (Thermo Scientific, Wilmington, Delaware, USA) and normalized to 2 ng/µL. Positive and negative controls were included to detect contamination during the sample processing. We used *Saccharomyces cerevisiae* as a fungal positive control and *Escherichia coli* as a bacterial positive control. Molecular grade RNA- and DNA-free H_2O was used as a negative control.

The normalized templates were PCR-amplified using bacterial and fungal forward and reverse primers with 12bp barcodes. For fungi, we targeted Internal Transcribed Spacer 2 (ITS2) using forward fITS7 (Ihrmark et al. 2012) and reverse ITS4 (White et al. 1990) primers. For bacteria, we targeted the variable region v4 of the small subunit of the ribosomal RNA gene using forward 515f and reverse 806r primers (Caporaso et al. 2011). All PCR reactions were performed in triplicate 50µL reactions. Each PCR reaction included 10µL or 20ng of the template, 200 µM of each deoxynucleotide, 1µmol of forward and reverse primers, 10 µL of 5X Green HF PCR buffer (Thermo Scientific,Wilmington, Delaware, USA), 14.75 µL of molecular grade water and 0.5 units of the proofreading Phusion Green Hot Start II High-Fidelity DNA polymerase (Thermo Scientific, Wilmington, Delaware, USA). PCR amplification was performed using Eppendorf MasterCyclers (Eppendorf, Hamburg, Germany). The bacterial PCR conditions included an initial denaturation at 98°C for 30 s, followed by 30 cycles with denaturation at 98°C for 10 s, annealing for 30 s at 50°C, extension for 1min at 72°C, with final extension for 10 min at 72°C. Positive and negative controls were included in every PCR amplification. The fungal PCR cycle conditions were identical except for the 54°C annealing temperature. Positive and negative controls were included in every PCR amplification.

All PCR products were visualized by agarose gel (1.5%) electrophoresis to ensure the successful amplification and correct amplicon sizes. The triplicate amplicons were combined into one per experimental unit and cleaned using Omega Mag-bind® RXNPure Plus system following a modified manufacturer protocol using 1:1 ration of magnetic beads to the PCR volume and two rinse steps with 80% ethanol. The cleaned product was quantified using Nanodrop ND2000 spectrophotometer (Thermo Scientific, Wilmington, Delaware, USA) and 200ng of bacterial and fungal amplicons from each experimental unit pooled separately for sequencing. Illumina-specific primers and adapters were added in four PCR cycles with KAPA Hyper Prep Kit (Roche, Pleasenton, CA USA) and 0.5µg starting DNA. Libraries were sequenced (2 x 300 cycles) using Illumina MiSeq Personal Sequencing System at the Integrated Genomic Facility at Kansas State University.

Sequence data processing

A total of 21,605,332 bacterial and 12,597,100 fungal raw sequences were processed using the mothur pipeline (v. 1.38.0; Schloss et al. 2009) as per the MiSeq standard operational protocol (Kozich et al. 2013) where possible. Sequences were extracted from paired-end .fastq files, contiged and any sequences with ambiguous bases, sequences with more than 1base pair (bp) mismatch with primer and any mismatches to the sample-specific 12 bp molecular identifiers (MIDs), or homopolymers longer than 9 bp were omitted. This resulted in a total of 13,481,728 bacterial and 11,691,826 fungal sequences.

We aligned bacterial sequences against SILVA (v. 132; Yilmaz et al. 2014) reference and pre-clustered near-identical (>99% similar) sequences (Huse et al. 2008) to minimize potentially erroneous reads. The sequences were screened for chimeras using UCHIME algorithm (Edgar et al. 2011) and putative chimeras were removed. The remaining sequences were assigned to taxa using the Naïve Bayesian Classifier (Wang et al. 2007) and the RDP training set (v. 10; Cole et al. 2014) with 51% threshold. Any sequences assigned to mitochondria, chloroplast, Archaea were removed. The remaining sequence data were clustered to OTUs at 97% similarity level using the nearest neighbor algorithm. OTUs that were detected in the negative control or rare OTUs represented by fewer than 100 reads (<0.0001% of all retained sequence data) in the dataset were removed.

As reliable alignment of ITS2 data is challenging, the fungal sequences were truncated to the length equal of the shortest high-quality read (236 bp excluding primer and MIDs). The >99% similar sequences were pre-clustered (Huse et al. 2008), checked for potential chimeras using UCHIME algorithm (Edgar et al. 2011) and putative chimeras were removed. The remaining sequences were assigned to the Operational Taxonomic Units (OTUs) at 97% similarity and clustered using vsearch (Rognes et al. 2016). Rare OTUs (fewer than 100 or contributing less than 0.0001% in the dataset) and those that were detected in the negative controls were removed from the further analysis. Remaining OTUs were assigned to taxon using the Naïve Bayesian Classifier (Wang et al. 2007) and International Nucleotide Sequence Database – reference database (UNITE) (Koljalg et al. 2013). Non-target OTUs which did not match the UNITE dataset or were assigned to groups outside of the Kingdom of Fungi were removed.

We iteratively (100 iterations) estimated bacterial and fungal richness and diversity for each sample using mothur (v. 1.38.0; Schloss et al. 2009). To minimize biases resulting from differences in sequencing depths among the libraries, we rarefied the bacterial and fungal data to 2 750 and 10 000 sequences per sample, respectively, as recommended in Gihring et al. (2012). To determine how well our sampling represented the resident diversity, we estimated Good's coverage (the ratio between singleton OTUs and total number of OTUs in a sample). To estimate richness and diversity we estimated observed (S_{Obs}) and extrapolated (Chao1) OTU richness, Shannon's diversity (H'), and evenness (E_H).

Data analysis

Bacterial and fungal richness and diversity data were ln-transformed prior to analyses because of non-normality and heteroscedasticity. We analyzed our data to specifically address following three questions. *First*, to test the overall effects of the planting density and variety, we analyzed soil chemistry as well as bacterial richness (S_{Obs}, Chao I), diversity (Shannon's $_{H'}$) and evenness ($E_{H'}$) using mixed effect models where "Block" and "Time" were included in the model as random effects. In these analyses, "Variety" was included as a fixed main effect and "Density" nested within "Variety" to account for the split-plot design. *Second,* in addition to testing for the overall management effects, we also aimed to test if management choices differed at any of the six sampling points. In these analyses, each time of sampling was analyzed separately using mixed effects models with "Variety" and "Density" nested within "Variety" as fixed effects and "Block" as a random effect. *Third*, we also aimed to elucidate temporal dynamics in our study system. Although these analyses focused specifically on temporal component of our study, the mixed effect models included fixed and random effects similar to those in our second set of analyses, but the models were amended with “Time” as an additional fixed linear effect along with its interactions with “Variety” and “Density” within “Variety” and “Block” as a random effect.

To visualize the soil- and root-inhabiting bacterial and fungal communities we calculated Bray-Curtis dissimilarity matrices and visualized these data using principal coordinate analysis (PCoA). To test for the effect of management choices (variety and density) on the composition of these communities, we used permutational multivariate analysis of variance (PERMANOVA) and, to test for community dispersion and differences in community heterogeneity, we used dispersion analyses (betadisper). These analyses were consistent with the three strategies described above. First, we analyzed these data with a simple model that included “variety” and “density’ nested within variety. Second, we repeated these analyses but conducted them separately for each of the six sampling time points. Third, we amended the models from the first analyses with “time” effect to focus on the temporal dynamics of the communities in the course of our 38-week sampling. To identify those root and soil fungi and bacteria that were disproportionally more abundant in one treatment than in others, we analyzed these data for indicators for each week and variety using the multipatt function (P = 0.001) of the indicspecies package in R (De Cáceres & Legendre 2009) Bacterial indicators in roots and soils were characterized on the phylum level, whereas fungal indicators were characterized on the family level.

Following the community analyses, we aimed to identify those environmental factors correlated with the soil bacterial and fungal community data using the Bray-Curtis dissimilarity matrices PCoA and plotted the environmental vectors onto a PCoA ordination using the enfit function of the vegan package in R (v. 2.5-7; Oksanen et al. 2020). In these analyses, we included soil pH, NH_4^+, NO_3^-, total N%, total C%, C:N, organic matter %, P, K, Ca and Mg.

Results

We analyzed soil chemistry and bacterial and fungal communities in the switchgrass roots and soils. After removal of poor quality, chimeric and rare sequences the final dataset included 7,148,883 bacterial and 11,477,980 fungal sequences distributed across 9,360 and 2,490 OTUs, respectively, and representing 2,386 ± 1,164 bacterial OTUs and 12,884 ± 8,099 sequences from switchgrass roots and 4,506 ± 914 bacterial OTUs and 24,598 ± 11,072 sequences from switchgrass soils, or 262 ± 108 fungal OTUs and 31,590 ± 18,387 sequences from switchgrass roots and 851 ± 268 bacterial OTUs and 24,818 ± 13,694 sequences from switchgrass soils.

Overall soil property responses

Our analyses of four switchgrass varieties and two planting densities on the soil chemistry revealed no strong variety ($F_{3,40} < 2.66$; $P > 0.0608$) or any planting density ($F_{4,40} < 1.27$; $P > 0.2969$) effects when analyzed by the repeated measures across the six sampling times (Table 3.1). Only soil magnesium differed marginally among the varieties ($F_{3,40} = 2.66$; $P = 0.0608$), a result attributable to low concentration in plots planted with Kanlow compared to highest in plots planted with Alamo. Similar to soil chemistry, we observed no variety or planting density effects on either soil PLFAs (Variety: $F_{3,40} < 0.74$; $P > 0.5355$; Density: $F_{4,40} < 1.08$; $P > 0.3774$) or EEAs (Variety: $F_{3,40} < 0.29$; $P > 0.8306$; Density: $F_{4,40} < 0.42$; $P > 0.7955$) in the repeated measures analysis across the six sampling times (Table 3.2 and Table 3.3).

Soil property responses to management choices at different time points

We further tested for variety and planting density effects separately for each of the six sampling times during the growing season. These analyses indicated that if any variety and/or planting density effects occurred, they did so exclusively early in the growing season (weeks 1-8). In general, these analyses suggested that switchgrass variety and planting density effects on soil were minimal. Further, although we observed some variety effects on several soil parameters that we recorded, these effects were not consistently specific to any one variety (Table 3.1 and Figure 3.2).

The greatest number of abiotic attributes varied among the management choices in the first sampling (week 1) when soil pH, K(ppm), Mg(ppm), total K%, Ca%, H% and K:Mg varied among the switchgrass varieties (Table 3.1). For example, soil pH under BoMaster (pH = 5.93 ± 0.05) in week 1 was lower than under Colony (pH = 6.1 ± 0.16) or Kanlow (pH= 6.13 ± 0.12) ($F_{3,21}$ = 6.65; P = 0.0025). Some of the varieties differed in total C% , K(ppm) and K:Mg ratio when grown in HDP or LDP in week 1 (Table 3.1). For example, K(ppm) was higher when associated with BoMaster (K = 151.5 ± 28.45) and Kanlow (149.75 ± 28.03) growing under HDP compared to Alamo (110.0 ± 32.54) and Colony (104.0 ± 14.72)($F_{4,21}$ = 3.54; P = 0.032) growing under the same density. After week 1, we observed no evidence for any density effects. In contrast to the planting densities that did not vary after the first sampling, a few abiotic variables still varied among the switchgrass varieties. Switchgrass varieties differed in Ca(ppm) and K:Mg ratio in the second sampling (week 2) (Table 3.1). Soil Ca(ppm) under Colony in week 2 was higher than under Kanlow ($F_{3,21}$ = 3.28; P = 0.041). The K:Mg ratio in week 2 was lower under Alamo compared to BoMaster ($F_{3,21}$ = 5.40; P = 0.007) (Table 3.1). Further, H(%) varied in week 4 among varieties ($F_{3,21}$ = 3.36; P=0.038), although the pairwise comparisons of provided no support for differences among the varieties ($P > 0.23$). Finally, Ca% was higher when in soils under Alamo and BoMaster than Kanlow in week 8 ($F_{3,21} = 5.39$; $P = 0.007$). Later in the growing season, after week 8, there was no evidence for any switchgrass variety effects on the soil chemistry.

Planting densities differed in neither soil PLFA-inferred microbial biomasses nor EEAs. In contrast, PLFAs varied among the switchgrass variety, but did so only in the first half of the growing season (weeks 2, 4 and 16) (Table 3.2). Switchgrass varieties differed in total bacterial ($F_{3,21} = 3.48$; $P = 0.030$) and total fungal ($F_{3,21} = 6.19$; $P = 0.004$) biomass as well as in F:B ratio ($F_{3,21} = 5.72$; $P = 0.005$) in week 2 (Table 3.2). The differences in total fungal biomass were attributable to differences in non-mycorrhizal fungi, as the AM fungi did not differ. Total bacterial biomass in soil under Kanlow was lowest and lower than that under Colony (Table 3.2). In contrast, total fungal biomass in soil was highest under Kanlow and higher than that under Colony. These differences were attributable to the biomass of non-mycorrhizal fungi, whose biomass was greatest under Kanlow and higher than that under Alamo or Colony. In contrast to the non-mycorrhizal fungi, the switchgrass varieties did not vary in their PLFA-inferred AM fungus biomass. The differences in total bacterial and fungal biomarkers resulted in subsequent differences in the F:B ratio that was higher under Kanlow than under Alamo. In addition, soils under the variety BoMaster had a higher total fungal biomass than Colony and higher F:B ratio than Alamo. In week 4, total bacterial biomass ($F_{3,21} = 3.88$; $P = 0.023$) and that of actinomycetes ($F_{3,21} = 5.07$; $P = 0.009$) differed among the varieties (Table 3.2). Similar to week 2, total bacterial biomass was lowest under Kanlow and differed from that under BoMaster. Actinomycete biomass in week 4 was lower under variety BoMaster and differed from Colony and Kanlow. In week 8, we observed no evidence for differences in PLFA-inferred microbial biomasses among the switchgrass varieties. In week 16, total fungal biomass varied again among the varieties ($F_{3,21} = 4.07$; $P = 0.020$). In contrast to week 2, when soils under Colony had the lowest fungal biomass, in week 16, total fungal biomass was highest under Colony and higher than that under Alamo (Table 3.2). While we never observed any differences in soil EEAs between the planting densities, the EEAs varied among the varieties but only in week 16 ($F_{3,21} = 3.22$; $P = 0.040$) (Table 3.3). Soils under Kanlow had low EEAs overall. Under Kanlow, CBH activity was lower than under any of the other three varieties, βG activity was lower than under Alamo and Colony, and phosphatase activity was lower than under Alamo (Table 3.3).

Temporal dynamics of the soil properties

To test for temporal dynamics in soil chemistry, PLFAs and EEAs, we explored general trends using mixed effect model ANOVAs with “Time” included as an additional continuous fixed effect. Then, to better focus on where distinct difference occur during the growing, we used pairwise comparisons with “time” as a categorical value in a similar mixed effects ANOVA.

Our analyses of soil chemistry highlighted that soil pH ($F_{1,173} =40.22$; $P < 0.001$), total N% ($F_{1,173} = 10.40$; $P < 0.002$), total C% ($F_{1,173} = 16.36$; $P < 0.001$), C:N ratio ($F_{1,173} = 9.73$; $P < 0.002$), P(ppm) ($F_{1,173} = 53.13$; $P < 0.001$) and K(ppm) ($F_{1,173} = 56.81$; $P < 0.001$) declined over time, whereas NH_4^+ ($F_{1,173} = 17.68$; $P < 0.001$) and NO_3^- ($F_{1,173} =8.60$; $P < 0.004$) increased over time (Figure 3.2). In the pairwise post-hoc tests of the categorical “Time” effect, soil pH was higher in weeks 1, 2, 4 and 8 than in weeks 16 and 38 ($P < 0.012$). In addition, pH in week 8 was lower than in weeks 1 and 4 ($P < 0.023$). Total N% declined in the last sampling point (week 38) compared to weeks 1, 4, 8 and 16 ($P < 0.044$), but not week 2 ($P = 0.079$). Total C% in soil was higher in weeks 2, 4, 8 than in week 1 ($P < 0.021$), and lower in week 38 than weeks 1,4, 8 and 16 ($P < 0.002$), but not week 1 ($P = 0.349$). Similar to total C%, C:N ratio was higher in weeks 2, 4, 8, and 16 ($P < 0.002$) compared to week 1 and lower in week 38 compared to earlier in the growing season (2, 4, 8, and 16) ($P < 0.007$), except week 1 ($P = 0.563$). P (ppm) concentration in late growing season (weeks 16 and 38) was lower than in early growing season (weeks 1, 2, 4 and 8) ($P < 0.001$), and lower in week 8 than week 2 ($P < 0.003$). Soil K (ppm) was highest in week 2, higher than at any other time during the season ($P > 0.0025$). Conversely, soil K (ppm) was lowest late in the fall (week 38) and lower than any time earlier in the season ($P < 0.035$). Soil NH_4^+ was lower in the beginning of the growing season (weeks 1 and 2) than later in the growing season (weeks 8, 16 and 38) ($P > 0.038$), and soil NH_4^+ in week 1 was also lower than in week 4 ($P = 0.008$). In addition, soil NH_4^+ in week 16 was higher than in weeks 4 ($P = 0.006$) and 8 ($P = 0.027$). Soil NO_3^- decreased towards the middle of the season and was lower in weeks 4, 8 and 16 than in the first two weeks of the season (weeks 1 and 2) or the last week of the season (week 38) ($P < 0.040$). It is interesting to note the decline in soil pH and soil macronutrients (P and K) and the contrasting increase of NO_3^- and NH_4^+ over the time that likely reflect the balance between the seasonal immobilization by plants and microbial communities and the microbial mineralization. While we observed no strong evidence for density effects for any of the tested soil chemistry variables ($F_{4,173} < 2.40$; $P > 0.052$), soil pH differed among varieties ($F_{3,173} < 4.23$; $P > 0.007$) in these broader analyses. The pairwise comparisons among varieties indicated that soil planted with Colony had higher soil pH than varieties Alamo ($P = 0.048$) and BoMaster ($P = 0.003$), and soil planted with variety BoMaster had lower pH than those planted with variety Kanlow ($P = 0.020$). It is interesting to note that Colony is also highest yielding variety which might explain its impact on the soil chemistry.

Analyses of PLFAs with “Time” as a continuous fixed effect indicated that total bacteria ($F_{1,173} = 12.54$; $P < 0.001$) and Gram- bacteria % ($F_{1,173} = 28.48$; $P < 0.001$) decreased over the growing season, whereas PLFA-inferred total fungal biomass ($F_{1,173} = 6.19$; $P = 0.014$) and F:B ($F_{1,173} = 12.70$; $P < 0.001$) increased over time. No increase or decrease in Gram+ bacteria, actinobacteria, or AM fungi % were observed across the growing season ($F_{1,173} < 2.56$; $P > 0.111$) (Figure 3.3). Similar to the analyses of temporal dynamics in soil chemistry, we performed the pairwise comparisons of the weeks by treating “time” as a categorical factor to dissect the temporal dynamics in greater detail. Pairwise comparisons revealed that total bacteria % week 1 was lower compared to weeks 4, 8 and 16 ($P < 0.033$). Gram- bacteria % was higher in a week 4 than in weeks 1, 2, 8, 16 and 38 ($P < 0.001$), and lower in weeks 16 and 38 than in weeks 1 and 8 ($P < 0.048$). In contrast with Gram- bacteria, % of Gram+ bacteria in week 4 was lower compared to weeks 1, 2, 8, 16 and 38 ($P < 0.001$). Gram+ bacteria % was also lower in week 1 compared to weeks 2, 8, 16 and 38 ($P < 0.001$). Actinobacteria % in week 4 was higher than in weeks 1, 2, 8, 16 and 38 ($P < 0.001$). Actinobacteria in week 16 was also lower than in weeks 1, 2 and 8 ($P < 0.003$). Total fungi % in week 4 was lower than other weeks during the growing season ($P < 0.011$), and in week 8 was also lower than in weeks 1, 2, 16 and 38 ($P < 0.028$). AM fungi (%) was lowest in week 4 ($P < 0.001$) and highest in week 16 and differed from the other weeks ($P < 0.001$). In addition, AM fungi % was also higher in week 8 than in week 1 ($P < 0.001$). Similar to AM fungi, F:B ratio was lowest in week 4 and lower than weeks 1, 2, 8, 16 and 38 ($P < 0.001$), while week 8 was also lower than weeks 1, 2, 16 and 38 ($P < 0.001$). We observed no strong evidence for variety ($F_{3,173} < 2.36$; $P > 0.074$) or density ($F_{4,173} < 1.71$; $P > 0.152$) effects or interactions with time for any of the tested PLFAs variables.

The analyses of EEAs that included the temporal component showed that βG ($F_{1,173} = 10.45$; $P < 0.002$) and NAG ($F_{1,173} = 6.77$; $P = 0.010$) enzymes declined in soil over the growing season, whereas Phos ($F_{1,173} = 3.08$; $P = 0.081$) and CBH ($F_{1,173} = 2.31$; $P = 0.130$) did not decline or increase over time (Figure 3.4). In the pairwise comparisons βG was higher in weeks 2 and 8 than weeks 1, 4, 16 and 38 ($P < 0.001$). In addition, βG in week 4 was lower than in weeks 1, 16 and 38 ($P < 0.003$), whereas it was higher in week 1 than in weeks 16 and 38 ($P < 0.002$). Similar to βG, NAG was highest in week 2 ($P < 0.044$) and lowest in week 4 ($P < 0.001$) compared to the rest of the season. In addition, NAG during weeks 1 and 8 was higher than in weeks 16 and 38 ($P < 0.001$). Phos was higher in weeks 1, 2, 8, 16 and 38 compared to week 4 ($P < 0.001$), while Phos in weeks 2 and 8 was also higher than in weeks 16 and 38 ($P < 0.001$). Similar to other tested soil enzymes, CBH was lower in week 4 compared to other weeks ($P < 0.012$). In addition, CBH in week 8 was higher than in weeks 1, 2, 16 and 38 ($P < 0.001$), while also higher in week 38 compared to weeks 2 and 16 ($P < 0.018$). We observed no strong evidence for the variety ($F_{3,173} < 0.87$; $P > 0.458$) or density ($F_{4,173} < 0.95$; $P > 0.439$) effects or interactions with time for any of the tested EEAs.

Overall responses of soil- and root- inhibiting bacterial and fungal richness and diversity

To focus on the effects of management choices on the bacterial and fungal communities, we analyzed observed (S_{Obs}) and extrapolative (Chao1) richness, diversity (Shannon's $_{H'}$), and evenness (E_H) in roots and soils using mixed models with time as a random effect. These analyses provided no evidence for variety or planting density effects on the richness and diversity metrics for bacteria or fungi in switchgrass roots or soil (Table 3.4 and Table 3.5).

Soil- and root-inhibiting bacterial and fungal diversity at different time points

To dissect the dynamics of bacterial and fungal communities during the growing season, we analyzed richness, diversity, and evenness separately at each of six time points. Similar to the analyses of soil chemistry, responses to management choices in bacterial richness and diversity were rare and exclusive to early growing season (Table 3.4). Soil bacterial extrapolated (Chao1) ($F_{3,21} = 3.59$; $P = 0.03$), but not observed (S_{Obs}) ($F_{3,21} = 1.21$; $P = 0.33$) richness varied among the varieties in week 2. Bacterial extrapolative richness was higher in soils under Alamo than under Kanlow ($P = 0.036$). We observed no strong evidence for planting density effects for any of the estimated bacterial richness or diversity metrics in soil at any of the six time points ($F_{4,21} < 1.68$; $P > 0.19$). Similar time-wise analyses of bacteria inhabiting the switchgrass roots revealed no strong evidence of variety ($F_{3,21} < 2.79$; $P > 0.07$) or planting density ($F_{4,21} < 2.63$; $P > 0.06$) effects on bacterial richness or diversity metrics. Similar to bacteria, the switchgrass variety and planting density effects on the fungal richness and diversity were observed only in the beginning of the season (Table 3.5). Analyses of fungal communities associated with soil and roots revealed that Kanlow had lower observed (S_{Obs}) and extrapolated species richness (Chao1) as well as diversity (Shannon's H') than other varieties in week 2. We observed no strong evidence for planting density effects on fungal richness or diversity estimates in soil ($F_{4,21} < 2.17$; $P > 0.108$) or roots ($F_{4,21} < 2.61$; $P > 0.064$) across the season. An exception was the marginal effect of density in roots where HDP in variety Alamo differed from LDP in BoMaster in a week 8 ($P = 0.044$).

Temporal dynamics of microbial richness and diversity

To elucidate the temporal dynamics of the soil and root microbial richness and diversity, we used mixed models ANOVAs with "Time" included as an additional continuous fixed effect. These analyses highlighted the temporal dynamics in the bacterial and fungal richness and diversity in the course of a growing season. Bacterial richness (S_{Obs}) in soil ($F_{1,171} = 160.24$; $P < 0.001$) and roots ($F_{1,170} = 53.66$; $P < 0.001$) as well as diversity (Shannon's H') in soil ($F_{1,171} = 82.82$; $P < 0.001$) and roots ($F_{1,170} = 33.59$; $P < 0.001$) declined in the course of the growing season (Figure 3.5). To better identify where these temporal dynamics emerged from, we used a categorical "Time" effect in pairwise comparisons. These post-hoc analyses indicated that soil bacterial richness and diversity in the last sampling in late fall (week 38) were lower than in any time point before ($P < 0.001$). In addition, soil bacterial richness in week 16 was lower than in week 1 ($P = 0.020$) and in week 4 ($P = 0.001$). Bacterial richness in roots in late growing season (weeks 8, 16 and 38) was lower than in early growing season (weeks 1, 2 and 4) ($P < 0.023$). Bacterial diversity in roots was higher in early season (weeks 1, 2 and 4) than in week 8 ($P < 0.015$) and was higher in week 2 than in week 16 ($P = 0.003$) and week 1 ($P = 0.033$). Similar to soil bacteria, bacterial diversity in roots was lowest in the last sampling in late fall (week 38) and lower than that any time earlier in the growing season ($P = 0.003$), except for weeks 8 ($P = 0.429$) and 16 ($P = 0.714$).

Similar to bacteria, fungal richness ($F_{1,160} = 69.06$; $P < 0.001$) and diversity in soil ($F_{1,160} = 16.99$; $P = 0.010$) declined over time (Figure 3.6). In the pairwise post-hoc tests of the categorical "Time" effect, soil fungal richness was higher in weeks 1, 2 and 8 than in week 16 ($P < 0.004$), and lower in the last sampling (week 38) than any time earlier in the growing season ($P < 0.002$). Like fungal richness in soil, fungal diversity in soil at the end of the growing season (week 38) was lower than any time earlier in the growing season ($P < 0.0384$). In contrast to bacteria and soil fungi, fungal richness in roots increased over time ($F_{1,170} = 15.47$; $P < 0.001$) (Figure 3.6). This was largely attributable to the high fungal richness in roots at the end of the growing season (week 38) that was higher than any time earlier in the growing season ($P < 0.044$). Although there was no strong evidence for temporal effects ($F_{1,170} = 0.20$ and $P = 0.658$) for root fungal diversity across the season in our analyses with "Time" as a continuous variable, pairwise comparisons of the categorical "Time" effect revealed that fungal diversity in roots was lower in week 16 than in weeks 1, 2, 8 and 38 (P < 0.011), but not week 4 (P = 0.128). Additionally, fungal diversity in roots was higher in week 4 than in weeks 1 (P = 0.003) and 38 (P = 0.011).Corroborating our other analyses, the richness and diversity responses to varieties or their planting densities were absent when ”Time” was included as a fixed effect in our analyses. We observed no strong support for switchgrass variety effects on bacterial richness (S_{Obs}) in either soil ($F_{3,174}$ = 1.12; P = 0.241) or roots ($F_{3,173}$ = 0.64; P = 0.589). This was also true for bacterial diversity (Shannon's $_{H'}$) in soil ($F_{3,174}$ = 1.41; P = 0.24) and roots ($F_{3,173}$ = 0.22; P = 0.881). Similar to bacteria, neither fungal richness (S_{Obs}) in soil ($F_{3,163}$ = 0.34; P = 0.797) or roots ($F_{3,173}$ = 0.08; P = 0.97) nor diversity in soil ($F_{3,163}$ = 0.87; P =0.459) or roots ($F_{3,173}$ = 0.16; P = 0.922) varied among the switchgrass varieties. Consistent with our overall analyses, these analyses provided no support for planting density effects on bacterial or fungal richness and diversity. Neither bacterial richness in soil ($F_{4,174}$ = 0.37; P = 0.832) or roots ($F_{4,173}$ = 0.52; P = 0.722) nor diversity in soil ($F_{4,174}$ = 0.28; P = 0.888) or roots ($F_{4,173}$ = 0.12; P = 0.975) varied between the two planting densities. Again, fungal responses were consistent with those of bacteria and neither fungal richness in soil ($F_{4,163}$ = 1.51; P = 0.202) or roots ($F_{4,173}$ = 0.19; P = 0.945) nor diversity in soil ($F_{4,163}$ = 0.87; P = 0.486) or roots ($F_{4,173}$ = 0.36; P = 0.840) were affected by the planting density.

Overall responses of soil- and root-inhibiting bacterial and fungal community composition

To understand whether varieties or planting density affect assembly of bacterial and fungal communities in soil and roots, we compared the communities pooled across the six time points. These analyses provided no evidence for a planting density effect either in bacterial communities associated with soil ($F_{4,182}$ = 1.066; P = 0.271) and roots ($F_{4,182}$ = 0.77; P > 0.995) or fungal soil ($F_{4,181} = 0.85$; $P = 0.873$) and roots ($F_{4,181} = 0.83$; $P = 0.97$) communities in switchgrass. However, in contrast to our analyses of richness and diversity, bacterial and fungal communities in roots and soil varied among the varieties. Differences among the varieties ($F_{3,182} = 2.682$; $P = 0.001$) were attributable to soil bacterial communities inhabiting soil underneath BoMaster that were distinct from those underneath Colony ($P_{adj} = 0.018$) and from those underneath Kanlow ($P_{adj} = 0.04$). Indicator taxon analyses identified a large number of indicators for the switchgrass varieties. Of the total of 416 soil bacterial indicators, a majority was associated with BoMaster (286), whereas fewer were associated with Colony (53) and Kanlow (77) and none with Alamo (Table A.1) Majority of soil bacterial indicator OTUs were assigned to Acidobacteria (67), Actinobacteria (46) and Proteobacteria (169). These indictors included nitrogen fixing taxa – 2 Nitrospirales (phylum Nitrospirae) indicators associated with BoMaster (1) and Kanlow (1) as well as 4 Rhizobiales (phylum Proteobacteria) indicators for BoMaster (2), Colony (1) and Kanlow (1) (Table A.1). The varieties also varied ($F_{3,182} = 1.29$; $P = 0.038$) in their root bacterial community composition. Despite this variety effect, the FDR adjusted pairwise comparisons identified no pairs of varieties that differed ($P_{adj} > 0.167$).

Indicator taxon analyses identified a smaller, compared to soil, number of bacterial indicators for the switchgrass varieties in roots. Of the total of 37 root bacterial indicators, a majority was associated with Colony (19), whereas fewer were associated with BoMaster (13), Kanlow (4) and Alamo (1) (Table A.2).

Fungal communities in soil also differed compositionally among the varieties ($F_{3,181} = 1.29$; $P = 0.038$). These differences were attributable to distinct soil fungal communities underneath Kanlow and Alamo ($P_{adj} = 0.012$) or BoMaster ($P_{adj} = 0.042$) as well as those underneath BoMaster and Colony ($P_{adj} = 0.009$). Our indicator taxon analyses identified a total of

30 fungal indicators in switchgrass soil, including four for Alamo, six for BoMaster and nine and eleven for Colony and Kanlow, respectively (Table A.3). Examples of these indicators include a common soil-inhabiting *Mortierella* sp. (Phylum Zygomycota) and leaf pathogen *Phaeosphaeria* sp. (Phylum Ascomycota) associated with Kanlow and representatives of the arbuscular mycorrhizal Glomeromycota that had two indicators for variety BoMaster and one indicator for Colony. Also, fungal communities in switchgrass roots differed among the varieties ($F_{3,181}$ = 1.45; P = 0.002). Fungal communities inhabiting Kanlow roots differed from those inhabiting Alamo (P = 0.012). The indicator taxon analyses revealed only a total of six indicators, all representing BoMaster including one AM fungus indicator of family Glomeraceae (Table A.4)

Soil- and root-inhibiting bacterial and fungal community analysis by week

In general, bacterial and fungal communities associated with roots and soils varied compositionally among varieties only in the beginning of the season (from weeks 1 to 4), except for root bacterial communities that showed no variety effect at any time during the growing season ($F_{3,23/24}$ < 0.92; P > 0.07). In contrast to the early season variety effects, we observed no evidence for planting density effect for root- or soil-inhabiting communities, except for a planting density effect on soil bacterial communities in week 8 ($F_{4,24}$ < 0.92; P > 0.04). Indicator taxon analyses identified taxa that differed in week 8 and included OTUs representing Acidobacteria (10), Bacteroidetes (4) and Proteobacteria (12) (Table A.5). Soil bacterial communities differed among varieties in weeks 1 ($F_{3,23}$ = 1.73; P = 0.017) and 2 ($F_{3,24}$ = 1.41; P = 0.025). Pairwise comparisons indicated that in week 1 BoMaster differed from Alamo and BoMaster different from Colony and Kanlow. However, after the FDR correction for multiple comparisons resulted in only marginal differences among varieties (P > 0.07) Similar to the week 1, soil bacterial communities differed among switchgrass varieties in week 2 when communities in soils underneath BoMaster differed from Alamo and Kanlow. Again after the correction for multiple comparisons varieties were not different from each other ($P = 0.096$). We also observed a switchgrass variety effect of in the soil fungal communities during week 2 ($F_{3,23} = 1.48$; $P = 0.012$), with no significant difference in varieties after adjustment ($P > 0.054$). The root fungal communities differed among the varieties in weeks 2 ($F_{3,24} =1.415$; $P = 0.004$) and 4 ($F_{3,22} =1.633$; $P = 0.001$). Fungal communities in BoMaster roots differed compositionally from Alamo ($P = 0.018$) and Kanlow ($P = 0.018$) during week 2. Indicator taxon analyses of communities in week 2 identified two indicators associated with BoMaster, both representing the AM fungus family Glomeraceae. In a week 4, root-inhabiting fungal communities associated with Kanlow differed from those associated with Alamo ($P = 0.006$) or Colony ($P = 0.010$) with only two indicators representing phylum Ascomycota and associated with Kanlow. (Table A.6).

Temporal dynamics of the root and soil bacterial and fungal communities

Analyses of the temporal dynamics of bacterial and fungal communities in the roots and soil were consistent for density, variety, and time effects. The mixed effects analyses of PCoA axis scores that included “Time” as a linear fixed effect provided no strong evidence for the planting density effects on soil bacterial ($F_{4,177} = 1.249$; $P = 0.081$), root bacterial ($F_{4,177} = 0.917$; $P = 0.713$), soil fungal ($F_{4,176} = 0.949$; $P = 0.612$) or root fungal ($F_{4,176} =0.891$; $P = 0.059$) communities, a result consistent with minimal planting density effects on soil chemistry and/or bacterial and fungal richness and diversity. Although our broader analysis suggested a strong variety effect on bacterial communities in soil ($F_{3,177} = 3.15$; $P = 0.001$) and roots ($F_{3,177} = 1.14$; $P = 0.004$) or fungal communities in soil ($F_{3,176} = 1.19$; $P = 0.001$) and roots ($F_{3,176} = 1.57$; $P = 0.001$), these results were not consistently supported in pairwise comparisons. Each of the four switchgrass varieties differed in bacterial communities in soil ($P < 0.03$), but not in roots ($P >$

0.157). Fungal communities in soil underneath Kanlow differed from other varieties: Alamo (P_{adj} = 0.012), BoMaster (P_{adj} = 0.012) and Colony (P_{adj} = 0.006), whereas fungal communities in roots differed only between Kanlow and Alamo (P_{adj} = 0.012).

We used PCoA axis scores as fixed linear terms in our mixed effects models to identify general trends in ordination space over the growing season. The first PCoA ($F_{1,171}$ = 64.09; P < 0.001) and second PCoA ($F_{1,171}$ = 20.32; P < 0.001) axis scores characterizing soil bacterial communities decreased over time, suggesting a gradual directional shift in the ordination space. In a similar manner, first PCoA axis scores characterizing root bacterial communities increased over the growing season ($F_{1,171}$ = 53.60; P < 0.001), whereas no such linear trends were obvious for the second PCoA axis scores ($F_{1,171}$ = 1.93; P = 0.167) (Figure A.1). First PCoA axis scores characterizing soil fungal communities declined over time ($F_{1,170}$ = 31.03; P < 0.001), whereas the second PCoA axis scores did so only marginally ($F_{1,170}$ = 5.27; P = 0.022). First PCoA axis scores for the switchgrass root fungal community increased($F_{1,170}$ = 20.32; P < 0.001), whereas those of second PCoA axis declined ($F_{1,170}$ = 92.20; P < 0.001) (Figure A.2).

Our analyses highlighted a very strong temporal effect on the bacterial and fungal community composition associated with switchgrass soils and roots. In pairwise comparisons, bacterial and fungal communities in roots and soils at each sampling time differed after FDR correction. Dispersion analysis of the soil bacterial communities provided no evidence for community convergence or divergence over time (P = 0.670) and two planting densities (P = 0.504). In contrast, our analyses suggested marginal variety effect (P = 0.046) indicating that Kanlow hosted more heterogeneous (divergent) soil bacterial communities than the Colony. Dispersion analyses of the root bacterial communities provided no consistent evidence for convergence or divergence between planting densities (P = 0.770) and varieties (P = 0.170).

However, root bacterial community dispersion varied over the growing season ($P < 0.001$). Weeks 1 and 2 more dispersed compared to weeks 4 and 8 suggesting bacterial community convergence towards the peak growing season. Similarly to bacteria, fungal community dispersion analyses provided no evidence for community convergence or divergence for switchgrass planting densities ($P = 0.850$) in soil and roots ($P = 0.310$) or among switchgrass varieties ($P = 0.350$) in soil or ($P = 0.311$) in roots. However, like root bacteria, these analyses indicated a greater soil fungal community dispersion ($P < 0.001$) early in the growing season: dispersion in week 1 was greater than in week 8, and week 2 was greater than weeks 4 and 8 suggesting community filtering from a more heterogeneous community early in the growing season. Similar to fungal communities in soil, root fungal communities in week 1 were more dispersed than in weeks 2, 4, and 8, and those in week 2 had greater dispersion than those in weeks 4 and 8.

We used indicator taxon analysis to identify soil and root fungi and bacteria that drove the observed temporal differences. Species indicator analysis revealed total of 1,737 bacterial indicator OTUs in soil ($P = 0.001$) (Table A.7). The number of indicators increased over the growing season from 71 indicators in week 1 to 814 indicators in week 38. These indicators represented mainly the bacterial phyla Actinobacteria (104), Acidobacteria (151), Protobacteria (253) and Planctomycetes (118). Root bacterial communities had fewer bacterial indicators (800) with peaks in number of indicator OTUs in weeks 1 (313) and 16 (243) (Table A.8). Similar to soil, majority of root indicator bacteria belonged to Acidobacteria (71), Actinobacteria (196), Proteobacteria (271) and Planctomycetes (96). Soil (218) and root (232) fungal indicators had similar distribution during the season with peaks in numbers of indicator OTUs in week 38 with

102 fungal indicators in soil and 206 in roots. The indicators represented mainly Ascomycota (soil 30, roots 68) and Basidiomycota (soil 49, roots 87) (Table A.9 and Table A.10).

Soil chemistry correlations with microbial communities

To understand the correlations between soil microorganisms and soil chemistry characteristics, we performed the environmental fit analysis (Figure A.3). Although a few soil factors correlated with soil fungal community ordination (NH_4^+ – $P = 0.001$; P – $P = 0.004$; Ca – $P = 0.009$; K – $P = 0.001$; C:N – $P = 0.026$), their correlation coefficients (r2) were generally very low with the highest correlation co-efficient (7%) for Ca. The environmental correlates appear more driven by the early (weeks 1-8) vs late (weeks 16 – 38) season division (Figure 3.6). Soil bacteria had a larger number of correlates (pH – $P = 0.001$; NH_4^+ – $P = 0.001$; total N% – $P = 0.001$; total C% – $P = 0.001$; C:N – $P = 0.001$; OM% – $P = 0.001$; Ca – $P = 0.001$; K – $P = 0.001$; P – $P = 0.001$). Interestingly, the three correlates with highest correlation coefficients were all carbon related: total C% with a correlation coefficient of 20.5% and OM% and total C:N with coefficients of 19% and 18%, respectively. PCoA visualization revealed that bacterial soil factors mostly correlated with weeks 4 and 8 (Figure 3.7).

Discussion

We aimed to evaluate how abiotic and biotic attributes vary over one growing season among four switchgrass varieties planted in two different densities and maintained under the conservation agriculture principles. Our data indicate that switchgrass varieties and their planting densities minimally affect soil chemistry or bacterial and fungal communities in soil or switchgrass roots, particularly when compared to the temporal dynamics over a growing season. Our findings suggest that the temporal dynamics have a greater effect on the switchgrass microbiome and its assembly than do the management choices that our research targeted (planting density and varieties).

Soil chemistry responses

Although our analyses overall suggested minimal effects of switchgrass varieties or planting densities on soil chemistry, various soil attributes differed in the early growing season. Any observed differences among the varieties in the early growing season were no longer obvious beyond eight weeks after the leaf emergence. Although our data do not permit identification of the mechanisms that best explain these observations, we hypothesize that these early season differences are attributable to differences in the timing of leaf emergence and corresponding initiation of the plant metabolic activity in the spring. These early season developmental differences likely play a role in our observed differences in soil abiotic attributes. For example, variety “BoMaster” was last to emerge in the spring, appearing almost a week later than other varieties (Mandyam and Kazarina personal observation), thus likely resuming its metabolic activity and rhizodeposition later than the other varieties. Our data on the soil chemistry dynamics support this hypothesis: after two weeks, soils planted with BoMaster had higher P, Ca, and K concentrations than those planted with other varieties, likely attributable to the delay in nutrient uptake by “BoMaster”. The ephemeral early season differences in varieties’ activity and their disappearance before the peak growing season lend further support to our hypothesis. Developmental differences in biological activity of the switchgrass varieties have been observed in other studies (Chen et al. 2019; Ghimire et al. 2011; Rodrigues at al. 2017). However, these metabolic differences seem inconsistent throughout the plant development. For example, in a greenhouse experiment, Rodrigues et al. (2017) observed that the relative soluble amino acid abundances differed among two varieties at six weeks, but not earlier (at 1.5 weeks) or later (16 weeks). Like other variety-specific traits such as differences in survival and productivity among others (Sanderson et al. 1999; Casler et al. 2003, 2004, 2007), differences in the early season performance reflect the underlying differences in the variety genetic background. However, the fact that differences were not observed later in the course of the growing season in our study may reflect the minimal effect that varieties may have on the abiotic soil characteristics.

The abiotic and biotic soil characteristics varied temporally. Nutrient availability in soil is affected by biotic factors such as plant and microbial activity and metabolism (Binkley et at. 1998) as well as by abiotic factors such as soil moisture (Mitchell et al. 1992). As an example of temporal variability, the two plant available N sources (NH_4^+ and NO_3^-) varied during the growing season and increased in the course of the growing season. Our observations corroborate those of others (Casals et al. 1995; Amos et al. 2015): plant available N sources vary during the growing season likely reflecting microbial soil N transformations. In our experiment, soil NH_4^+ was highest in the middle of the growing season likely correlating with conditions favorable to ammonification (high moisture and high temperature in the summer). In addition, we observed a plateau in NH_4^+ and an increase in NO_3^- concentration in our last sampling at week 38. These observations are in line with the conceptual model of soil N cycle by Schimel and Bennett (2004) describing the plant-microbe competition for available N and likely reflect high mineralization of N from the senescent plant biomass that maintained microbial activity during minimal plant metabolic activity and resulted in N mineralization at the end of the growing season.

Seasonal variability of environmental conditions, *e.g.*, precipitation, may affect microbial community biomass and activity. We observed an unexpectedly low EEAs and fungal PLFA biomass measures in week 4. In contrast, we observed no corresponding changes in soil chemistry or bacterial and fungal alpha diversity and community composition at that time. In search for possible explanations, we acquired and analyzed the weather data (https://www.weather.gov/wrh/Climate?wfo=jan). However, we did not observe any strong evidence for weather anomalies – for drought, in particular – that might help explain the low PLFA-inferred fungal biomass and the corresponding low EEAs (Žifčáková et al. 2016). The local NRCS weather station reported 54-mm precipitation five days before the week 4 sampling and 24-mm percipitation in the day of the sampling. It is unlikely that this precipitation would explain the unexpectedly low PLFAs and EEAs estimates.

Our experiment is analogous to so called common garden experiments; all our switchgrass varieties were grown adjacent to each other and thus under identical environmental conditions in a split-plot design wherein spatial blocking aimed to minimize the variability in soil characteristics and environmental conditions. Even though the experiment had been in place for six years at the time of sampling and should highlight the variety and management effects, our data strongly suggests that soil nutrients vary temporally, but less so among switchgrass varieties or their planting densities.

Microbial responses

Similar to soil chemistry, we observed no strong evidence for an overall variety or planting density effects on the microbiome richness and diversity in switchgrass roots or associated soils. Although richness and diversity were not impacted, varieties hosted distinct bacterial and fungal communities corroborating results of others (Emery et al. 2018; Rodrigues et al. 2017; Revillini et al. 2019), who concluded that varieties could affect root and soil microbial communities. As the richness and diversity were unaffected, the compositional differences are likely attributable to species rank reordering among the varieties (see Avolio et al. 2019; Collins et al. 2008; Cleland et al. 2013).

In general, our observed communities matched compositionally those reported for switchgrass by others (Chen et al. 2019; Revillini et al. 2019; Singer et al. 2019 and Brodsky et al. 2019). Bacterial communities in soils were dominated by Phyla Actinobacteria, Acidobacteria, Bacteroides, Proteobacteria and Planctomycetes and dominated in roots by bacterial phyla Acidobacteria, Bacteroides, Proteobacteria, Firmicutes corroborating previous reports (Chen et al. 2019; Grady et al. 2019; He et al. 2017; Mao et al. 2011; Revillini et al. 2019; Singer et al. 2019). Similar to bacteria, our fungal communities were similar to those reported previously (Brodsky et al. 2019; Rodrigues et al. 2017; Singer et al. 2019) and composed primarily of classes Agaricomycetes, Dothideomycetes and Sordariomycetes in switchgrass-associated soils and roots.

We also utilized indicator taxon analyses to identify bacteria and fungi that may have been disproportionately more abundant with one switchgrass variety compared to others. These analyses identified a large number of potential indicators. The two lowest yielding varieties “BoMaster” and “Kanlow” that appeared most distinct from the other two varieties in soil chemistry also tended to have a higher number of bacterial and fungal indicators (Table A.1 and Table A.2). These indicators included bacteria assigned to taxa representing potential nitrogen-fixers (Rhizobia) and fungi assigned to phylum Glomeromycota representing the AM fungi as well as putative pathogens (Mycosphearella). Taken together, these observations suggest that varieties may host microbiomes that positively or negatively affect variety performance and/or nutrient acquisition. Based on these indicator taxon analyses, some varieties may potentially serve as superior candidates for sustainable conservation agriculture because they may attract beneficial microbes, require lesser nutrient inputs and/or differ in their disease susceptibility (Lowman et al. 2016; Roley et al. 2019), whereas others may be more susceptible to bacterial or fungal antagonists.

Soil and root microbial community richness and diversity as well as composition were temporally dynamic. Our studies primarily tested hypotheses on the effects of switchgrass varieties and their planting densities and neither fungal nor bacterial community richness or diversity strongly responded to these management choices. Although richness and diversity metrics were minimally affected by the variety choices, bacterial and fungal community composition seemed to differ among the varieties in the broader analyses that also addressed the temporal dynamics. This was not true for planting densities which did not affect the bacterial or fungal community in these analyses. Closer analyses of the variety effects suggested that the observed differences were minimal and mainly inconsistent. However, it is interesting to note that similar to overall community responses, the differences among varieties were mostly attributable to the low-yielding variety “Kanlow”.

Whilst the variety or planting density choices may have had small impacts on the root and soil inhabiting bacterial and fungal communities, their richness and diversity, as well as their composition were dynamic during the growing season. In general, richness and diversity tended to decline over the season except for root fungi whose richness increased over the season. Interestingly, the number of indicators generally increased toward the end of the season suggesting a seasonal change of the microbial communities and its associated functions. We also often observed general linear trends in the PCoA axis scores that suggest gradual shifts in the community composition supporting the greatest differences between early and late season.

Other studies have reported large seasonal shifts in plant-associated bacterial and fungal communities. For example, Chen et al. (2019), Rodrigues et al. (2017) and Sawyer et al. (2019) concluded that the seasonal variation in switchgrass microbiome is a result of the combination of the abiotic environmental changes as well as seasonal changes in the plant metabolic and biochemical activity. However, our findings are in contrast with Carson et al. (2019) who observed no community trajectory in the ordination space over the growing season but observed very strong treatment effects of prescribed burning and fertilization (N addition) in tallgrass prairie system. We hypothesize that in hierarchy of the factors shaping microbial communities, our management effects were minor and masked by the strong temporal dynamics, contrasting the strong treatment effects reported in a study by Carson et al. (2019) in which 30 years of nitrogen addition masked the subtle temporal dynamics of fungal communities.

We also expected that switchgrass varieties would differ temporally in their soil and root microbiomes such that in switchgrass microbiomes can change temporally over the growing season and vary across varieties (Ghimire et al. 2011; Rodrigues et al. 2017). However, similar to our soil chemistry results, of those weeks across the season that we targeted, the differences in planting densities were minimal or absent, whereas the effect of varieties on the microbial richness and diversity metrics as well as microbial communities were rare and observed only at the beginning of the season. The indicator taxon analyses confirm the microbial community data and reflect that varieties are similar in composition and have fewer indicators toward the end of the season, supporting the soil chemistry hypothesis that varieties differ only in the initial developmental stage.

References

Abubaker, S. (2008). Effect of Plant Density on Flowering Date, Yield and Quality Attribute of Bush Beans (Phaseolus Vulgaris L.) under Center Pivot Irrigation System. American

Journal of Agricultural and Biological Science, 3. https://doi.org/10.3844/ajabssp.2008.666.668

Avolio, M. L., Forrestel, E. J., Chang, C. C., La Pierre, K. J., Burghardt, K. T., & Smith, M. D. (2019). Demystifying dominant species [https://doi.org/10.1111/nph.15789]. New Phytologist, 223(3), 1106-1126. https://doi.org/https://doi.org/10.1111/nph.15789

Binkley, D., & Giardina, C. (1998). Why do Tree Species Affect Soils? The Warp and Woof of Tree-soil Interactions. Biogeochemistry, 42(1), 89-106. https://doi.org/10.1023/A:1005948126251

Bligh, E. G., & Dyer, W. J. (1959). A rapid method of total lipid extraction and purification. Can J Biochem Physiol, 37(8), 911-917. https://doi.org/10.1139/o59-099

Brant, J. B., Myrold, D. D., & Sulzman, E. W. (2006). Root controls on soil microbial community structure in forest soils. Oecologia, 148(4), 650-659. https://doi.org/10.1007/s00442-006-0402-7

Broadbent, F.E. (1965). Organic Matter, Methods of Soil Analysis. Part 1, Physical and Mineralogical Methods. American Society of Agronomy Monograph No. 9. pp. 1397-1400. https://doi.org/10.2134/agronmonogr9.2.c41

Brodsky, O. L., Shek, K. L., Dinwiddie, D., Bruner, S. G., Gill, A. S., Hoch, J. M., . . . McGuire, K. L. (2019). Microbial Communities in Bioswale Soils and Their Relationships to Soil Properties, Plant Species, and Plant Physiology. Frontiers in Microbiology, 10, Article 2368. https://doi.org/10.3389/fmicb.2019.02368

Burns, J. C., Godshalk, E. B., & Timothy, D. H. (2008). Registration of ‘BoMaster’ Switchgrass [https://doi.org/10.3198/jpr2007.02.0094crc]. Journal of Plant Registrations, 2(1), 31-32. https://doi.org/https://doi.org/10.3198/jpr2007.02.0094crc

Burns, J. C., Godshalk, E. B., & Timothy, D. H. (2010). Registration of ‘Colony’ Lowland Switchgrass [https://doi.org/10.3198/jpr2009.12.0722crc]. Journal of Plant Registrations, 4(3), 189-194. https://doi.org/https://doi.org/10.3198/jpr2009.12.0722crc

Bååth, E., & Anderson, T. H. (2003). Comparison of soil fungal/bacterial ratios in a pH gradient using physiological and PLFA-based techniques. Soil Biology and Biochemistry, 35(7), 955-963. https://doi.org/https://doi.org/10.1016/S0038-0717(03)00154-8

Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Huntley, J., Fierer, N., . . . Knight, R. (2012). Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. Isme Journal, 6(8), 1621-1624. https://doi.org/10.1038/ismej.2012.8

Carson, C. M., Jumpponen, A., Blair, J. M., & Zeglin, L. H. (2019). Soil fungal community changes in response to long-term fire cessation and N fertilization in tallgrass prairie. Fungal Ecology, 41, 45-55. https://doi.org/10.1016/j.funeco.2019.03.002

Casals, P., Romanyà, J., Cortina, J., Fons, J., Bode, M., & Vallejo, V. R. (1995). Nitrogen supply rate in Scots pine (Pinus sylvestris L.) forests of contrasting slope aspect. Plant and Soil, 168(1), 67-73. https://doi.org/10.1007/BF00029314

Casler, M. D. (2012). Switchgrass Breeding, Genetics, and Genomics. In A. Monti (Ed.), Switchgrass: A Valuable Biomass Crop for Energy (pp. 29-53). Springer London. https://doi.org/10.1007/978-1-4471-2903-5_2

Casler, M. D., & Boe, A. R. (2003). Cultivar × Environment Interactions in Switchgrass [https://doi.org/10.2135/cropsci2003.2226]. Crop Science, 43(6), 2226-2233. https://doi.org/https://doi.org/10.2135/cropsci2003.2226

Casler, M. D., Vogel, K. P., Taliaferro, C. M., Ehlke, N. J., Berdahl, J. D., Brummer, E. C., . . . Mitchell, R. B. (2007). Latitudinal and Longitudinal Adaptation of Switchgrass Populations [https://doi.org/10.2135/cropsci2006.12.0780]. Crop Science, 47(6), 2249-2260. https://doi.org/https://doi.org/10.2135/cropsci2006.12.0780

Casler, M. D., Vogel, K. P., Taliaferro, C. M., & Wynia, R. L. (2004). Latitudinal Adaptation of Switchgrass Populations [https://doi.org/10.2135/cropsci2004.2930]. Crop Science, 44(1), 293-303. https://doi.org/https://doi.org/10.2135/cropsci2004.2930

Chamberlain, J. F., & Miller, S. A. (2012). Policy incentives for switchgrass production using valuation of non-market ecosystem services. Energy Policy, 48, 526-536.

Chaudhary, D. R., Saxena, J., Lorenz, N., Dick, L. K., & Dick, R. P. (2012). Microbial Profiles of Rhizosphere and Bulk Soil Microbial Communities of Biofuel Crops Switchgrass (<i>Panicum virgatum</i> L.) and Jatropha (<i>Jatropha curcas</i> L.). Applied and Environmental Soil Science, 2012, 906864. https://doi.org/10.1155/2012/906864

Chen, H., Yang, Z. K., Yip, D., Morris, R. H., Lebreux, S. J., Cregger, M. A., . . . Schadt, C. W. (2019). One-time nitrogen fertilization shifts switchgrass soil microbiomes within a context of larger spatial and temporal variation. Plos One, 14(6), Article e0211310. https://doi.org/10.1371/journal.pone.0211310

Clark, R. B., Baligar, V. C., & Zobel, R. W. (2005). Response of mycorrhizal switchgrass to phosphorus fractions in acidic soil. Communications in Soil Science and Plant Analysis, 36(9-10), 1337-1359. https://doi.org/10.1081/css-200056950

Cleland, E. E., Collins, S. L., Dickson, T. L., Farrer, E. C., Gross, K. L., Gherardi, L. A., . . . Suding, K. N. (2013). Sensitivity of grassland plant community composition to spatial vs. temporal variation in precipitation [https://doi.org/10.1890/12-1006.1]. Ecology, 94(8), 1687-1696. https://doi.org/https://doi.org/10.1890/12-1006.1

Cole, J. R., Wang, Q., Fish, J. A., Chai, B., McGarrell, D. M., Sun, Y., . . . Tiedje, J. M. (2014). Ribosomal Database Project: data and tools for high throughput rRNA analysis. Nucleic Acids Res, 42(Database issue), D633-642. https://doi.org/10.1093/nar/gkt1244

Collins, S. L., Suding, K. N., Cleland, E. E., Batty, M., Pennings, S. C., Gross, K. L., . . . Clark, C. M. (2008). RANK CLOCKS AND PLANT COMMUNITY DYNAMICS [https://doi.org/10.1890/07-1646.1]. Ecology, 89(12), 3534-3541. https://doi.org/https://doi.org/10.1890/07-1646.1

Combs, S.M. and Nathan, M.V. (1998) Soil Organic Matter. In: Brown, J.R., Ed., Recommended Chemical Soil Test Procedures for the North Central Region, NCR Publication No. 221, Missouri Agricultural Experiment Station, Columbia, MO, 53-58.

da C. Jesus, E., Susilawati, E., Smith, S. L., Wang, Q., Chai, B., Farris, R., . . . Tiedje, J. M. (2010). Bacterial Communities in the Rhizosphere of Biofuel Crops Grown on Marginal Lands as Evaluated by 16S rRNA Gene Pyrosequences. BioEnergy Research, 3(1), 20-27. https://doi.org/10.1007/s12155-009-9073-7

De Cáceres, M., Legendre, P., & Moretti, M. (2010). Improving indicator species analysis by combining groups of sites [https://doi.org/10.1111/j.1600-0706.2010.18334.x]. Oikos, 119(10), 1674-1684. https://doi.org/https://doi.org/10.1111/j.1600-0706.2010.18334.x

Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 27(16), 2194-2200. https://doi.org/10.1093/bioinformatics/btr381

Emery, S. M., Kinnetz, E. R., Bell-Dereske, L., Stahlheber, K. A., Gross, K. L., & Pennington, D. (2018). Low variation in arbuscular mycorrhizal fungal associations and effects on biomass among switchgrass cultivars. Biomass and Bioenergy, 119, 503-508. https://doi.org/https://doi.org/10.1016/j.biombioe.2018.10.012

Emery, S. M., Reid, M. L., Bell-Dereske, L., & Gross, K. L. (2017). Soil mycorrhizal and nematode diversity vary in response to bioenergy crop identity and fertilization. Global Change Biology Bioenergy, 9(11), 1644-1656. https://doi.org/10.1111/gcbb.12460

Follett, R. F., Vogel, K. P., Varvel, G. E., Mitchell, R. B., & Kimble, J. (2012). Soil Carbon Sequestration by Switchgrass and No-Till Maize Grown for Bioenergy. BioEnergy Research, 5(4), 866-875. https://doi.org/10.1007/s12155-012-9198-y

Frostegård, A., & Bååth, E. (1996). The use of phospholipid fatty acid analysis to estimate bacterial and fungal biomass in soil. Biology and Fertility of Soils, 22(1), 59-65. https://doi.org/10.1007/BF00384433

Gamalero, E., Berta, G., Massa, N., Glick, B. R., & Lingua, G. (2008). Synergistic interactions between the ACC deaminase-producing bacterium Pseudomonas putida UW4 and the AM fungus Gigaspora rosea positively affect cucumber plant growth. Fems Microbiology Ecology, 64(3), 459-467. https://doi.org/10.1111/j.1574-6941.2008.00485.x

Gelderman, R., and Beegle D. (1998) Nitrate-Nitrogen. In: Recommended chemical soil test procedures for the north central region. North Central Regional Publication No.

221(Revised), 1998. University of Missouri Agricultural Experiment Station, Columbia, MO. p. 17–20.

Ghimire, S. R., & Craven, K. D. (2011). Enhancement of Switchgrass (Panicum virgatum L.) Biomass Production under Drought Conditions by the Ectomycorrhizal Fungus Sebacina vermifera. Applied and Environmental Microbiology, 77(19), 7063-7067. https://doi.org/10.1128/aem.05225-11

Gihring, T. M., Green, S. J., & Schadt, C. W. (2012). Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. Environ Microbiol, 14(2), 285-290. https://doi.org/10.1111/j.1462-2920.2011.02550.x

Gonzalezlopez, J., Martineztoledo, M. V., Rodelas, B., Pozo, C., & Salmeron, V. (1995). PRODUCTION OF AMINO-ACIDS BY FREE-LIVING HETEROTROPHIC NITROGEN-FIXING BACTERIA. Amino Acids, 8(1), 15-21. https://doi.org/10.1007/bf00806540

Grady, K. L., Sorensen, J. W., Stopnisek, N., Guittar, J., & Shade, A. (2019). Assembly and seasonality of core phyllosphere microbiota on perennial biofuel crops. Nature Communications, 10, Article 4135. https://doi.org/10.1038/s41467-019-11974-4

Grubbs, F. E. (1969). PROCEDURES FOR DETECTING OUTLYING OBSERVATIONS IN SAMPLES. Technometrics, 11(1), 1-&. https://doi.org/10.2307/1266761

Hargreaves, S. K., Williams, R. J., & Hofmockel, K. S. (2015). Environmental Filtering of Microbial Communities in Agricultural Soil Shifts with Crop Growth. Plos One, 10(7), Article e0134345. https://doi.org/10.1371/journal.pone.0134345

Hestrin, R., Lee, M. R., Whitaker, B. K., & Pett-Ridge, J. (2021). The Switchgrass Microbiome: A Review of Structure, Function, and Taxonomic Distribution. Phytobiomes Journal, 5(1), 14-28. https://doi.org/10.1094/pbiomes-04-20-0029-fi

Hoorman, J., Sundermeier, Islam, R., & Reeder, R. (2009). Using Cover Crops to Convert to No-till. Crops and Soils, 42, 9-13.

Hou, S., He, H., Zhang, W., Xie, H., & Zhang, X. (2009). Determination of soil amino acids by high performance liquid chromatography-electro spray ionization-mass spectrometry derivatized with 6-aminoquinolyl-N-hydroxysuccinimidyl carbamate. Talanta, 80(2), 440-447. https://doi.org/10.1016/j.talanta.2009.07.013

Howard Skinner, R., Zegada-Lizarazu, W., & Schmidt, J. P. (2012). Environmental Impacts of Switchgrass Management for Bioenergy Production. In A. Monti (Ed.), Switchgrass: A Valuable Biomass Crop for Energy (pp. 129-152). Springer London. https://doi.org/10.1007/978-1-4471-2903-5_6

Huse, S. M., Dethlefsen, L., Huber, J. A., Welch, D. M., Relman, D. A., & Sogin, M. L. (2008). Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag

Sequencing. Plos Genetics, 4(11), Article e1000255. https://doi.org/10.1371/journal.pgen.1000255

Ihrmark, K., Bodeker, I. T. M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., . . . Lindahl, B. D. (2012). New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. Fems Microbiology Ecology, 82(3), 666-677. https://doi.org/10.1111/j.1574-6941.2012.01437.x

Jach-Smith, L. C., & Jackson, R. D. (2018). N addition undermines N supplied by arbuscular mycorrhizal fungi to native perennial grasses. Soil Biology & Biochemistry, 116, 148-157. https://doi.org/10.1016/j.soilbio.2017.10.009

Jach-Smith, L. C., & Jackson, R. D. (2020). Inorganic N addition replaces N supplied to switchgrass (Panicum virgatum) by arbuscular mycorrhizal fungi. Ecological Applications, 30(2). https://doi.org/10.1002/eap.2047

Jesus, E. d. C., Liang, C., Quensen, J. F., Susilawati, E., Jackson, R. D., Balser, T. C., & Tiedje, J. M. (2016). Influence of corn, switchgrass, and prairie cropping systems on soil microbial communities in the upper Midwest of the United States. Global Change Biology Bioenergy, 8(2), 481-494. https://doi.org/10.1111/gcbb.12289

Ker, K., Seguin, P., Driscoll, B. T., Fyles, J. W., & Smith, D. L. (2012). Switchgrass establishment and seeding year production can be improved by inoculation with rhizosphere endophytes. Biomass & Bioenergy, 47, 295-301. https://doi.org/10.1016/j.biombioe.2012.09.031

Kleczewski, N. M., Bauer, J. T., Bever, J. D., Clay, K., & Reynolds, H. L. (2012). A survey of endophytic fungi of switchgrass (Panicum virgatum) in the Midwest, and their putative roles in plant growth. Fungal Ecology, 5(5), 521-529. https://doi.org/https://doi.org/10.1016/j.funeco.2011.12.006

Klindworth, A., Pruesse, E., Schweer, T., Peplies, J., Quast, C., Horn, M., & Gloeckner, F. O. (2013). Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Research, 41(1), Article e1. https://doi.org/10.1093/nar/gks808

Koljalg, U., Nilsson, R. H., Abarenkov, K., Tedersoo, L., Taylor, A. F. S., Bahram, M., . . . Larsson, K. H. (2013). Towards a unified paradigm for sequence-based identification of fungi. Molecular Ecology, 22(21), 5271-5277. https://doi.org/10.1111/mec.12481

Kozich, J. J., Westcott, S. L., Baxter, N. T., Highlander, S. K., & Schloss, P. D. (2013). Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. Appl Environ Microbiol, 79(17), 5112-5120. https://doi.org/10.1128/aem.01043-13

Langille, M. G. I., Zaneveld, J., Caporaso, J. G., McDonald, D., Knights, D., Reyes, J. A., . . . Huttenhower, C. (2013). Predictive functional profiling of microbial communities using

16S rRNA marker gene sequences. Nature Biotechnology, 31(9), 814-+. https://doi.org/10.1038/nbt.2676

Lea, P. J., Sodek, L., Parry, M. A. J., Shewry, R., & Halford, N. G. (2007). Asparagine in plants. Annals of Applied Biology, 150(1), 1-26. https://doi.org/10.1111/j.1744-7348.2006.00104.x

Ledgard, S. F., & Steele, K. W. (1992). BIOLOGICAL NITROGEN-FIXATION IN MIXED LEGUME GRASS PASTURES. Plant and Soil, 141(1-2), 137-153. https://doi.org/10.1007/bf00011314

Lesuffleur, F., Paynel, F., Bataille, M.-P., Le Deunff, E., & Cliquet, J.-B. (2007). Root amino acid exudation: measurement of high efflux rates of glycine and serine from six different plant species. Plant and Soil, 294(1-2), 235-246. https://doi.org/10.1007/s11104-007-9249-x

Li, A., Niu, K., & Du, G. (2011). Resource availability, species composition and sown density effects on productivity of experimental plant communities. Plant and Soil, 344(1), 177-186. https://doi.org/10.1007/s11104-011-0738-6

Li, X., Rui, J., Mao, Y., Yannarell, A., & Mackie, R. (2014). Dynamics of the bacterial community structure in the rhizosphere of a maize cultivar. Soil Biology & Biochemistry, 68, 392-401. https://doi.org/10.1016/j.soilbio.2013.10.017

Liebig, M. A., Schmer, M. R., Vogel, K. P., & Mitchell, R. B. (2008). Soil Carbon Storage by Switchgrass Grown for Bioenergy. BioEnergy Research, 1(3), 215-222. https://doi.org/10.1007/s12155-008-9019-5

Lodwig, E. M., Hosie, A. H. F., Bordes, A., Findlay, K., Allaway, D., Karunakaran, R., . . . Poole, P. S. (2003). Amino-acid cycling drives nitrogen fixation in the legume - Rhizobium symbiosis. Nature, 422(6933), 722-726. https://doi.org/10.1038/nature01527

Lopez-Bucio, J., Campos-Cuevas, J. C., Hernandez-Calderon, E., Velasquez-Becerra, C., Farias-Rodriguez, R., Macias-Rodriguez, L. I., & Valencia-Cantero, E. (2007). Bacillus megatenum rhizobacteria promote growth and alter root-system architecture through an auxin-and ethylene-independent signaling mechanism in Arabidopsis thaliana. Molecular Plant-Microbe Interactions, 20(2), 207-217. https://doi.org/10.1094/mpmi-20-2-0207

Lowman, S., Kim-Dura, S., Mei, C., & Nowak, J. (2016). Strategies for enhancement of switchgrass (Panicum virgatum L.) performance under limited nitrogen supply based on utilization of N-fixing bacterial endophytes. Plant and Soil, 405(1-2), 47-63. https://doi.org/10.1007/s11104-015-2640-0

Lowry, D. B., Behrman, K. D., Grabowski, P., Morris, G. P., Kiniry, J. R., & Juenger, T. E. (2014). Adaptations between Ecotypes and along Environmental Gradients in Panicum virgatum. The American Naturalist, 183(5), 682-692. https://doi.org/10.1086/675760

Lozupone, C., Lladser, M. E., Knights, D., Stombaugh, J., & Knight, R. (2011). UniFrac: an effective distance metric for microbial community comparison. Isme Journal, 5(2), 169-172. https://doi.org/10.1038/ismej.2010.133

Lozupone, C. A., Hamady, M., Kelley, S. T., & Knight, R. (2007). Quantitative and qualitative beta diversity measures lead to different insights into factors that structure microbial communities. Applied and Environmental Microbiology, 73(5), 1576-1585. https://doi.org/10.1128/aem.01996-06

Malmberg, C., & Smith, H. (1982). Relationship between Plant Weight and Density in Mixed Populations of Medicago Sativa and Trifolium Pratense. Oikos, 38(3), 365-368. https://doi.org/10.2307/3544678

Mao, Y., Li, X., Smyth, E. M., Yannarell, A. C., & Mackie, R. I. (2014). Enrichment of specific bacterial and eukaryotic microbes in the rhizosphere of switchgrass (Panicum virgatum L.) through root exudates. Environ Microbiol Rep, 6(3), 293-306. https://doi.org/10.1111/1758-2229.12152

Mao, Y., Yannarell, A. C., Davis, S. C., & Mackie, R. I. (2013). Impact of different bioenergy crops on N-cycling bacterial and archaeal communities in soil. Environmental Microbiology, 15(3), 928-942. https://doi.org/10.1111/j.1462-2920.2012.02844.x

Mao, Y., Yannarell, A. C., & Mackie, R. I. (2011). Changes in N-Transforming Archaea and Bacteria in Soil during the Establishment of Bioenergy Crops. Plos One, 6(9), Article e24750. https://doi.org/10.1371/journal.pone.0024750

Maposse, I. C., D. I. Bransby, S. E. Sladden, and D. D. Kee. 1995. Biomass yields from eight switchgrass varieties in Alabama. p. 138. In Agronomy Abstracts. ASA, Madison, Wis

Marquard, E., Weigelt, A., Roscher, C., Gubsch, M., Lipowsky, A., & Schmid, B. (2009). Positive biodiversity–productivity relationship due to increased plant density [https://doi.org/10.1111/j.1365-2745.2009.01521.x]. Journal of Ecology, 97(4), 696-704. https://doi.org/https://doi.org/10.1111/j.1365-2745.2009.01521.x

Masella, A. P., Bartram, A. K., Truszkowski, J. M., Brown, D. G., & Neufeld, J. D. (2012). PANDAseq: PAired-eND Assembler for Illumina sequences. Bmc Bioinformatics, 13, Article 31. https://doi.org/10.1186/1471-2105-13-31

McDonald, D., Price, M. N., Goodrich, J., Nawrocki, E. P., DeSantis, T. Z., Probst, A., . . . Hugenholtz, P. (2012). An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. Isme Journal, 6(3), 610-618. https://doi.org/10.1038/ismej.2011.139

Mendes, R., Garbeva, P., & Raaijmakers, J. M. (2013). The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms. FEMS Microbiol Rev, 37(5), 634-663. https://doi.org/10.1111/1574-6976.12028

Mehlich, A. (1984). Mehlich 3 soil test extractant: A modification of Mehlich 2 extractant. Communications in Soil Science and Plant Analysis, 15(12), 1409-1416. https://doi.org/10.1080/00103628409367568

Miller, H. J., Henken, G., & Vanveen, J. A. (1989). VARIATION AND COMPOSITION OF BACTERIAL-POPULATIONS IN THE RHIZOSPHERES OF MAIZE, WHEAT, AND GRASS CULTIVARS. Canadian Journal of Microbiology, 35(6), 656-660. https://doi.org/10.1139/m89-106

Mitchell, M. J., Burke, M. K., & Shepard, J. P. (1992). Seasonal and spatial patterns of S, Ca, and N dynamics of a Northern Hardwood forest ecosystem. Biogeochemistry, 17(3), 165-189. https://doi.org/10.1007/BF00004040

Mitchell, R., Vogel, K. P., & Sarath, G. (2008). Managing and enhancing switchgrass as a bioenergy feedstock [https://doi.org/10.1002/bbb.106]. Biofuels, Bioproducts and Biorefining, 2(6), 530-539. https://doi.org/https://doi.org/10.1002/bbb.106

Oates, L. G., Duncan, D. S., Gelfand, I., Millar, N., Robertson, G. P., & Jackson, R. D. (2016). Nitrous oxide emissions during establishment of eight alternative cellulosic bioenergy cropping systems in the North Central United States [https://doi.org/10.1111/gcbb.12268]. GCB Bioenergy, 8(3), 539-549. https://doi.org/https://doi.org/10.1111/gcbb.12268

Oksanen, J. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner (2020). vegan: Community Ecology Package. R package version 2.5-7. https://CRAN.R-project.org/package=vegan

Quaye, A. K., Volk, T. A., & Schoenau, J. J. (2015). Seasonal Dynamics of N, P, and K in an Organic and Inorganic Fertilized Willow Biomass System. Applied and Environmental Soil Science, 2015, 471248. https://doi.org/10.1155/2015/471248

Revillini, D., Wilson, G. W. T., Miller, R. M., Lancione, R., & Johnson, N. C. (2019). Plant Diversity and Fertilizer Management Shape the Belowground Microbiome of Native Grass Bioenergy Feedstocks [10.3389/fpls.2019.01018]. Frontiers in Plant Science, 10, 1018.

Rodrigues, R. R., Moon, J., Zhao, B., & Williams, M. A. (2017). Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. Global Change Biology Bioenergy, 9(6), 1057-1070. https://doi.org/10.1111/gcbb.12396

Rognes, T., Flouri, T., Nichols, B., Quince, C., & Mahé, F. (2016). VSEARCH: a versatile open source tool for metagenomics. PeerJ, 4, e2584. https://doi.org/10.7717/peerj.2584

Roley, S. S., Xue, C., Hamilton, S. K., Tiedje, J. M., & Robertson, G. P. (2019). Isotopic evidence for episodic nitrogen fixation in switchgrass (Panicum virgatum L.). Soil

Biology and Biochemistry, 129, 90-98. https://doi.org/https://doi.org/10.1016/j.soilbio.2018.11.006

Sanderson, M. A., Reed, R. L., Ocumpaugh, W. R., Hussey, M. A., Van Esbroeck, G., Read, J. C., . . . Hons, F. M. (1999). Switchgrass cultivars and germplasm for biomass feedstock production in Texas. Bioresource Technology, 67(3), 209-219. https://doi.org/https://doi.org/10.1016/S0960-8524(98)00132-1

Sawyer, A., Staley, C., Lamb, J., Sheaffer, C., Kaiser, T., Gutknecht, J., . . . Rosen, C. (2019). Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. Applied Microbiology and Biotechnology, 103(4), 1973-1987. https://doi.org/10.1007/s00253-018-9535-y

Schimel, J., & Bennett, J. (2004). Nitrogen mineralization: Challenges of a changing paradigm [Review]. Ecology, 85(3), 591-602. https://doi.org/10.1890/03-8002

Schloss Patrick, D., Westcott Sarah, L., Ryabin, T., Hall Justine, R., Hartmann, M., Hollister Emily, B., . . . Weber Carolyn, F. (2009). Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 75(23), 7537-7541. https://doi.org/10.1128/AEM.01541-09

Singer, E., Bonnette, J., Kenaley, S. C., Woyke, T., & Juenger, T. E. (2019). Plant compartment and genetic variation drive microbiome composition in switchgrass roots [https://doi.org/10.1111/1758-2229.12727]. Environmental Microbiology Reports, 11(2), 185-195. https://doi.org/https://doi.org/10.1111/1758-2229.12727

Stachová, T., Fibich, P., & Lepš, J. (2013). Plant density affects measures of biodiversity effects. Journal of Plant Ecology, 6(1), 1-11. https://doi.org/10.1093/jpe/rts015

USDA-NRCS. Release brochure for ‘Kanlow’ switchgrass (Panicum virgatum) (2011). Manhattan (KS): USDA-Natural Resources Conservation Service, Manhattan PMC.

USDA-NRCS. Released brochure for “Alamo” switchgrass (Panicum virgatum) (2012). James E.”Bud” Smith Plant Materials Center. Knox City, TX 79529.

U.S. Department of Energy. (2011). U.S. Billion-Ton Update: Biomass Supply for a Bioenergy and Bioproducts Industry. R.D. Perlack and B.J. Stokes (Leads), ORNL/TM-2011/224. Oak Ridge National Laboratory, Oak Ridge, TN. 227p.

Vacher, C., Hampe, A., Porté, A. J., Sauer, U., Compant, S., & Morris, C. E. (2016). The Phyllosphere: Microbial Jungle at the Plant–Climate Interface. Annual Review of Ecology, Evolution, and Systematics, 47(1), 1-24. https://doi.org/10.1146/annurev-ecolsys-121415-032238

Vogel, K. P., Brejda, J. J., Walters, D. T., & Buxton, D. R. (2002). Switchgrass biomass production in the Midwest USA: Harvest and nitrogen management. Agronomy Journal, 94(3), 413-420. https://doi.org/10.2134/agronj2002.0413

Wang, B., Seiler, J. R., & Mei, C. (2016). A microbial endophyte enhanced growth of switchgrass under two drought cycles improving leaf level physiology and leaf development. Environmental and Experimental Botany, 122, 100-108. https://doi.org/10.1016/j.envexpbot.2015.09.004

Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Applied and Environmental Microbiology, 73(16), 5261-5267. https://doi.org/10.1128/aem.00062-07

Werling, B. P., Dickson, T. L., Isaacs, R., Gaines, H., Gratton, C., Gross, K. L., . . . Landis, D. A. (2014). Perennial grasslands enhance biodiversity and multiple ecosystem services in bioenergy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 111(4), 1652-1657. https://doi.org/10.1073/pnas.1309492111

Whitaker, B. K., Reynolds, H. L., & Clay, K. (2018). Foliar fungal endophyte communities are structured by environment but not host ecotype in Panicum virgatum (switchgrass). Ecology, 99(12), 2703-2711. https://doi.org/10.1002/ecy.2543

White, T., Bruns, T., Lee, S., Taylor, J., Innis, M., Gelfand, D., & Sninsky, J. (1990). Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In (Vol. 31, pp. 315-322).

Wright, L., & Turhollow, A. (2010). Switchgrass selection as a “model” bioenergy crop: A history of the process. Biomass and Bioenergy, 34(6), 851-868. https://doi.org/https://doi.org/10.1016/j.biombioe.2010.01.030

Yilmaz, P., Parfrey, L. W., Yarza, P., Gerken, J., Pruesse, E., Quast, C., . . . Glöckner, F. O. (2014). The SILVA and “All-species Living Tree Project (LTP)” taxonomic frameworks. Nucleic Acids Research, 42(D1), D643-D648. https://doi.org/10.1093/nar/gkt1209

Zalapa, J. E., Price, D. L., Kaeppler, S. M., Tobias, C. M., Okada, M., & Casler, M. D. (2011). Hierarchical classification of switchgrass genotypes using SSR and chloroplast sequences: ecotypes, ploidies, gene pools, and cultivars. Theoretical and Applied Genetics, 122(4), 805-817. https://doi.org/10.1007/s00122-010-1488-1

Zhang, Y., Zalapa, J. E., Jakubowski, A. R., Price, D. L., Acharya, A., Wei, Y., . . . Casler, M. D. (2011). Post-glacial evolution of Panicum virgatum: centers of diversity and gene pools revealed by SSR markers and cpDNA sequences. Genetica, 139(7), 933-948. https://doi.org/10.1007/s10709-011-9597-6

Žifčáková, L., Vetrovsky, T., Howe, A., & Baldrian, P. (2016). Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter [Article]. Environmental Microbiology, 18(1), 288-301. https://doi.org/10.1111/1462-2920.13026

Tables and figures

Figure 3.1.

Experimental Design of Panicum virgatum Plot Located in Alcorn State University Biological Station

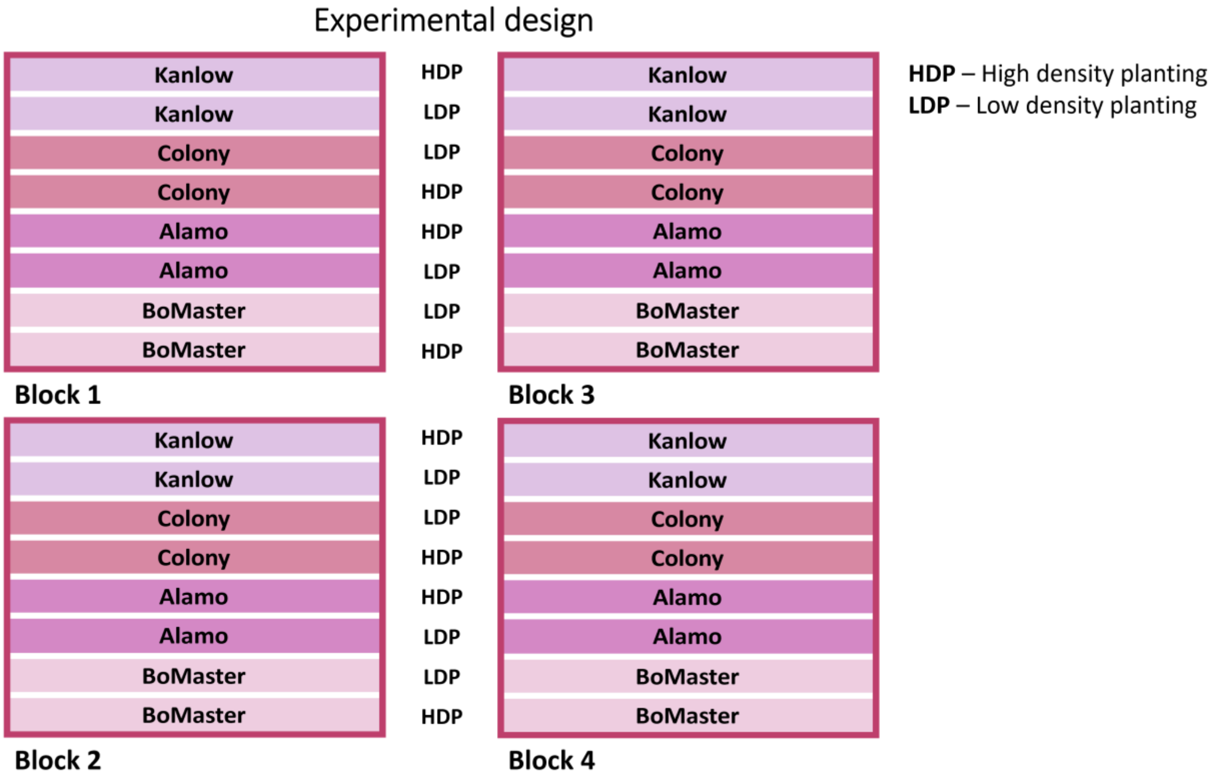


Table 3.1.

Soil Chemistry Table.

Soil Superscripts after each soil chemistry variable (Y) indicate mixed effects tests for a model Y =“Variety” (V) + “Density[Variety]” (D[V]) wherein “Density” is nested within variety. Degrees of freedom for Mixed effect ANOVA fixed terms are 3 for “Variety” and 4 for “Density[Variety]” numerator with 21 degrees of freedom for denominator. “Block” was included as a random effect in these model. Caps are pairwise differences based on Students t-tests, lower-case letters are “slice effects” testing planting density difference within the variety. NO_3^- is often below detection level and questionable. This is true particularly in the beginning of the growing season. ns = P ≥ 0.05; * = 0.05 > P ≥ 0.01; ** = 0.01 > P ≥ 0.001; *** = 0.001 > P

	ALAMO		**BOMASTER**		**COLONY**		**KANLOW**	
	HDP	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**
WEEK 1								
pH $^{V(**)\ D[V](ns)}$	*5.98±0.10*$^{AB\ a}$	*6.03±0.05*$^{AB\ a}$	*5.93±0.05*$^{A\ a}$	*5.93±0.05*$^{A\ a}$	*6.03±0.15*$^{BC\ a}$	*6.18±0.17B*$^{BC\ a}$	*6.08±0.05*$^{C\ a}$	*6.18±0.19*$^{C\ a}$
NH_4-N (PPM) $_{V(NS)\ D[V](NS)}$	5.38±0.71$^{A\ a}$	5.5±0.62$^{A\ a}$	5.28±0.51$^{A\ a}$	5.75±0.19$^{A\ a}$	6.28±2.66$^{A\ a}$	5.63±1.13$^{A\ a}$	5.68±0.6$^{A\ a}$	5.45±1.44$^{A\ a}$
NO_3-N (ppm) $^{V(ns)}$ $_{D[V](ns)}$	1.75±1.50$^{A\ a}$	1.50±1.00$^{A\ a}$	2.0±1.15$^{A\ a}$	1.25±0.5$^{A\ a}$	1.25±0.50$^{A\ a}$	1.75±0.96$^{A\ a}$	5.25±5.32$^{A\ a}$	1.75±0.96$^{A\ a}$
TOTAL N % $^{V(NS)}$ $_{D[V](NS)}$	0.12±0.01$^{A\ a}$	0.13±0.0$^{A\ a}$ 1	0.13±0.01$^{A\ a}$	0.13±0.01$^{A\ a}$	0.13±0.02$^{A\ a}$	0.12±0.02$^{A\ a}$	0.14±0.01$^{A\ a}$	0.13±0.01$^{A\ a}$
Total C % $^{V(ns)}$ $_{D[V](*)}$	*0.90±0.03*$^{A\ a}$	*0.83±0.05*$^{A\ a}$	*0.85±0.10*$^{A\ a}$	*0.79±0.04*$^{A\ a}$	*0.82±0.04*$^{A\ a}$	*0.78±0.07*$^{A\ a}$	*0.94±0.13*$^{A\ b}$	*0.76±0.06*$^{A\ a}$
TOTAL C:N $^{V(NS)}$ $_{D[V](NS)}$	7.37±0.52$^{A\ a}$	6.72±1.03$^{A\ a}$	6.69±0.76$^{A\ a}$	6.35±0.69$^{A\ a}$	6.64±0.94$^{A\ a}$	6.89±1$^{A\ a}$	6.83±0.95$^{A\ a}$	5.84±0.52$^{A\ a}$

OM (%)$^{V(ns)}$ **D[V](ns)**	2.00±0.08$^{A\ a}$	1.93±0.1$^{A\ a}$	1.95±0.24$^{A\ a}$	1.85±0.06$^{A\ a}$	1.98±0.10$^{A\ a}$	1.85±0.21$^{A\ a}$	2.1±0.29$^{A\ a}$	1.83±0.36$^{A\ a}$
P (PPM)$^{V(NS)}$ **D[V](NS)**	28.8±4.27$^{A\ a}$	31.0±6.06$^{A\ a}$	34.25±4.43$^{A\ a}$	30±2.94$^{A\ a}$	29.0±5.48$^{A\ a}$	26.75±2.99$^{A\ a}$	31.75±3.59$^{A\ a}$	27.25±2.63$^{A\ a}$
K (ppm)$^{V(*)\ D[V](*)}$	*110.0±32.54*$^{C\ a}$	*97.5±17.41*$^{C\ a}$	*151.5±28.45*$^{A\ b}$	*111.25±13.5*$^{A\ a}$	*104.0±14.72*$^{BC\ a}$	*107±15.58*$^{BC\ a}$	*149.75±29.03*$^{AB\ b}$	*108±25.6*$^{AB\ a}$
CA (PPM)$^{V(NS)}$ **D[V](NS)**	776.5±57.41$^{A\ a}$	795.25±66.68$^{A\ a}$	755±66.44$^{A\ a}$	768±51.63$^{A\ a}$	754±50.73$^{A\ a}$	719.25±36.01$^{A\ a}$	761±38.03$^{A\ a}$	737.75±35.08$^{A\ a}$
Mg (ppm)$^{V(*)}$ **D[V](ns)**	*130.75±13.23*$^{A\ a}$	*128.5±11.9*$^{A\ a}$	*129±8.72*$^{AB\ a}$	*120.75±6.85*$^{AB\ a}$	*116.75±4.57*$^{B\ a}$	*118±10.23*$^{B\ a}$	*123±2.94*$^{B\ a}$	*112.25±11.81*$^{B\ a}$
cec (meq:100g) **V(*) D[V](ns)**	*6.25±0.50*$^{B\ a}$	*6.23±0.51*$^{B\ a}$	*6.28±0.34*$^{B\ a}$	*6.15±0.35*$^{B\ a}$	*5.90±0.29*$^{A\ a}$	*5.55±0.17*$^{A\ a}$	*6.08±0.30*$^{A\ a}$	*5.6±0.29*$^{A\ a}$
K (%sat)$^{V(*)}$ **D[V](ns)**	*4.48±1.04*$^{A\ a}$	*4.05±0.72*$^{A\ a}$	*6.23±1.43*$^{B\ a}$	*4.65±0.65*$^{B\ a}$	*4.53±0.74*$^{AB\ a}$	*4.95±0.79*$^{AB\ a}$	*6.33±1.10*$^{B\ a}$	*4.9±0.93*$^{B\ a}$
CA (%SAT)$^{V(*)}$ **D[V](NS)**	*62.15±0.6*$^{AB\ a}$	*63.88±0.68*$^{AB\ a}$	*60.1±2.48*$^{A\ a}$	*62.43±1.3*$^{A\ a}$	*63.93±3.33*$^{B\ a}$	*64.78±1.38*$^{B\ a}$	*62.68±1.74*$^{B\ a}$	*65.93±3.01*$^{B\ a}$
Mg (%sat)$^{V(ns)}$ **D[V](ns)**	17.43±0.52$^{A\ a}$	17.23±0.56$^{A\ a}$	17.13±0.54$^{A\ a}$	16.38±1.19$^{A\ a}$	16.53±1.01$^{A\ a}$	17.75±1.81$^{A\ a}$	16.88±0.74$^{A\ a}$	16.68±1.25$^{A\ a}$
H (%SAT)$^{V(**)}$ **D[V](NS)**	*15.63±1.27*$^{BC\ a}$	*14.85±0.54*$^{BC\ a}$	*16.35±0.52*$^{C\ a}$	*16.65±0.91*$^{C\ a}$	*15.2±2.53*$^{AB\ a}$	*12.6±2.43*$^{AB\ a}$	*14.35±0.97*$^{A\ a}$	*12.5±2.42*$^{A\ a}$
K:Mg$^{V(**)\ D[V](*)}$	*0.26±0.06*$^{A\ a}$	*0.24±0.04*$^{A\ a}$	*0.37±0.08*$^{BC\ b}$	*0.28±0.02*$^{BC\ a}$	*0.28±0.03*$^{AB\ a}$	*0.28±0.02*$^{AB\ a}$	*0.38±0.07*$^{C\ b}$	*0.30±0.04*$^{C\ a}$
CA:MG$^{V(NS)}$ **D[V](NS)**	3.57±0.12$^{A\ a}$	3.71±0.14$^{A\ a}$	3.52±0.23$^{A\ a}$	3.83±0.35$^{A\ a}$	3.88±0.37$^{A\ a}$	3.68±0.39$^{A\ a}$	3.72±0.19$^{A\ a}$	3.97±0.40$^{A\ a}$

WEEK 2								
pH $^{V(ns)\ D[V](ns)}$	6.05±0.06 $^{A\ a}$	6.03±0.1 $^{A\ a}$	6.03±0.26 $^{A\ a}$	6.05±0.13 $^{A\ a}$	6.03±0.1 $^{A\ a}$	6.03±0.05 $^{A\ a}$	5.98±0.15 $^{A\ a}$	5.9±0.20 $^{A\ a}$
NH_4-N (PPM) **V(NS) D[V](NS)**	6±1.37 $^{A\ a}$	6.08±2.31 $^{A\ a}$	7.2±0.27 $^{A\ a}$	6.83±3.66 $^{A\ a}$	5.75±0.99 $^{A\ a}$	6.05±1.85 $^{A\ a}$	6.1±0.87 $^{A\ a}$	7.48±2.29 $^{A\ a}$
NO_3-N (ppm) $^{V(ns)}$ **D[V](ns)**	2.25±1.5 $^{A\ a}$	1.5±0.58 $^{A\ a}$	2.25±1.5 $^{A\ a}$	2.75±1.71 $^{A\ a}$	1.75±0.96 $^{A\ a}$	1.75±0.5 $^{A\ a}$	1.75±0.5 $^{A\ a}$	4.5±4.51 $^{A\ a}$
TOTAL N % $^{V(NS)}$ **D[V](NS)**	0.12±0.01 $^{A\ a}$	0.12±0.01 $^{A\ a}$	0.15±0.03 $^{A\ a}$	0.12±0.01 $^{A\ a}$	0.12±0.01 $^{A\ a}$	0.13±0.01 $^{A\ a}$	0.12±0.01 $^{A\ a}$	0.11±0.02 $^{A\ a}$
Total C % $^{V(ns)}$ **D[V](ns)**	*0.92±0.08* $^{A\ a}$	*0.95±0.16* $^{A\ a}$	*1.17±0.23* $^{A\ a}$	*1.04±0.12* $^{A\ a}$	*0.91±0.1* $^{A\ a}$	*1.01±0.17* $^{A\ a}$	*0.86±0.15* $^{A\ a}$	*0.86±0.08* $^{A\ a}$
TOTAL C:N $^{V(NS)}$ **D[V](NS)**	7.7±0.46 $^{A\ a}$	7.71±0.7 $^{A\ a}$	7.99±1.52 $^{A\ a}$	8.45±0.66 $^{A\ a}$	7.58±0.69 $^{A\ a}$	8.07±1 $^{A\ a}$	7.47±0.55 $^{A\ a}$	7.64±0.42 $^{A\ a}$
OM (%) $^{V(ns)}$ **D[V](ns)**	2.08±0.1 $^{A\ a}$	2.05±0.24 $^{A\ a}$	2.3±0.45 $^{A\ a}$	2.18±0.33 $^{A\ a}$	1.93±0.25 $^{A\ a}$	2±0.22 $^{A\ a}$	2±0.16 $^{A\ a}$	1.95±0.19 $^{A\ a}$
P (PPM) $^{V(NS)}$ **D[V](NS)**	31.75±6.08 $^{A\ a}$	26.25±5.85 $^{A\ a}$	36.25±9.6 $^{A\ a}$	37.75±8.54 $^{A\ a}$	35.5±9.88 $^{A\ a}$	32.75±5.25 $^{A\ a}$	30.5±5.26 $^{A\ a}$	31±6 $^{A\ a}$
K (ppm) $^{V(ns)}$ **D[V](ns)**	132.25±17.23 $^{A\ a}$	110.5±17.71 $^{A\ a}$	185.75±53.5 $^{A\ a}$	187±72.76 $^{A\ a}$	154.25±66.3 $^{A\ a}$	138.75±39.36 $^{A\ a}$	170.5±46.15 $^{A\ a}$	134.75±36.22 $^{A\ a}$
CA (PPM) $^{V(*)}$ **D[V](NS)**	*729.5±78.73* $^{AB\ a}$	*775.5±42.91* $^{AB\ a}$	*744.75±72.3* $^{AB\ a}$	*796.75±65.9* $^{AB\ a}$	*795.5±58.41* $^{B\ a}$	*786.5±73.87* $^{B\ a}$	*679.75±161.2* $^{A\ a}$	*676.75±151.1* $^{A\ a}$
Mg (ppm) $^{V(ns)}$ **D[V](ns)**	126.75±3.4 $^{A\ a}$	129.25±13.4 $^{A\ a}$	124.25±16.5 $^{A\ a}$	130.25±19.9 $^{A\ a}$	127.5±32.31 $^{A\ a}$	135.5±13.77 $^{A\ a}$	112.75±19.77 $^{A\ a}$	123.75±22.91 $^{A\ a}$

cec(meq:100g) **V(ns) D[V](ns)**	5.93±0.44 $^{A a}$	6.15±0.44 $^{A a}$	6.18±0.66 $^{A a}$	6.48±0.53 $^{A a}$	6.38±0.79 $^{A a}$	6.33±0.51 $^{A a}$	5.7±1.15 $^{A a}$	5.75±1.33 $^{A a}$
K (%sat) $^{V(ns)}$ **D[V](ns)**	5.75±1.01 $^{A a}$	4.6±0.55 $^{A a}$	7.68±1.85 $^{A a}$	7.3±2.28 $^{A a}$	6.05±2.12 $^{A a}$	5.58±1.34 $^{A a}$	7.83±2.53 $^{A a}$	6.38±2.59 $^{A a}$
CA (%SAT) $^{V(NS)}$ **D[V](NS)**	61.45±2.31 $^{A a}$	63.15±2.11 $^{A a}$	60.53±5.27 $^{A a}$	61.58±3.41 $^{A a}$	62.78±4.75 $^{A a}$	62.15±2.36 $^{A a}$	59.28±4.1 $^{A a}$	59.05±4.78 $^{A a}$
Mg(%sat) $^{V(ns)}$ **D[V](ns)**	17.88±1.43 $^{A a}$	17.5±0.7 $^{A a}$	16.8±1.34 $^{A a}$	16.7±1.28 $^{A a}$	16.45±2.17 $^{A a}$	17.9±1.45 $^{A a}$	16.83±3.67 $^{A a}$	18.20±2.87 $^{A a}$
H(%SAT) $^{V(NS)}$ **D[V](NS)**	14.73±0.59 $^{A a}$	15.03±1.46 $^{A a}$	14.8±4.02 $^{A a}$	14.38±1.76 $^{A a}$	14.93±1.27 $^{A a}$	14.65±0.81 $^{A a}$	16.03±2.54 $^{A a}$	16.63±4.52 $^{A a}$
K:Mg $^{V(**)\ D[V](ns)}$	*0.32±0.03* $^{A a}$	*0.26±0.03* $^{A a}$	*0.45±0.1* $^{B a}$	*0.43±0.1* $^{B a}$	*0.36±0.09* $^{AB a}$	*0.31±0.08* $^{AB a}$	*0.46±0.07* $^{AB a}$	*0.35±0.10* $^{AB a}$
CA:MG $^{V(NS)}$ **D[V](NS)**	3.46±0.40 $^{A a}$	3.62±0.21 $^{A a}$	3.63±0.47 $^{A a}$	3.71±0.45 $^{A a}$	3.90±0.81 $^{A a}$	3.5±0.41 $^{A a}$	3.67±0.88 $^{A a}$	3.32±0.68 $^{A a}$
WEEK 4								
pH $^{V(ns)\ D[V](ns)}$	5.95±0.1 $^{A a}$	6.03±0.17 $^{A a}$	5.98±0.15 $^{A a}$	6±0.08 $^{A a}$	5.98±0.1 $^{A a}$	6.13±0.13 $^{A a}$	6.18±0.17 $^{A a}$	6.15±0.26 $^{A a}$
NH_4-N (PPM) **V(NS) D[V](NS)**	7.4±0.9 $^{A a}$	6.45±1.22 $^{A a}$	8.6±3.24 $^{A a}$	7.55±1.37 $^{A a}$	8.33±2.34 $^{A a}$	6.98±0.6 $^{A a}$	7.4±1.66 $^{A a}$	7.3±1.36 $^{A a}$
NO_3-N (ppm) $^{V(ns)}$ **D[V](ns)**	1±0 $^{A a}$	1.25±0.5 $^{A a}$	1±0 $^{A a}$	1.75±0.96 $^{A a}$	1.5±1 $^{A a}$	1.5±0.58 $^{A a}$	1±0 $^{A a}$	1±0 $^{A a}$
TOTAL N % $^{V(NS)}$ **D[V](NS)**	0.13±0.01 $^{A a}$	0.12±0.02 $^{A a}$	0.12±0.02 $^{A a}$	0.14±0.01 $^{A a}$	0.12±0.01 $^{A a}$	0.13±0.01 $^{A a}$	0.12±0.01 $^{A a}$	0.12±0.01 $^{A a}$

Total C % $^{V(ns)}$ **D[V](ns)**	0.99±0.08 $^{A\,a}$	1.01±0.17 $^{A\,a}$	0.91±0.27 $^{A\,a}$	0.97±0.09 $^{A\,a}$	1.02±0.14 $^{A\,a}$	0.97±0.13 $^{A\,a}$	0.96±0.05 $^{A\,a}$	0.89±0.12 $^{A\,a}$
TOTAL C:N $^{V(NS)}$ **D[V](NS)**	7.8±0.56 $^{A\,a}$	8.19±0.62 $^{A\,a}$	7.33±1.06 $^{A\,a}$	7.17±0.37 $^{A\,a}$	8.46±0.53 $^{A\,a}$	7.57±0.79 $^{A\,a}$	8.02±0.99 $^{A\,a}$	7.31±1.01 $^{A\,a}$
OM (%) $^{V(ns)}$ **D[V](ns)**	2.15±0.1 $^{A\,a}$	2.1±0.35 $^{A\,a}$	2±0.41 $^{A\,a}$	2.13±0.13 $^{A\,a}$	2.15±0.31 $^{A\,a}$	2.1±0.18 $^{A\,a}$	2±0.08 $^{A\,a}$	1.98±0.24 $^{A\,a}$
P (PPM) $^{V(NS)}$ **D[V](NS)**	28.75±2.75 $^{A\,a}$	30.75±3.59 $^{A\,a}$	31.25±3.86 ^{A} a	30±2.71 $^{A\,a}$	28.25±4.57 $^{A\,a}$	31.5±8.35 $^{A\,a}$	33.25±6.29 $^{A\,a}$	30.75±7.27 $^{A\,a}$
K (ppm) $^{V(ns)}$ **D[V](ns)**	111.5±22.58 $^{A\,a}$	133.75±27.15 ^{A} a	103.75±11 $^{A\,a}$	113.5±32.01 A a	119.25±45.7 ^{A} a	154.5±28.57 ^{A} a	129.75±35.31 A a	133.25±33.84 A a
CA (PPM) $^{V(NS)}$ **D[V](NS)**	876.75±101.63 A a	819.25±80.23 ^{A} a	811.25±63.2 A a	847±65.25 $^{A\,a}$	813.75±49.6 ^{A} a	808.75±43.5 ^{A} a	839.5±55.87 ^{A} a	819.5±67.2 $^{A\,a}$
Mg (ppm) $^{V(ns)}$ **D[V](ns)**	137±27.81 $^{A\,a}$	135.5±16.34 $^{A\,a}$	124±12.62 $^{A\,a}$	138.25±13.7 A a	125.5±16.9 $^{A\,a}$	145.5±19.21 ^{A} a	105.75±63.7 ^{A} a	125.5±13.48 ^{A} a
cec(meq:100g) **V(ns) D[V](ns)**	6.93±0.76 $^{A\,a}$	6.58±0.48 $^{A\,a}$	4.9±3.15 $^{A\,a}$	6.7±0.43 $^{A\,a}$	6.43±0.44 $^{A\,a}$	6.58±0.25 $^{A\,a}$	6.45±0.29 $^{A\,a}$	6.3±0.24 $^{A\,a}$
K (%sat) $^{V(ns)}$ **D[V](ns)**	4.15±0.94 $^{A\,a}$	5.18±0.84 $^{A\,a}$	4.15±0.24 $^{A\,a}$	4.4±1.39 $^{A\,a}$	4.75±1.69 $^{A\,a}$	6.05±1.33 $^{A\,a}$	5.25±1.43 $^{A\,a}$	5.4±1.41 $^{A\,a}$
CA (%SAT) $^{V(NS)}$ **D[V](NS)**	63.28±1.14 $^{A\,a}$	62.25±1.82 $^{A\,a}$	63.35±2.53 ^{A} a	63.18±1.3 $^{A\,a}$	63.38±1.66 $^{A\,a}$	61.45±1.07 $^{A\,a}$	65.18±5.1 $^{A\,a}$	65.1±5.46 $^{A\,a}$
Mg(%sat) $^{V(ns)}$ **D[V](ns)**	16.4±2.2 $^{A\,a}$	17.15±1.2 $^{A\,a}$	16.15±1.57 ^{A} a	17.15±0.65 ^{A} a	16.25±1.42 $^{A\,a}$	18.48±2.68 $^{A\,a}$	16.85±1.32 $^{A\,a}$	16.6±1.64 $^{A\,a}$
H(%SAT) $^{V(*)}$ **D[V](NS)**	*16±2.27* $^{A\,a}$	*15.33±2.91* $^{A\,a}$	*16.08±2.36* ^{A} *a*	*15.3±0.84* $^{A\,a}$	*15.58±0.97* $^{A\,a}$	*13.65±1.85* $^{A\,a}$	*12.38±2.53* $^{A\,a}$	*13.08±3.64* $^{A\,a}$
K:Mg $^{V(ns)\ D[V](ns)}$	0.26±0.1 $^{A\,a}$	0.3±0.03 $^{A\,a}$	0.26±0.02 $^{A\,a}$	0.26±0.09 $^{A\,a}$	0.3±0.12 $^{A\,a}$	0.33±0.09 $^{A\,a}$	0.31±0.07 $^{A\,a}$	0.33±0.08 $^{A\,a}$

CA:MG $^{V(NS)}$ **D[V](NS)**	3.91±0.53 $^{A a}$	3.64±0.23 $^{A a}$	3.96±0.45 $^{A a}$	3.69±0.09 $^{A a}$	3.92±0.35 $^{A a}$	3.39±0.53 $^{A a}$	3.9±0.59 $^{A a}$	3.97±0.65 $^{A a}$
WEEK 8								
pH $^{V(ns)\ D[V](ns)}$	6.00±0.14 $^{A a}$	5.9±0.24 $^{A a}$	5.88±0.1 $^{A a}$	5.9±0.14 $^{A a}$	5.83±0.05 $^{A a}$	6.03±0.1 $^{A a}$	6.05±0.13 $^{A a}$	6.03±0.15 $^{A a}$
NH_4-N (PPM) **V(NS) D[V](NS)**	9.15±4.86 $^{A a}$	6.53±1.1 $^{A a}$	7.65±1.64 $^{A a}$	8.35±2.59 $^{A a}$	7.43±0.94 $^{A a}$	6.93±0.64 $^{A a}$	9.73±4.16 $^{A a}$	7.28±0.53 $^{A a}$
NO_3-N (ppm) $^{V(ns)}$ **D[V](ns)**	1.25±0.5 $^{A a}$	1±0 $^{A a}$	1±0 $^{A a}$	1.25±0.5 $^{A a}$	1±0 $^{A a}$	1±0 $^{A a}$	1.5±1 $^{A a}$	1±0 $^{A a}$
TOTAL N % $^{V(NS)}$ **D[V](NS)**	0.13±0.02 $^{A a}$	0.12±0.02 $^{A a}$	0.13±0.01 $^{A a}$	0.13±0.03 $^{A a}$	0.12±0.02 $^{A a}$	0.12±0.01 $^{A a}$	0.13±0.02 $^{A a}$	0.11±0 $^{A a}$
Total C % $^{V(ns)}$ **D[V](ns)**	1.14±0.36 $^{A a}$	0.96±0.12 $^{A a}$	0.95±0.13 $^{A a}$	1.17±0.46 $^{A a}$	0.95±0.18 $^{A a}$	0.89±0.15 $^{A a}$	1.02±0.19 $^{A a}$	0.84±0.12 $^{A a}$
TOTAL C:N $^{V(NS)}$ **D[V](NS)**	8.47±1.38 $^{A a}$	8.01±0.39 $^{A a}$	7.4±0.91 $^{A a}$	8.72±1.65 $^{A a}$	7.85±0.34 $^{A a}$	7.34±0.43 $^{A a}$	7.84±0.88 $^{A a}$	7.47±0.77 $^{A a}$
OM (%) $^{V(ns)}$ **D[V](ns)**	2.28±0.77 $^{A a}$	1.68±0.53 $^{A a}$	2±0.26 $^{A a}$	2.28±0.61 $^{A a}$	2.03±0.39 $^{A a}$	1.85±0.06 $^{A a}$	2±0.29 $^{A a}$	1.75±0.17 $^{A a}$
P (PPM) $^{V(NS)}$ **D[V](NS)**	28.5±8.27 $^{A a}$	26±3.74 $^{A a}$	29.25±3.86 ^{A} a	32.5±16.66 ^{A} a	25.25±7.41 $^{A a}$	26.25±8.66 $^{A a}$	31±7.16 $^{A a}$	26.75±5.74 $^{A a}$
K (ppm) $^{V(ns)}$ **D[V](ns)**	120.5±45.27 $^{A a}$	105.5±30.62 $^{A a}$	117.75±17.5 A a	108.5±37.7 ^{A} a	94.5±44.58 $^{A a}$	120.75±48.09 A a	121.25±31.63 A a	102±22.73 $^{A a}$

CA (PPM) $^{V(NS)}$ D[V](NS)	840.75±55.92 $^{A\ a}$	868±43.49 $^{A\ a}$	788.75±63.8 $^{A\ a}$	861±72.24 $^{A\ a}$	855.75±42.6 $^{A\ a}$	840.75±39.25 $^{A\ a}$	839.5±60.67 $^{A\ a}$	844.25±115.8 $^{A\ a}$
Mg (ppm) $^{V(ns)}$ D[V](ns)	145.75±26.32 $^{A\ a}$	131.25±16.84 $^{A\ a}$	125±4.76 $^{A\ a}$	144.5±22.04 $^{A\ a}$	124±12.41 $^{A\ a}$	130.25±14.17 $^{A\ a}$	124.5±6.86 $^{A\ a}$	100±60.32 $^{A\ a}$
cec(meq:100g) V(ns) D[V](ns)	6.75±0.44 $^{A\ a}$	6.93±0.38 $^{A\ a}$	6.4±0.37 $^{A\ a}$	6.98±0.59 $^{A\ a}$	6.8±0.5 $^{A\ a}$	6.6±0.39 $^{A\ a}$	6.48±0.35 $^{A\ a}$	6.45±0.65 $^{A\ a}$
K (%sat) $^{V(ns)}$ D[V](ns)	4.6±1.81 $^{A\ a}$	3.9±1.12 $^{A\ a}$	4.7±0.54 $^{A\ a}$	3.98±1.23 $^{A\ a}$	3.53±1.45 $^{A\ a}$	4.73±1.88 $^{A\ a}$	4.8±1.27 $^{A\ a}$	4.08±1.02 $^{A\ a}$
CA (%SAT) $^{V(**)}$ D[V](NS)	*62.35±3.39* $^{A\ a}$	*62.7±2.17* $^{A\ a}$	*61.55±1.87* $^{A\ a}$	*61.88±4.25* $^{A\ a}$	*63.03±2.5* $^{AB\ a}$	*63.75±2.04* $^{AB\ a}$	*64.8±2.74* $^{B\ a}$	*65.3±3.61* $^{B\ a}$
Mg(%sat) $^{V(ns)}$ D[V](ns)	17.9±2.15 $^{A\ a}$	15.78±1.51 $^{A\ a}$	16.3±0.42 $^{A\ a}$	17.18±1.35 $^{A\ a}$	15.18±0.7 $^{A\ a}$	16.43±1.07 $^{A\ a}$	16.05±0.24 $^{A\ a}$	16.15±0.9 $^{A\ a}$
H(%SAT) $^{V(NS)}$ D[V](NS)	15.18±2.28 $^{A\ a}$	17.68±4.55 $^{A\ a}$	17.25±1.82 $^{A\ a}$	17.18±2.69 $^{A\ a}$	18.38±1.34 $^{A\ a}$	15.1±1.24 $^{A\ a}$	14.3±1.58 $^{A\ a}$	14.85±2.35 $^{A\ a}$
K:Mg $^{V(ns)\ D[V](ns)}$	0.26±0.09 $^{A\ a}$	0.25±0.05 $^{A\ a}$	0.29±0.04 $^{A\ a}$	0.23±0.07 $^{A\ a}$	0.23±0.1 $^{A\ a}$	0.29±0.11 $^{A\ a}$	0.3±0.08 $^{A\ a}$	0.25±0.07 $^{A\ a}$
CA:MG $^{V(NS)}$ D[V](NS)	3.53±0.54 $^{A\ a}$	4±0.29 $^{A\ a}$	3.78±0.21 $^{A\ a}$	3.63±0.46 $^{A\ a}$	4.16±0.22 $^{A\ a}$	3.9±0.37 $^{A\ a}$	4.04±0.22 $^{A\ a}$	4.06±0.39 $^{A\ a}$
WEEK 16								
pH $^{V(ns)\ D[V](ns)}$	5.7±0.14 $^{A\ a}$	5.85±0.13 $^{A\ a}$	5.85±0.17 $^{A\ a}$	5.9±0.12 $^{A\ a}$	5.88±0.21 $^{A\ a}$	5.93±0.1 $^{A\ a}$	5.88±0.3 $^{A\ a}$	5.85±0.13 $^{A\ a}$
NH_4-N (PPM) V(NS) D[V](NS)	9.28±0.97 $^{A\ a}$	8.38±0.79 $^{A\ a}$	10.58±4.57 $^{A\ a}$	9.23±2.33 $^{A\ a}$	8.83±3.13 $^{A\ a}$	10.25±5.06 $^{A\ a}$	11.08±7.28 $^{A\ a}$	8.05±1.43 $^{A\ a}$

NO$_3$-N (ppm) $^{V(ns)}$ **D[V](ns)**	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$	1±0 $^{A\,a}$
TOTAL N % $^{V(NS)}$ **D[V](NS)**	0.14±0.02 $^{A\,a}$	0.13±0.02 $^{A\,a}$	0.12±0.01 $^{A\,a}$	0.11±0.01 $^{A\,a}$	0.13±0.02 $^{A\,a}$	0.12±0.03 $^{A\,a}$	0.16±0.06 $^{A\,a}$	0.12±0.01 $^{A\,a}$
Total C % $^{V(ns)}$ **D[V](ns)**	1.22±0.34 $^{A\,a}$	0.83±0.19 $^{A\,a}$	0.76±0.07 $^{A\,a}$	0.74±0.08 $^{A\,a}$	0.96±0.35 $^{A\,a}$	0.93±0.32 $^{A\,a}$	1.24±0.76 $^{A\,a}$	0.85±0.16 $^{A\,a}$
TOTAL C:N $^{V(NS)}$ **D[V](NS)**	8.59±1.41 $^{A\,a}$	6.55±0.53 $^{A\,a}$	6.59±0.65 $^{A\,a}$	6.6±0.45 $^{A\,a}$	7.55±1.87 $^{A\,a}$	7.49±0.64 $^{A\,a}$	7.32±1.44 $^{A\,a}$	7.12±1.31 $^{A\,a}$
OM (%) $^{V(ns)}$ **D[V](ns)**	2.33±0.52 $^{A\,a}$	1.75±0.31 $^{A\,a}$	1.65±0.13 $^{A\,a}$	1.65±0.06 $^{A\,a}$	1.88±0.44 $^{A\,a}$	1.85±0.4 $^{A\,a}$	1.9±0.39 $^{A\,a}$	1.88±0.22 $^{A\,a}$
P (PPM) $^{V(NS)}$ **D[V](NS)**	25.5±8.66 $^{A\,a}$	20.75±2.5 $^{A\,a}$	20.5±3.7 $^{A\,a}$	22.75±5.06 ^{A} a	19.25±4.92 $^{A\,a}$	20.5±6.24 $^{A\,a}$	25.25±5.85 $^{A\,a}$	19±5.48 $^{A\,a}$
K (ppm) $^{V(ns)}$ **D[V](ns)**	70±21.43 $^{A\,a}$	46.25±11.32 $^{A\,a}$	50.25±7.85 ^{A} a	67.75±37.19 A a	53.5±19.47 $^{A\,a}$	80.75±58.09 ^{A} a	76±27.75 $^{A\,a}$	59.75±23.37 ^{A} a
CA (PPM) $^{V(NS)}$ **D[V](NS)**	739.75±72.36 ^{A} a	762.75±71.27 ^{A} a	746.25±43.8 A a	804.25±37.7 A a	771.75±35.5 ^{A} a	766.25±71.8 ^{A} a	728.75±76.6 ^{A} a	768±57.25 $^{A\,a}$
Mg (ppm) $^{V(ns)}$ **D[V](ns)**	104.25±11.53 ^{A} a	109±7.87 $^{A\,a}$	84.75±48.23 A a	119±9.83 $^{A\,a}$	118±18.02 $^{A\,a}$	114.5±16.9 $^{A\,a}$	103.25±6.9 $^{A\,a}$	104.25±11.32 A a
cec(meq:100g) **V(ns) D[V](ns)**	6±0.29 $^{A\,a}$	5.88±0.25 $^{A\,a}$	5.83±0.05 $^{A\,a}$	6.25±0.24 $^{A\,a}$	6.05±0.3 $^{A\,a}$	6±0.66 $^{A\,a}$	5.73±0.38 $^{A\,a}$	5.95±0.26 $^{A\,a}$
K (%sat) $^{V(ns)}$ **D[V](ns)**	3±0.93 $^{A\,a}$	2.05±0.57 $^{A\,a}$	2.2±0.35 $^{A\,a}$	2.8±1.57 $^{A\,a}$	2.28±0.86 $^{A\,a}$	3.38±2.17 $^{A\,a}$	3.5±1.48 $^{A\,a}$	2.55±0.93 $^{A\,a}$
CA (%SAT) $^{V(NS)}$ **D[V](NS)**	61.55±3.45 $^{A\,a}$	64.8±3.37 $^{A\,a}$	64.08±4.16 ^{A} a	64.35±1.88 ^{A} a	63.95±4.96 $^{A\,a}$	64.03±3.55 $^{A\,a}$	63.63±4.98 $^{A\,a}$	64.55±3.86 $^{A\,a}$

Mg(%sat) $^{V(ns)}$ **D[V](ns)**	14.48±1.42 $^{A\,a}$	15.45±0.72 $^{A\,a}$	15.33±1.32 $^{A\,a}$	15.83±0.74 $^{A\,a}$	16.2±1.87 $^{A\,a}$	15.88±0.79 $^{A\,a}$	15.05±1.17 $^{A\,a}$	14.55±0.97 $^{A\,a}$
H(%SAT) $^{V(NS)}$ **D[V](NS)**	21.33±2.71 $^{A\,a}$	17.93±2.87 $^{A\,a}$	18.03±2.88 $^{A\,a}$	16.8±1.88 $^{A\,a}$	17.63±4.1 $^{A\,a}$	16.65±1.45 $^{A\,a}$	18.28±5.96 $^{A\,a}$	18.13±2.79 $^{A\,a}$
K:Mg $^{V(ns)\ D[V](ns)}$	0.21±0.07 $^{A\,a}$	0.13±0.04 $^{A\,a}$	0.15±0.02 $^{A\,a}$	0.18±0.1 $^{A\,a\,A\,a}$	0.15±0.07 $^{A\,a}$	0.21±0.13 $^{A\,a}$	0.23±0.09 $^{A\,a}$	0.18±0.05 $^{A\,a}$
CA:MG $^{V(NS)}$ **D[V](NS)**	4.29±0.54 $^{A\,a}$	4.2±0.29 $^{A\,a}$	4.22±0.55 $^{A\,a}$	4.07±0.22 $^{A\,a}$	4.01±0.72 $^{A\,a}$	4.05±0.35 $^{A\,a}$	4.24±0.24 $^{A\,a}$	4.46±0.46 $^{A\,a}$
WEEK 38								
pH $^{V(ns)\ D[V](ns)}$	5.78±0.05 $^{A\,a}$	5.93±0.22 $^{A\,a}$	5.78±0.1 $^{A\,a}$	5.73±0.05 $^{A\,a}$	5.78±0.15 $^{A\,a}$	5.95±0.13 $^{A\,a}$	5.85±0.44 $^{A\,a}$	6.05±0.29 $^{A\,a}$
NH_4-N (PPM) **V(NS) D[V](NS)**	8.38±7.13 $^{A\,a}$	7.13±1.03 $^{A\,a}$	9.1±1.78 $^{A\,a}$	7.25±2.81 $^{A\,a}$	7.75±1.51 $^{A\,a}$	10.1±7.31 $^{A\,a}$	8.03±3.01 $^{A\,a}$	10.2±4.55 $^{A\,a}$
NO_3-N (ppm) $^{V(ns)}$ **D[V](ns)**	2.25±2.5 $^{A\,a}$	1.25±0.5 $^{A\,a}$	3.5±1.29 $^{A\,a}$	2.5±1.91 $^{A\,a}$	4.75±3.59 $^{A\,a}$	2.75±0.5 $^{A\,a}$	2.25±1.89 $^{A\,a}$	2.5±1.29 $^{A\,a}$
TOTAL N % $^{V(NS)}$ **D[V](NS)**	0.12±0.02 $^{A\,a}$	0.1±0.01 $^{A\,a}$	0.11±0.01 $^{A\,a}$	0.12±0.02 $^{A\,a}$	0.12±0.01 $^{A\,a}$	0.12±0.01 $^{A\,a}$	0.11±0.01 $^{A\,a}$	0.11±0.01 $^{A\,a}$
Total C % $^{V(ns)}$ **D[V](ns)**	0.85±0.28 $^{A\,a}$	0.76±0.08 $^{A\,a}$	0.75±0.03 $^{A\,a}$	0.7±0.1 $^{A\,a}$	0.76±0.2 $^{A\,a}$	0.82±0.28 $^{A\,a}$	0.76±0.11 $^{A\,a}$	0.78±0.09 $^{A\,a}$
TOTAL C:N $^{V(NS)}$ **D[V](NS)**	7.11±0.92 $^{A\,a}$	7.49±0.92 $^{A\,a}$	6.7±0.5 $^{A\,a}$	5.93±0.68 $^{A\,a}$	6.43±1.17 $^{A\,a}$	6.98±1.71 $^{A\,a}$	6.91±0.54 $^{A\,a}$	7.11±0.75 $^{A\,a}$

OM (%)$^{V(ns)}$ **D[V](ns)**	1.73±0.39 $^{A\,a}$	1.63±0.17 $^{A\,a}$	1.6±0.14 $^{A\,a}$	1.53±0.13 $^{A\,a}$	1.6±0.14 $^{A\,a}$	1.68±0.36 $^{A\,a}$	1.68±0.15 $^{A\,a}$	1.63±0.1 $^{A\,a}$
P (PPM) $^{V(NS)}$ **D[V](NS)**	25.5±10.15 $^{A\,a}$	23.25±6.95 $^{A\,a}$	24±3.92 $^{A\,a}$	22.5±3.7 $^{A\,a}$	21±5.35 $^{A\,a}$	23.5±8.39 $^{A\,a}$	25±3.74 $^{A\,a}$	23±4.55 $^{A\,a}$
K (ppm) $^{V(ns)}$ **D[V](ns)**	78.5±37 $^{A\,a}$	72.25±17.84 $^{A\,a}$	80±13.93 $^{A\,a}$	72.5±19.74 ^{A} a	90±31.27 $^{A\,a}$	76.25±31.15 ^{A} a	103±52.43 $^{A\,a}$	78.75±24.38 ^{A} a
CA (PPM) $^{V(NS)}$ **D[V](NS)**	1051.5±52.56 ^{A} a	1130.25±75.07 A a	1038.75±43 ^{A} a	1000.5±124 A a	1065.25±105 A a	1016.5±38.84 A a	1111±100.55 ^{A} a	1051.5±45.99 A a
Mg (ppm) $^{V(ns)}$ **D[V](ns)**	121.25±8.77 $^{A\,a}$	136.5±14.64 $^{A\,a}$	127±4.08 $^{A\,a}$	126.5±16.9 ^{A} a	128.25±15.3 ^{A} a	121±9.56 $^{A\,a}$	127±21.46 $^{A\,a}$	118.5±11.5 $^{A\,a}$
cec(meq:100g) **V(ns) D[V](ns)**	8.05±0.44 $^{A\,a}$	8.38±0.42 $^{A\,a}$	8.03±0.33 $^{A\,a}$	7.85±0.91 $^{A\,a}$	8.28±1.11 $^{A\,a}$	7.5±0.16 $^{A\,a}$	8.58±1.38 $^{A\,a}$	7.6±0.54 $^{A\,a}$
K (%sat) $^{V(ns)}$ **D[V](ns)**	2.48±1.1 $^{A\,a}$	2.25±0.69 $^{A\,a}$	2.58±0.54 $^{A\,a}$	2.43±0.77 $^{A\,a}$	2.83±1.11 $^{A\,a}$	2.6±1.04 $^{A\,a}$	3.13±1.6 $^{A\,a}$	2.65±0.85 $^{A\,a}$
CA (%SAT) $^{V(NS)}$ **D[V](NS)**	65.33±0.97 $^{A\,a}$	67.53±3.84 $^{A\,a}$	64.78±1.63 ^{A} a	63.7±0.98 $^{A\,a}$	64.6±2.46 $^{A\,a}$	67.78±2.53 $^{A\,a}$	65.58±8.3 $^{A\,a}$	69.4±5.13 $^{A\,a}$
Mg(%sat) $^{V(ns)}$ **D[V](ns)**	12.55±0.6 $^{A\,a}$	13.58±1.09 $^{A\,a}$	13.18±0.56 ^{A} a	13.45±1.03 ^{A} a	12.98±0.9 $^{A\,a}$	13.45±0.86 $^{A\,a}$	12.33±0.8 $^{A\,a}$	12.98±0.79 $^{A\,a}$
H(%SAT) $^{V(NS)}$ **D[V](NS)**	19.53±0.83 $^{A\,a}$	16.98±4.39 $^{A\,a}$	19.6±2.16 $^{A\,a}$	20.38±1 $^{A\,a}$	19.63±3.42 $^{A\,a}$	16.35±2.02 $^{A\,a}$	18.95±8.32 $^{A\,a}$	14.9±4.89 $^{A\,a}$
K:Mg $^{V(ns)\ D[V](ns)}$	0.2±0.1 $^{A\,a}$	0.17±0.06 $^{A\,a}$	0.2±0.04 $^{A\,a}$	0.19±0.07 $^{A\,a}$	0.23±0.09 $^{A\,a}$	0.2±0.08 $^{A\,a}$	0.25±0.12 $^{A\,a}$	0.2±0.05 $^{A\,a}$
CA:MG $^{V(NS)}$ **D[V](NS)**	5.22±0.26 $^{A\,a}$	4.99±0.25 $^{A\,a}$	4.92±0.16 $^{A\,a}$	4.76±0.38 $^{A\,a}$	5±0.36 $^{A\,a}$	5.05±0.31 $^{A\,a}$	5.35±0.82 $^{A\,a}$	5.37±0.62 $^{A\,a}$

Table 3.2.

PLFAs Table.

Relative abundances of bacteria and fungi (% of total nmol/g) and fungi to bacteria ratio (F:B) in soils of four Panicum virgatum cultivars (Alamo, Bomaster, Colony, and Kanlow) grown under conservation agriculture management after being sown in high (HDP) or low (LDP) seeding densities (mean ± standard deviation). Select soil PLFAs were classified as bacteria (15:0 iso, 15:0 anteiso, 15:0, 16:0 iso, 16:1x7c, 16:0 10Me, 17:0 iso, 17:0 anteiso, 17:0 cyclo, 17:0, 18:1x7c, 18:0 10Me, 19:0 cyclo), Gram negative bacteria (), Gram positive bacteria (), and actinobacteria () or fungi (18:2x6,9), arbuscular mycorrhizal fungi () and other fungi (). The estimates were followed from one week after the first leaf emergence and periodically to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects “Variety” (V) “Density[Variety]” D[V] and “Block” as a random effect with 3 degrees freedom for numerator for “Variety” and 4 degrees freedom for numerator for “Density[Variety]” with 21 degrees of freedom for the denominator, unless samples yielded no data (N/A). For each estimate, the uppercase letters indicate pairwise Student’s t-test comparisons of cultivars, the lowercase letters identify differences in planting densities for that cultivar. ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

	Alamo		***Bomaster***		***Colony***		***Kanlow***	
	HDP	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**
Week 1								
All Bacteria $^{V(ns)\ D[V]\ (ns)}$	92.25±1.53 $^{A\ a}$	92.29±1.24 $^{A\ a}$	92.33±1.38 $^{A\ a}$	92.07±1.48 $^{A\ a}$	92.04±1.58 $^{A\ a}$	91.88±1.99 $^{A\ a}$	91.29±3.09 $^{A\ a}$	91.44±2.80 $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	37.74±8.83 $^{A\ a}$	36.62±7.00 $^{A\ a}$	37.39±8.32 $^{A\ a}$	36.77±6.50 $^{A\ a}$	36.19±7.22 $^{A\ a}$	36.92±8.36 $^{A\ a}$	38.96±7.88 $^{A\ a}$	36.54±7.12 $^{A\ a}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	37.37±5.03 $^{A\ a}$	38.22±4.02 $^{A\ a}$	37.57±4.54 $^{A\ a}$	37.83±3.71 $^{A\ a}$	37.98±3.81 $^{A\ a}$	37.21±4.56 $^{A\ a}$	36.63±4.09 $^{A\ a}$	37.17±3.16 $^{A\ a}$
Actinomycetes $^{V(ns)\ D[V]\ (ns)}$	17.14±2.52 $^{A\ a}$	17.45±1.93 $^{A\ a}$	17.38±3.34 $^{A\ a}$	17.47±2.07 $^{A\ a}$	17.88±2.34 $^{A\ a}$	17.75±2.88 $^{A\ a}$	15.69±2.74 $^{A\ a}$	17.73±1.75 $^{A\ a}$

All Fungi $^{V(ns)\ D[V]\ (ns)}$	6.96±1.30 $^{\text{A a}}$	6.74±0.87 $^{\text{A a}}$	6.75±0.93 $^{\text{A a}}$	6.99±1.14 $^{\text{A a}}$	6.96±1.15 $^{\text{A a}}$	7.10±1.64 $^{\text{A a}}$	7.30±2.15 $^{\text{A a}}$	7.00±1.56 $^{\text{A a}}$
AM Fungi $^{V(ns)\ D[V]\ (ns)}$	4.83±0.98 $^{\text{A a}}$	4.65±0.79 $^{\text{A a}}$	4.64±0.88 $^{\text{A a}}$	5.06±0.64 $^{\text{A a}}$	4.79±0.77 $^{\text{A a}}$	4.78±0.85 $^{\text{A a}}$	4.93±1.15 $^{\text{A a}}$	4.92±1.04 $^{\text{A a}}$
Fungi $^{V(ns)\ D[V]\ (ns)}$	2.13±0.47 $^{\text{A a}}$	2.09±0.21 $^{\text{A a}}$	2.11±0.43 $^{\text{A a}}$	1.94±0.53 $^{\text{A a}}$	2.17±0.77 $^{\text{A a}}$	2.33±1.03 $^{\text{A a}}$	2.37±1.02 $^{\text{A a}}$	2.08±0.61 $^{\text{A a}}$
F:B $^{V(ns)\ D[V]\ (ns)}$	0.09±0.02 $^{\text{A a}}$	0.09±0.01 $^{\text{A a}}$	0.09±0.02 $^{\text{A a}}$	0.1±0.02 $^{\text{A a}}$	0.10±0.02 $^{\text{A a}}$	0.10±0.03 $^{\text{A a}}$	0.10±0.03 $^{\text{A a}}$	0.10±0.03 $^{\text{A a}}$
Week 2								
All Bacteria $^{V(*)\ D[V]\ (ns)}$	*92.24±1.03* $^{AB\ a}$	*92.74±0.36* $^{AB\ a}$	*91.70±0.90* $^{AB\ a}$	*92.79±0.59* $^{AB\ a}$	*93.53±0.97* $^{B\ a}$	*92.84±1.01* $^{B\ a}$	*91.39±1.56* $^{A\ a}$	*91.85±1.09* $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	33.89±1.29 $^{\text{A a}}$	33.88±0.38 $^{\text{A a}}$	33.18±0.91 $^{\text{A a}}$	33.49±2.49 $^{\text{A a}}$	36.31±8.07 $^{\text{A a}}$	38.01±7.45 $^{\text{A a}}$	34.84±2.53 $^{\text{A a}}$	33.12±3.71 $^{\text{A a}}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	40.91±0.18 $^{\text{A a}}$	41.34±0.64 $^{\text{A a}}$	41.03±0.84 $^{\text{A a}}$	41.93±1.58 $^{\text{A a}}$	40.10±4.76 $^{\text{A a}}$	39.13±4.65 $^{\text{A a}}$	40.94±0.85 $^{\text{A a}}$	41.12±1.18 $^{\text{A a}}$
Actinomycetes $^{V(ns)\ D[V]\ (ns)}$	17.44±1.41 $^{\text{A a}}$	17.52±0.87 $^{\text{A a}}$	17.50±1.16 $^{\text{A a}}$	17.37±0.64 $^{\text{A a}}$	17.12±3.02 $^{\text{A a}}$	15.71±2.64 $^{\text{A a}}$	15.61±2.26 $^{\text{A a}}$	17.61±2.21 $^{\text{A a}}$
All Fungi $^{V(**)\ D[V]\ (ns)}$	*6.78±0.40* $^{AB\ a}$	*6.93±0.37* $^{AB\ a}$	*7.42±0.91* $^{BC\ a}$	*6.77±0.40* $^{BC\ a}$	*5.94±0.8* $^{A\ a}$	*6.66±0.85* $^{A\ a}$	*7.67±0.73* $^{C\ a}$	*7.78±0.76* $^{C\ a}$

AM Fungi $^{V(ns)\ D[V]\ (ns)}$	4.96±0.15 $^{A\ a}$	5.05±0.30 $^{A\ a}$	5.07±0.08 $^{A\ a}$	5.13±0.25 $^{A\ a}$	4.68±0.65 $^{A\ a}$	4.94±0.58 $^{A\ a}$	5.14±0.84 $^{A\ a}$	5.20±0.39 $^{A\ a}$
Fungi $^{V(**)\ D[V]\ (ns)}$	1.82±0.52 $^{A\ a}$	1.88±0.30 $^{A\ a}$	2.35±0.86 $^{AB\ a}$	1.64±0.30 $^{AB\ a}$	1.26±0.20 $^{A\ a}$	1.72±0.60 $^{A\ a}$	2.53±0.47 $^{B\ a}$	2.58±1.12 $^{B\ a}$
F:B $^{V(**)\ D[V]\ (ns)}$	0.09±0.01 $^{AB\ a}$	0.09±0.01 $^{AB\ a}$	0.10±0.01 $^{BC\ a}$	0.09±0.01 $^{BC\ a}$	0.08±0.01 $^{A\ a}$	0.09±0.01 $^{A\ a}$	0.10±0.01 $^{C\ a}$	0.11±0.02 $^{C\ a}$
Week 4								
All Bacteria $^{V(*)\ D[V]\ (ns)}$	94.28±0.97 $^{AB\ a}$	94.24±1.29 $^{AB\ a}$	95.15±0.87 $^{B\ a}$	94.74±0.64 $^{B\ a}$	93.9±0.85 $^{AB\ a}$	94.17±0.65 $^{AB\ a}$	92.59±1.75 $^{A\ a}$	94.17±0.50 $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	46.86±3.61 $^{A\ a}$	45.84±1.87 $^{A\ a}$	44.11±4.11 $^{A\ a}$	43.83±1.03 $^{A\ a}$	45.72±2.29 $^{A\ a}$	46.09±1.98 $^{A\ a}$	47.83±2.61 $^{A\ a}$	46.13±2.82 $^{A\ a}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	33.36±2.33 $^{A\ a}$	33.96±1.21 $^{A\ a}$	35.45±2.42 $^{A\ a}$	35.70±0.94 $^{A\ a}$	34.35±1.77 $^{A\ a}$	34.8±1.58 $^{A\ a}$	31.81±2.08 $^{A\ a}$	34.57±1.92 $^{A\ a}$
Actinomycetes $^{V(**)\ D[V]\ (ns)}$	14.06±1.67 $^{AB\ a}$	14.44±1.00 $^{AB\ a}$	15.59±1.55 $^{B\ a}$	15.22±1.17 $^{B\ a}$	13.83±0.86 $^{A\ a}$	13.29±1.23 $^{A\ a}$	12.96±2.23 $^{A\ a}$	13.48±0.82 $^{A\ a}$
All Fungi $^{V(ns)\ D[V]\ (ns)}$	4.29±1.35 $^{A\ a}$	4.62±1.22 $^{A\ a}$	4.17±0.84 $^{A\ a}$	4.29±0.98 $^{A\ a}$	4.55±1.12 $^{A\ a}$	4.39±0.56 $^{A\ a}$	5.78±1.7 $^{A\ a}$	4.42±1.23 $^{A\ a}$
AM Fungi $^{V(ns)\ D[V]\ (ns)}$	3.70±0.20 $^{A\ a}$	3.80±0.32 $^{A\ a}$	3.45±0.3 $^{A\ a}$	3.89±0.29 $^{A\ a}$	4.00±0.19 $^{A\ a}$	4.07±0.16 $^{A\ a}$	3.75±0.22 $^{A\ a}$	3.67±0.48 $^{A\ a}$

Fungi $^{V(ns)\ D[V]\ (ns)}$	2.34±0.00 $^{A\ a}$	1.65±0.33 $^{A\ a}$	1.44±0.13 $^{A\ a}$	1.63±0.00 $^{A\ a}$	2.18±0.00 $^{A\ a}$	1.29±0.00 $^{A\ a}$	2.7±0.82 $^{A\ a}$	3.00±0.00 $^{A\ a}$
F:B $^{V(ns)\ D[V]\ (ns)}$	0.06±0.02 $^{A\ a}$	0.06±0.02 $^{A\ a}$	0.05±0.01 $^{A\ a}$	0.05±0.01 $^{A\ a}$	0.06±0.02 $^{A\ a}$	0.06±0.01 $^{A\ a}$	0.07±0.02 $^{A\ a}$	0.06±0.02 $^{A\ a}$
Week 8								
All Bacteria $^{V(ns)\ D[V]\ (ns)}$	91.59±3.16 $^{A\ a}$	92.65±0.67 $^{A\ a}$	92.62±1.64 $^{A\ a}$	92.99±0.65 $^{A\ a}$	92.29±1.85 $^{A\ a}$	92.92±0.71 $^{A\ a}$	93.08±0.87 $^{A\ a}$	92.31±1.33 $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	35.66±2.85 $^{A\ a}$	35.06±1.32 $^{A\ a}$	34.23±0.49 $^{A\ a}$	34.95±1.86 $^{A\ a}$	35.25±1.33 $^{A\ a}$	35.54±0.78 $^{A\ a}$	36.66±2.28 $^{A\ a}$	35.96±1.32 $^{A\ a}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	39.44±1.97 $^{A\ a}$	40.06±0.82 $^{A\ a}$	41.14±1.86 $^{A\ a}$	40.34±0.69 $^{A\ a}$	39.54±1.05 $^{A\ a}$	40.18±0.95 $^{A\ a}$	40.50±0.63 $^{A\ a}$	39.69±1.71 $^{A\ a}$
Actinomycetes $^{V(ns)\ D[V]\ (ns)}$	16.49±2.19 $^{A\ a}$	17.53±1.8 $^{A\ a}$	17.26±1.03 $^{A\ a}$	17.7±2.58 $^{A\ a}$	17.51±2.00 $^{A\ a}$	17.21±1.36 $^{A\ a}$	15.92±3.36 $^{A\ a}$	16.66±1.92 $^{A\ a}$
All Fungi $^{V(ns)\ D[V]\ (ns)}$	5.81±1.44 $^{A\ a}$	5.37±0.18 $^{A\ a}$	5.55±1.13 $^{A\ a}$	5.29±0.15 $^{A\ a}$	5.99±1.24 $^{A\ a}$	5.46±0.30 $^{A\ a}$	5.31±0.34 $^{A\ a}$	5.89±1.24 $^{A\ a}$
AM Fungi $^{V(ns)\ D[V]\ (ns)}$	5.01±0.57 $^{A\ a}$	5.37±0.18 $^{A\ a}$	5.01±0.11 $^{A\ a}$	5.29±0.15 $^{A\ a}$	5.40±0.24 $^{A\ a}$	5.46±0.30 $^{A\ a}$	5.31±0.34 $^{A\ a}$	5.30±0.12 $^{A\ a}$
Fungi $^{V(ns)\ D[V]\ (ns)}$	3.20±0.00 $^{A\ a}$	N/A	2.15±0 $^{A\ a}$	N/A	2.35±0.00 $^{A\ a}$	N/A	N/A	2.36±0.00 $^{A\ a}$
F:B $^{V(ns)\ D[V]\ (ns)}$	0.08±0.02 $^{A\ a}$	0.07±0.00 $^{A\ a}$	0.08±0.02 $^{A\ a}$	0.07±0.00 $^{A\ a}$	0.08±0.01 $^{A\ a}$	0.07±0.00 $^{A\ a}$	0.07±0.01 $^{A\ a}$	0.08±0.02 $^{A\ a}$

Week 16								
All Bacteria $^{V(ns)\ D[V]\ (ns)}$	91.52±0.87 $^{A\ a}$	92.28±0.11 $^{A\ a}$	92.43±0.47 $^{A\ a}$	91.86±1.21 $^{A\ a}$	91.66±1.3 $^{A\ a}$	90.07±1.84 $^{A\ a}$	91.31±1.69 $^{A\ a}$	91.15±1.09 $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	33.26±2.16 $^{A\ a}$	31.86±1.59 $^{A\ a}$	30.49±0.51 $^{A\ a}$	31.65±1.6 $^{A\ a}$	31.35±3.04 $^{A\ a}$	32.42±3.2 $^{A\ a}$	32.86±2.51 $^{A\ a}$	32.58±2.28 $^{A\ a}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	40.56±1.57 $^{A\ a}$	40.71±1.32 $^{A\ a}$	41.17±1.55 $^{A\ a}$	41±1.45 $^{A\ a}$	41.14±1.39 $^{A\ a}$	40.32±1.97 $^{A\ a}$	40.49±1.07 $^{A\ a}$	40.37±0.96 $^{A\ a}$
Actinomycetes $^{V(ns)\ D[V]\ (ns)}$	17.71±1.59 $^{A\ a}$	19.71±0.93 $^{A\ a}$	20.77±1.72 $^{A\ a}$	19.22±2.1 $^{A\ a}$	19.17±1.96 $^{A\ a}$	17.33±3.14 $^{A\ a}$	17.96±2.43 $^{A\ a}$	18.2±2.12 $^{A\ a}$
All Fungi $^{V(*)\ D[V]\ (ns)}$	6.55±1.17 $^{A\ a}$	6.36±0.45 $^{A\ a}$	6.49±1.14 $^{AB\ a}$	7.08±1.06 $^{AB\ a}$	7.05±1.22 $^{B\ a}$	8.39±0.96 $^{B\ a}$	7.26±1.3 $^{AB\ a}$	7.62±1.32 $^{AB\ a}$
AM Fungi $^{V(ns)\ D[V]\ (ns)}$	5.76±0.26 $^{A\ a}$	5.81±0.3 $^{A\ a}$	5.90±0.57 $^{A\ a}$	6.04±0.39 $^{A\ a}$	5.93±0.36 $^{A\ a}$	6.11±0.49 $^{A\ a}$	6.15±0.7 $^{A\ a}$	6.48±0.82 $^{A\ a}$
Fungi $^{V(ns)\ D[V]\ (ns)}$	1.58±0.49 $^{A\ a}$	1.10±0.05 $^{A\ a}$	1.18±0.16 $^{A\ a}$	1.38±0.37 $^{A\ a}$	1.5±0.6 $^{A\ a}$	2.28±1.35 $^{A\ a}$	1.48±0.72 $^{A\ a}$	1.53±0.42 $^{A\ a}$
F:B $^{V(ns)\ D[V]\ (ns)}$	0.09±0.02 $^{A\ a}$	0.09±0.01 $^{A\ a}$	0.09±0.02 $^{A\ a}$	0.10±0.01 $^{A\ a}$	0.10±0.02 $^{A\ a}$	0.11±0.01 $^{A\ a}$	0.10±0.02 $^{A\ a}$	0.11±0.02 $^{A\ a}$
Week 38								

All Bacteria $^{V(ns)\ D[V]\ (ns)}$	90.78±1.23 $^{A\ a}$	92.11±0.92 $^{A\ a}$	91.54±1.03 $^{A\ a}$	68.83±45.89 $^{A\ a}$	92.07±1.12 $^{A\ a}$	90.29±1.17 $^{A\ a}$	91.29±1.51 $^{A\ a}$	92.08±1.07 $^{A\ a}$
Gram– $^{V(ns)\ D[V]\ (ns)}$	34.11±1.33 $^{A\ a}$	33.59±2.33 $^{A\ a}$	33.64±1.32 $^{A\ a}$	33.14±0.49 $^{A\ a}$	33.37±2.24 $^{A\ a}$	34.52±3.36 $^{A\ a}$	33.77±2.38 $^{A\ a}$	32.18±0.83 $^{A\ a}$
Gram+ $^{V(ns)\ D[V]\ (ns)}$	39.47±1.40 $^{A\ a}$	41.22±2.28 $^{A\ a}$	39.94±1.18 $^{A\ a}$	39.87±1.38 $^{A\ a}$	40.39±1.55 $^{A\ a}$	39.39±1.42 $^{A\ a}$	40.45±1.51 $^{A\ a}$	40.47±0.24 $^{A\ a}$
Actinomycetes $^{V(ns)\ D[V]\ (ns)}$	17.21±1.22 $^{A\ a}$	17.31±2.59 $^{A\ a}$	17.97±1.75 $^{A\ a}$	18.76±1.01 $^{A\ a}$	18.31±0.88 $^{A\ a}$	16.38±1.83 $^{A\ a}$	17.08±1.82 $^{A\ a}$	19.43±1.03 $^{A\ a}$
All Fungi $^{V(ns)\ D[V]\ (ns)}$	7.88±0.91 $^{A\ a}$	6.83±0.60 $^{A\ a}$	7.08±0.44 $^{A\ a}$	5.18±3.46 $^{A\ a}$	7.02±1.01 $^{A\ a}$	8.36±1.21 $^{A\ a}$	7.72±1.66 $^{A\ a}$	6.94±0.79 $^{A\ a}$
AM Fungi $^{V(ns)\ D[V]\ (ns)}$	5.10±0.35 $^{A\ a}$	5.20±0.41 $^{A\ a}$	4.96±0.44 $^{A\ a}$	5.03±0.21 $^{A\ a}$	5.02±0.36 $^{A\ a}$	5.01±0.34 $^{A\ a}$	5.43±0.91 $^{A\ a}$	5.07±0.55 $^{A\ a}$
Fungi $^{V(ns)\ D[V]\ (ns)}$	2.78±0.88 $^{A\ a}$	1.63±0.19 $^{A\ a}$	2.13±0.61 $^{A\ a}$	1.88±0.49 $^{A\ a}$	2.00±0.72 $^{A\ a}$	3.34±1.37 $^{A\ a}$	2.29±0.76 $^{A\ a}$	1.87±0.49 $^{A\ a}$
F:B $^{V(ns)\ D[V]\ (ns)}$	0.11±0.01 $^{A\ a}$	0.09±0.01 $^{A\ a}$	0.10±0.01 $^{A\ a}$	0.09±0.00 $^{A\ a}$	0.10±0.02 $^{A\ a}$	0.11±0.02 $^{A\ a}$	0.10±0.02 $^{A\ a}$	0.10±0.01 $^{A\ a}$

Table 3.3.

***EEAs Table*.**

Extracellular enzyme activities (µmol h^{-1} g^{-1} dw) in soils of four Panicum virgatum cultivars (Alamo, Bomaster, Colony, and Kanlow) grown under conservation agriculture management after being sown in high or low seeding densities (mean ± standard deviation). The parameters were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects "Variety" (V) "Density[Variety]" D[V] and "Block" as a random effect with 3 degrees freedom for numerator for "Variety" and 4 degrees freedom for numerator for "Density[Variety]" with 21 degrees of freedom for the denominator. For each estimate, the uppercase letters indicate pairwise Student's t-test comparisons of cultivars, the lowercase letters identify differences in planting densities for that cultivar. ns = P ≥ 0.05; * = 0.05 > P ≥ 0.01; ** = 0.01 > P ≥ 0.001; *** = 0.001 > P

	Alamo		**Bomaster**		**Colony**		**Kanlow**	
	HDP	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**
Week 1								
Cellobiohydrolase $^{V(ns)\ D[V]\ (ns)}$	0.044±0.003 A a	0.041±0.006 A a	0.069±0.037 A a	0.051±0.012 A a	0.047±0.006 A a	0.033±0.011 A a	0.094±0.064 A a	0.049±0.019 A a
B-Glucosidase $^{V(ns)\ D[V]\ (ns)}$	0.265±0.027 A a	0.239±0.057 A a	0.362±0.155 A a	0.277±0.051 A a	0.284±0.036 A a	0.243±0.05 ^{A} a	0.476±0.282 A a	0.279±0.041 A a
B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.179±0.029 A a	0.147±0.024 A a	0.189±0.069 A a	0.180±0.042 A a	0.179±0.036 A a	0.161±0.036 A a	0.225±0.112 A a	0.168±0.012 A a

Phosphatase $^{V(ns)\ D[V]\ (ns)}$	1.098±0.119 A a	1.123±0.174 A a	1.367±0.395 A a	1.165±0.262 A a	1.257±0.397 A a	1.018±0.097 A a	1.313±0.317 A a	0.98±0.097 A a
Week 2								
Cellobiohydrolase $^{V(ns)\ D[V]\ (ns)}$	0.059±0.013 A a	0.058±0.023 A a	0.089±0.043 A a	0.062±0.025 A a	0.045±0.013 A a	0.059±0.021 A a	0.082±0.029 A a	0.065±0.035 A a
B-Glucosidase $^{V(ns)\ D[V]\ (ns)}$	0.340±0.046 A a	0.385±0.14 A a	0.543±0.232 A a	0.393±0.108 A a	0.268±0.054 A a	0.362±0.095 A a	0.483±0.186 A a	0.475±0.202 A a
B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.208±0.036 A a	0.22±0.046 A a	0.280±0.107 A a	0.209±0.068 A a	0.155±0.051 A a	0.220±0.055 A a	0.245±0.097 A a	0.217±0.096 A a
Phosphatase $^{V(ns)\ D[V]\ (ns)}$	1.403±0.156 A a	1.327±0.26 A a	1.468±0.358 A a	1.309±0.279 A a	1.213±0.217 A a	1.510±0.227 A a	1.401±0.435 A a	1.391±0.438 A a
Week 4								
Cellobiohydrolase $^{V(ns)\ D[V]\ (ns)}$	0.015±0.010 A a	0.010±0.006 A a	0.013±0.01 A a	0.011±0.004 A a	0.021±0.016 A a	0.016±0.008 A a	0.017±0.007 A a	0.019±0.011 A a
B-Glucosidase $^{V(ns)\ D[V]\ (ns)}$	0.124±0.093 A a	0.081±0.028 A a	0.112±0.07 A a	0.096±0.012 A a	0.136±0.057 A a	0.110±0.034 A a	0.139±0.060 A a	0.169±0.089 A a

B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.044±0.023 A a	0.023±0.006 A a	0.046±0.021 A a	0.035±0.01 ^{A} a	0.046±0.017 A a	0.043±0.013 A a	0.047±0.015 A a	0.054±0.023 A a
Phosphatase $^{V(ns)\ D[V]\ (ns)}$	0.300±0.131 A a	0.152±0.055 A a	0.247±0.066 A a	0.215±0.04 ^{A} a	0.315±0.033 A a	0.289±0.123 A a	0.287±0.128 A a	0.288±0.070 A a
Week 8								
Cellobiohydrolase $^{V(ns)\ D[V]\ (ns)}$	0.142±0.162 A a	0.091±0.028 A a	0.088±0.028 A a	0.104±0.071 A a	0.096±0.058 A a	0.075±0.029 A a	0.111±0.042 A a	0.096±0.042 A a
B-Glucosidase $^{V(ns)\ D[V]\ (ns)}$	0.500±0.356 A a	0.400±0.058 A a	0.381±0.032 A a	0.434±0.191 A a	0.422±0.104 A a	0.393±0.113 A a	0.5±0.191 $^{A\ a}$	0.442±0.122 A a
B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.196±0.081 A a	0.185±0.042 A a	0.173±0.018 A a	0.192±0.079 A a	0.167±0.025 A a	0.177±0.039 A a	0.221±0.054 A a	0.237±0.109 A a
Phosphatase $^{V(ns)\ D[V]\ (ns)}$	1.535±0.418 A a	1.436±0.153 A a	1.385±0.096 A a	1.648±0.47 ^{A} a	1.321±0.162 A a	1.332±0.151 A a	1.357±0.26 ^{A} a	1.287±0.148 A a
Week 16								

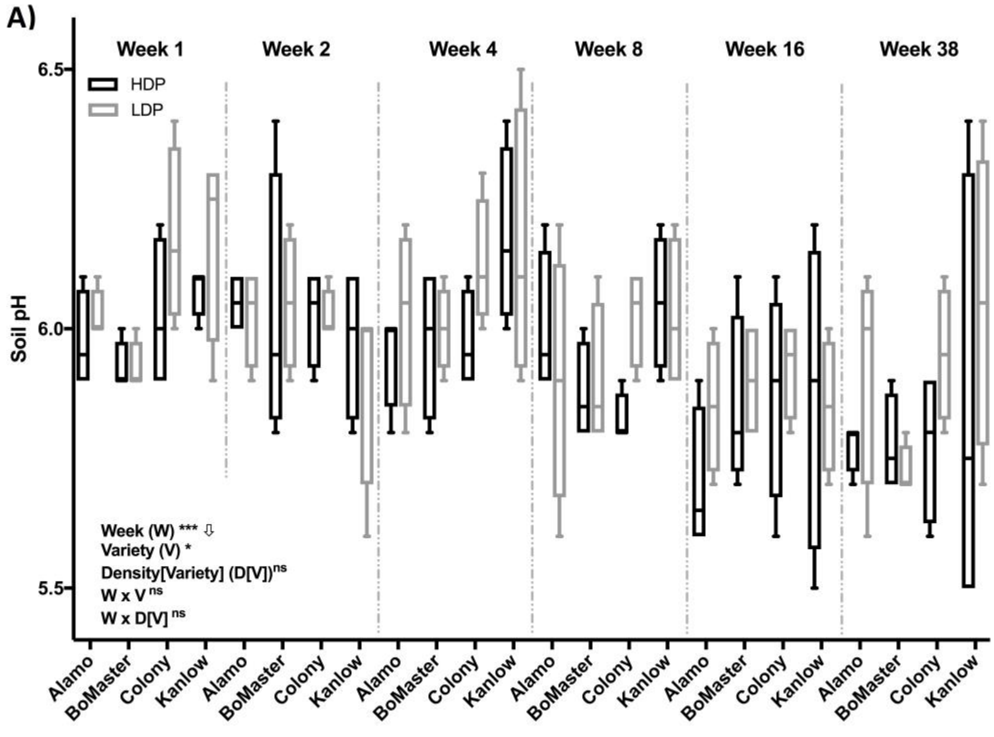
Cellobiohydrolase $^{V(*)\ D[V]\ (ns)}$	*0.090±0.041* $^{B\ a}$	*0.055±0.018* $^{B\ a}$	*0.07±0.06* $^{B\ a}$	*0.06±0.04* $^{B\ a}$	*0.089±0.053* $^{B\ a}$	*0.045±0.021* $^{B\ a}$	*0.038±0.009* $^{A\ a}$	*0.031±0.007* $^{A\ a}$
B-Glucosidase $^{V(*)\ D[V]\ (ns)}$	*0.307±0.104* $^{C\ a}$	*0.237±0.077* $^{C\ a}$	*0.223±0.129* $^{AB\ a}$	*0.205±0.128* $^{AB\ a}$	*0.277±0.112* $^{BC\ a}$	*0.181±0.059* $^{BC\ a}$	*0.168±0.083* $^{A\ a}$	*0.164±0.071* $^{A\ a}$
B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.135±0.036 $^{A\ a}$	0.118±0.032 $^{A\ a}$	0.128±0.056 $^{A\ a}$	0.096±0.033 $^{A\ a}$	0.144±0.053 $^{A\ a}$	0.106±0.022 $^{A\ a}$	0.102±0.020 $^{A\ a}$	0.085±0.01 $^{A\ a}$
Phosphatase $^{V(*)\ D[V]\ (ns)}$	*1.441±0.365* $^{B\ a}$	*1.068±0.104* $^{B\ a}$	*1.158±0.524* $^{A\ a}$	*0.924±0.204* $^{A\ a}$	*1.22±0.25* $^{AB\ a}$	*1.086±0.2* $^{AB\ a}$	*1.041±0.188* $^{A\ a}$	*0.921±0.098* $^{A\ a}$
Week 38								
Cellobiohydrolase $^{V(ns)\ D[V]\ (ns)}$	0.044±0.034 $^{A\ a}$	0.033±0.017 $^{A\ a}$	0.034±0.009 $^{A\ a}$	0.027±0.009 $^{A\ a}$	0.035±0.019 $^{A\ a}$	0.048±0.04 $^{A\ a}$	0.034±0.001 $^{A\ a}$	0.052±0.042 $^{A\ a}$
B-Glucosidase $^{V(ns)\ D[V]\ (ns)}$	0.244±0.123 $^{A\ a}$	0.196±0.038 $^{A\ a}$	0.19±0.039 $^{A\ a}$	0.154±0.037 $^{A\ a}$	0.189±0.042 $^{A\ a}$	0.245±0.132 $^{A\ a}$	0.223±0.062 $^{A\ a}$	0.249±0.087 $^{A\ a}$
B-N-acetylglucosaminidase $^{V(ns)\ D[V]\ (ns)}$	0.129±0.055 $^{A\ a}$	0.126±0.042 $^{A\ a}$	0.116±0.011 $^{A\ a}$	0.111±0.019 $^{A\ a}$	0.108±0.031 $^{A\ a}$	0.124±0.069 $^{A\ a}$	0.119±0.017 $^{A\ a}$	0.149±0.059 $^{A\ a}$

Phosphatase $^{V(ns)\ D[V]\ (ns)}$	1.202±0.296 A a	1.229±0.267 A a	1.179±0.195 A a	1.047±0.071 A a	1.100±0.161 A a	1.079±0.270 A a	1.152±0.131 A a	1.180±0.164 A a

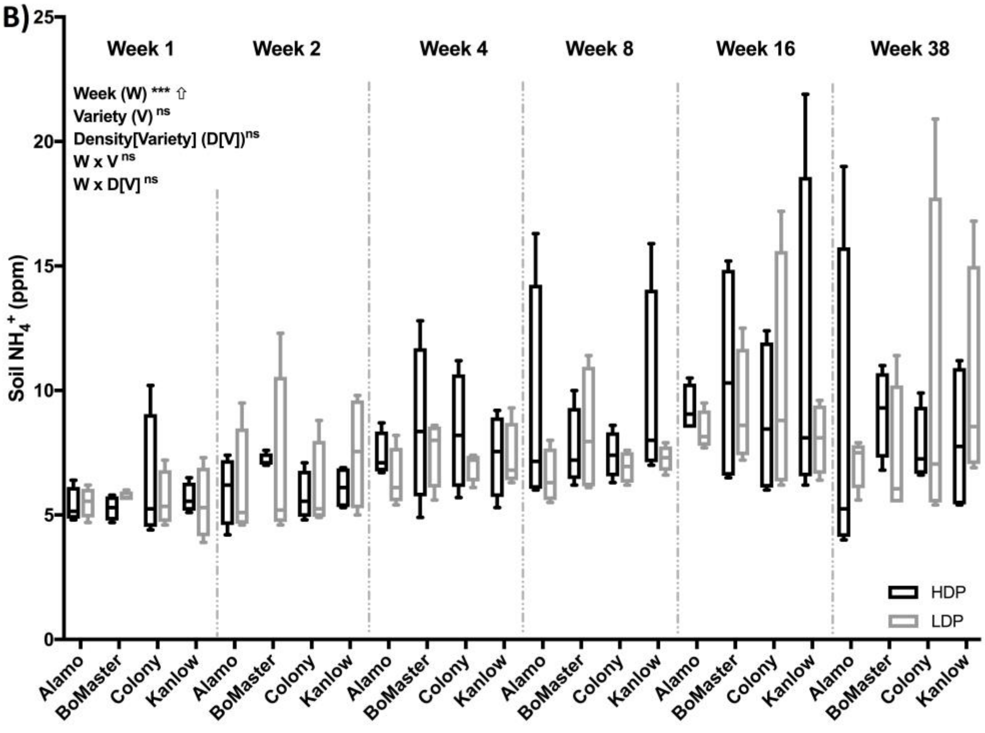
Figure 3.2.

Soil Chemistry Seasonal Dynamics

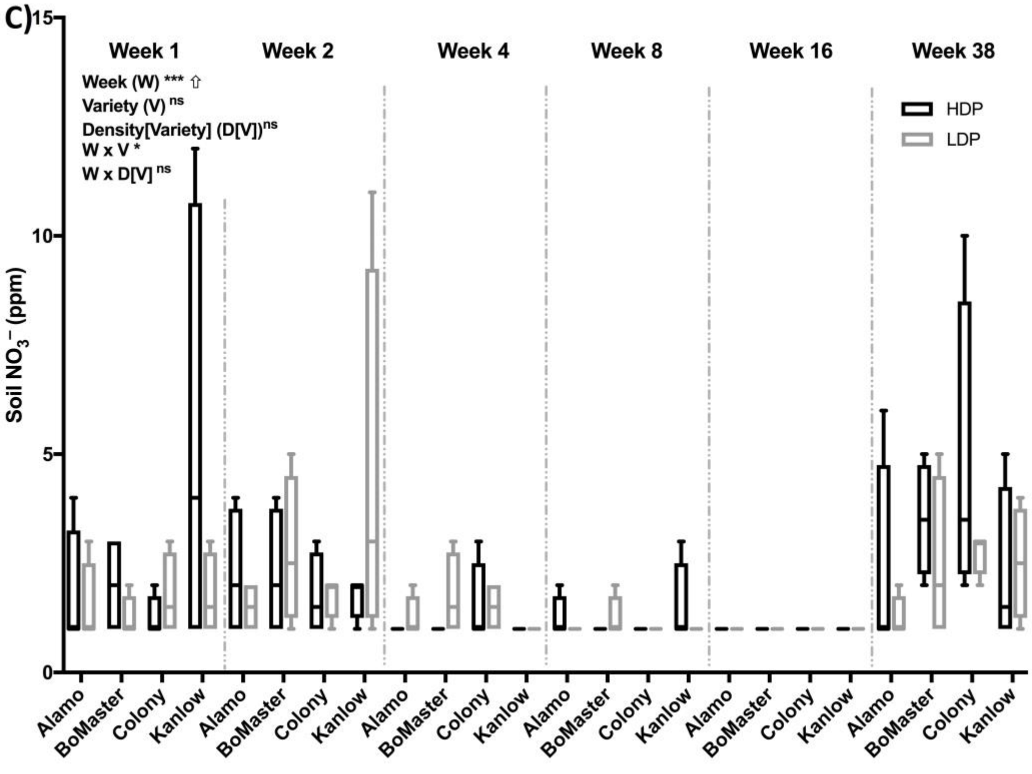
The parameters: (A) Soil pH (B) NH_4^+ (C) NO_3^- (D) Total N% (E)Total C% (F) C:N were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects "Week" (W) "Variety" (V) "Density[Variety]" D[V] interactions and "Block" as a random effect ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$



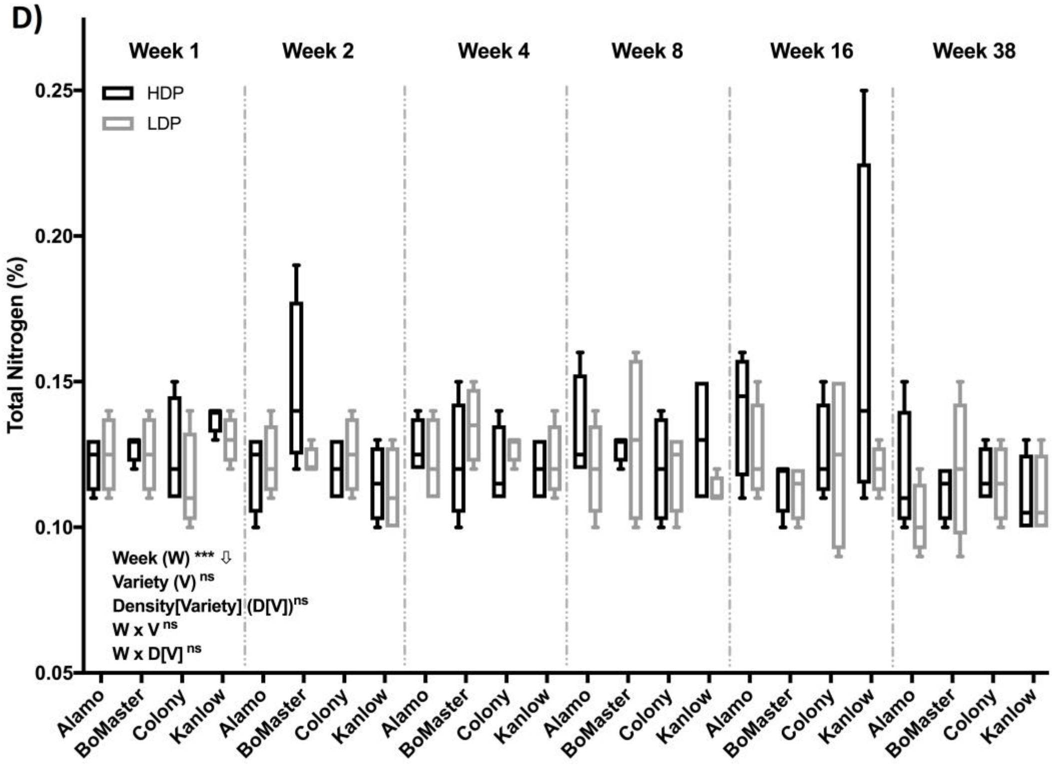
B)


25
20
15
10
5
0
Soil NH$_4^+$ (ppm)
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
Week (W) *** ⇧
Variety (V) ^{ns}
Density[Variety] (D[V])^{ns}
W x V ^{ns}
W x D[V] ^{ns}
HDP
LDP
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

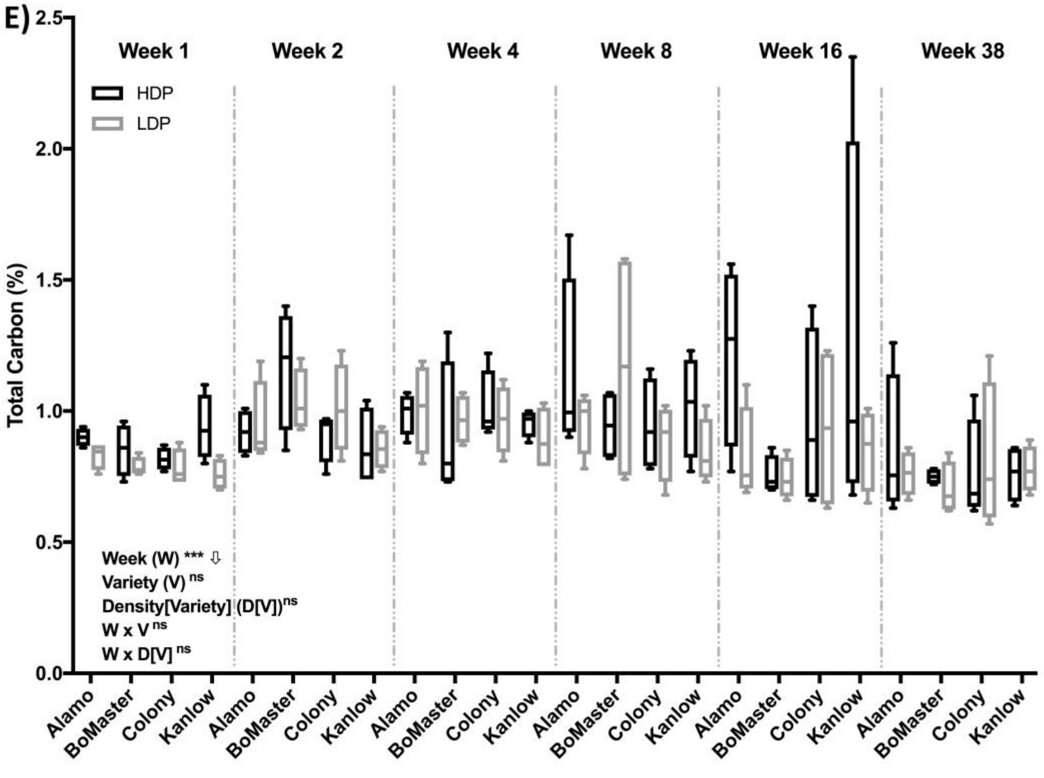
C)


15
10
5
0
Soil NO$_3^-$ (ppm)
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
Week (W) *** ⇧
Variety (V) ^{ns}
Density[Variety] (D[V])^{ns}
W x V *
W x D[V] ^{ns}
HDP
LDP
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

D)


Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Total Nitrogen (%)
0.25
0.20
0.15
0.10
0.05
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

E)


Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Total Carbon (%)
2.5
2.0
1.5
1.0
0.5
0.0
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

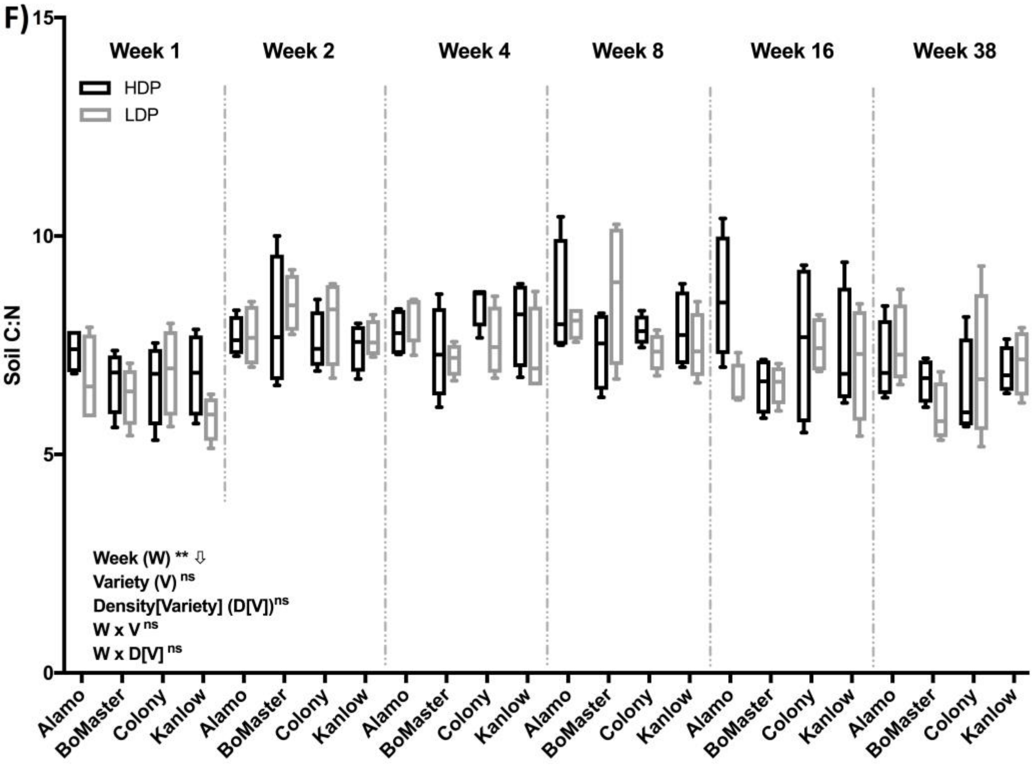
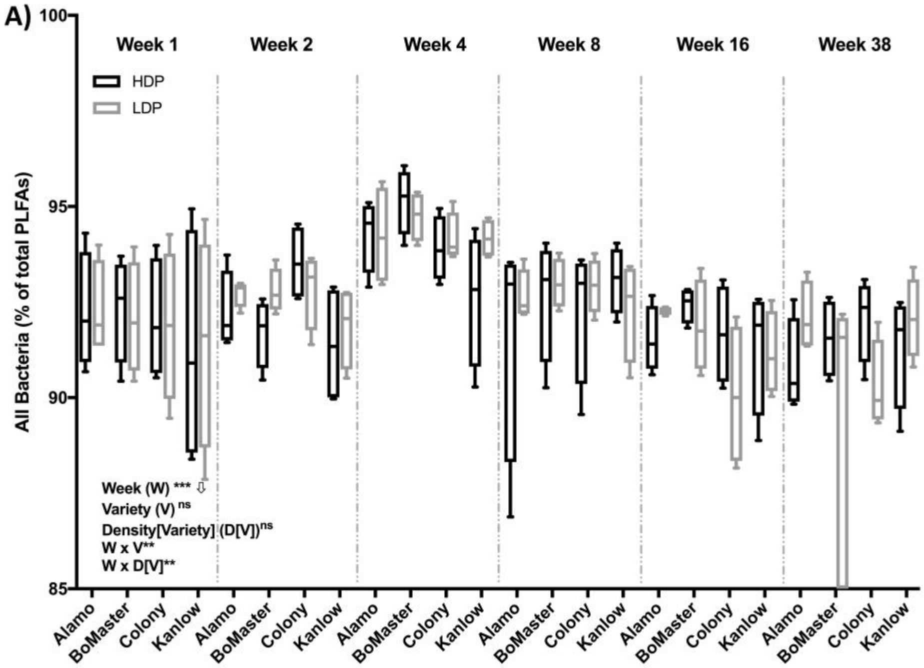

F)
15
10
5
0
Soil C:N
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) ** ⇩
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

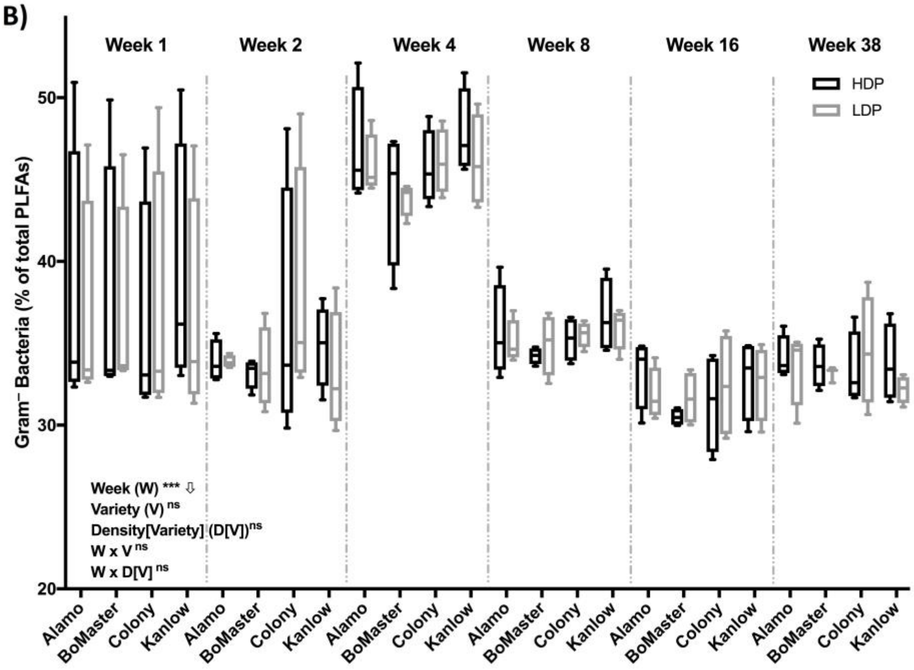
Figure 3.3.

PLFAs Dynamics over the Growing Season

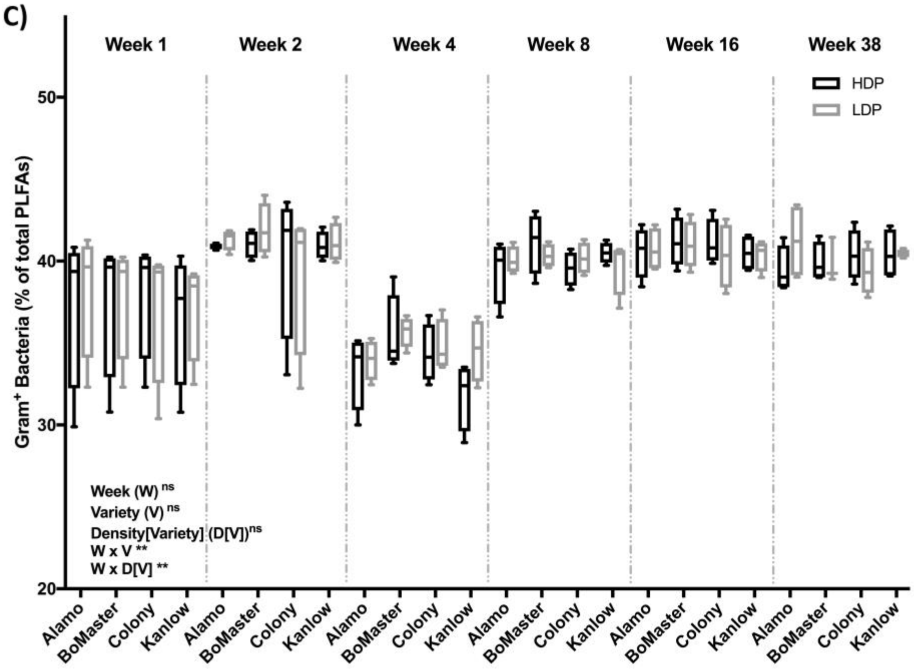
The parameters: (A) All Bacteria (B) Gram- bacteria (C) Gram+ bacteria (D) Actinobacteria (E) All fungi (F) AM fungi (G) Fungi:Bactera were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects “Week” (W) “Variety” (V) “Density[Variety]” D[V] interactions and “Block” as a random effect ns = P ≥ 0.05; * = 0.05 > P ≥ 0.01; ** = 0.01 > P ≥ 0.001; *** = 0.001 > P



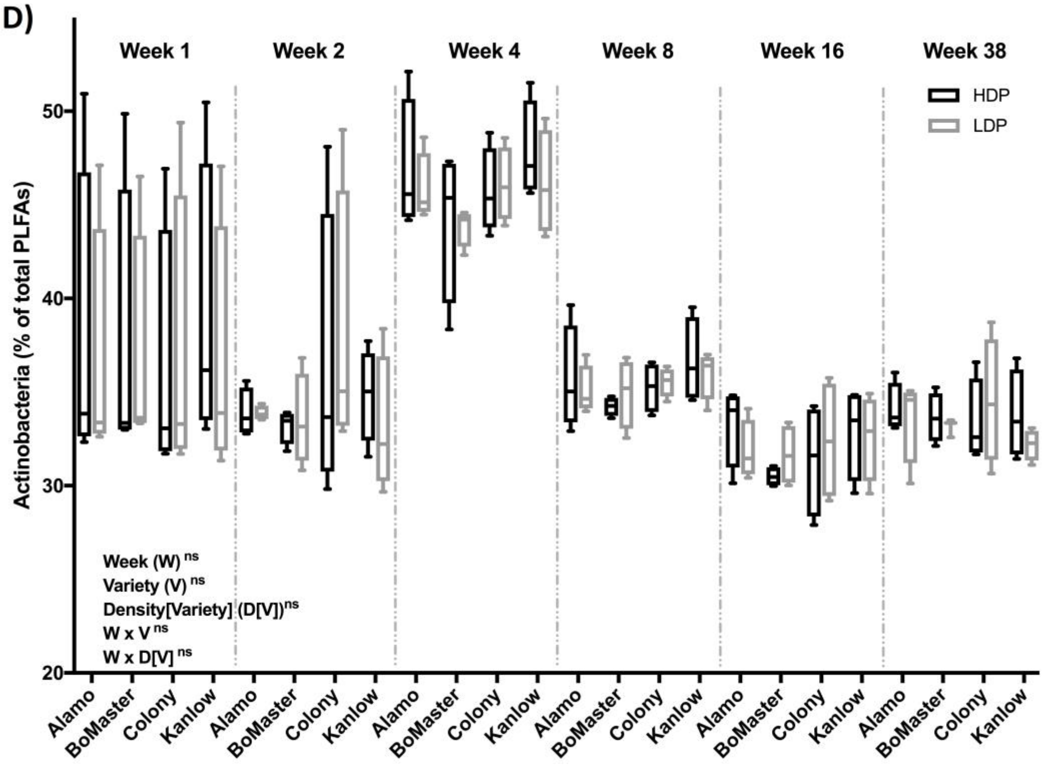
B)


Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Gram⁻ Bacteria (% of total PLFAs)
50
40
30
20
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

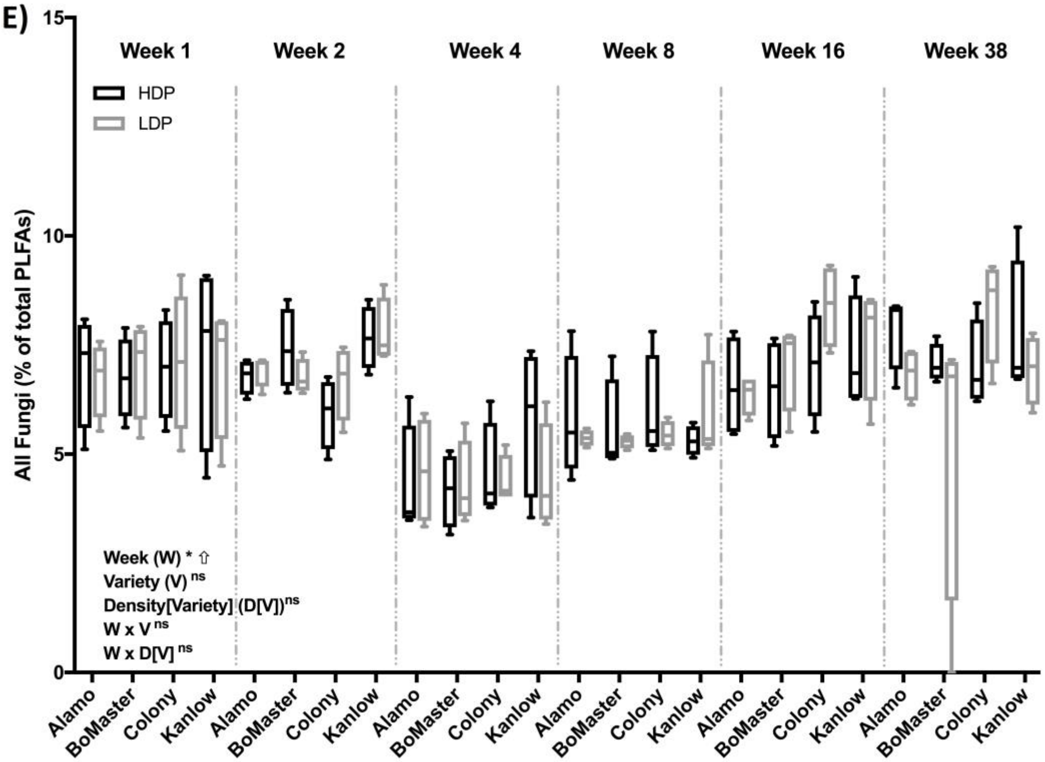
C)

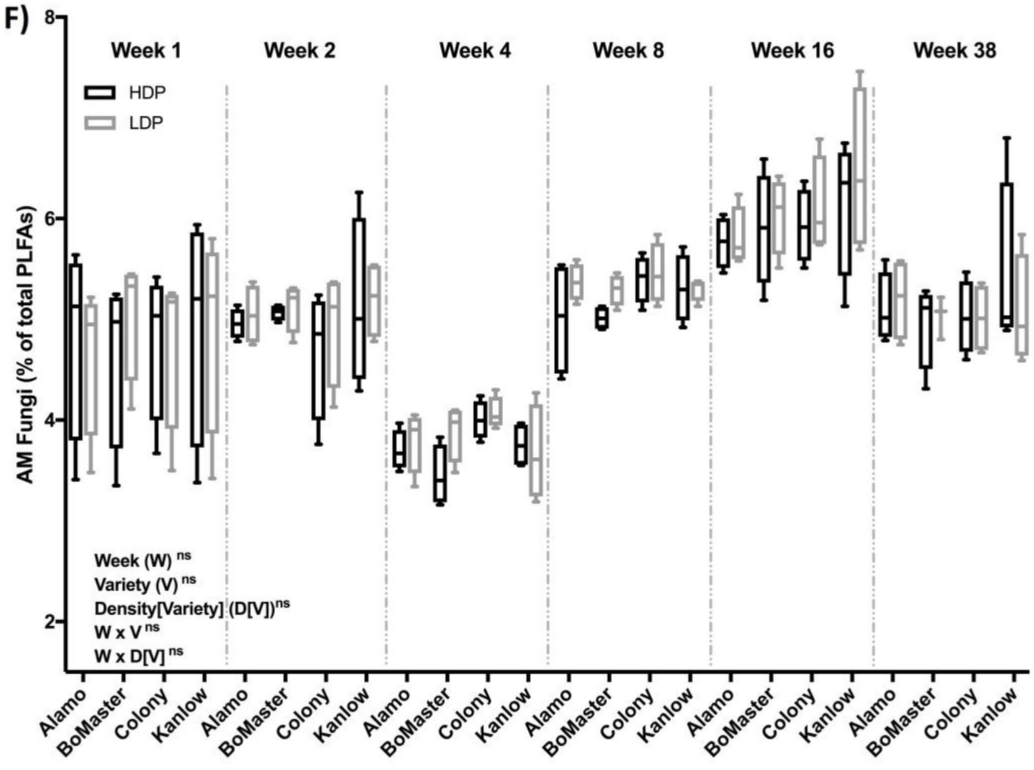

Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Gram⁺ Bacteria (% of total PLFAs)
50
40
30
20
Week (W) ns
Variety (V) ns
Density[Variety] (D[V])ns
W x V **
W x D[V] **
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

D)


Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Actinobacteria (% of total PLFAs)
50
40
30
20
Week (W) ns
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

E)


Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
All Fungi (% of total PLFAs)
15
10
5
0
Week (W) * ⇧
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow


F)
AM Fungi (% of total PLFAs)
8
6
4
2
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) ns
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

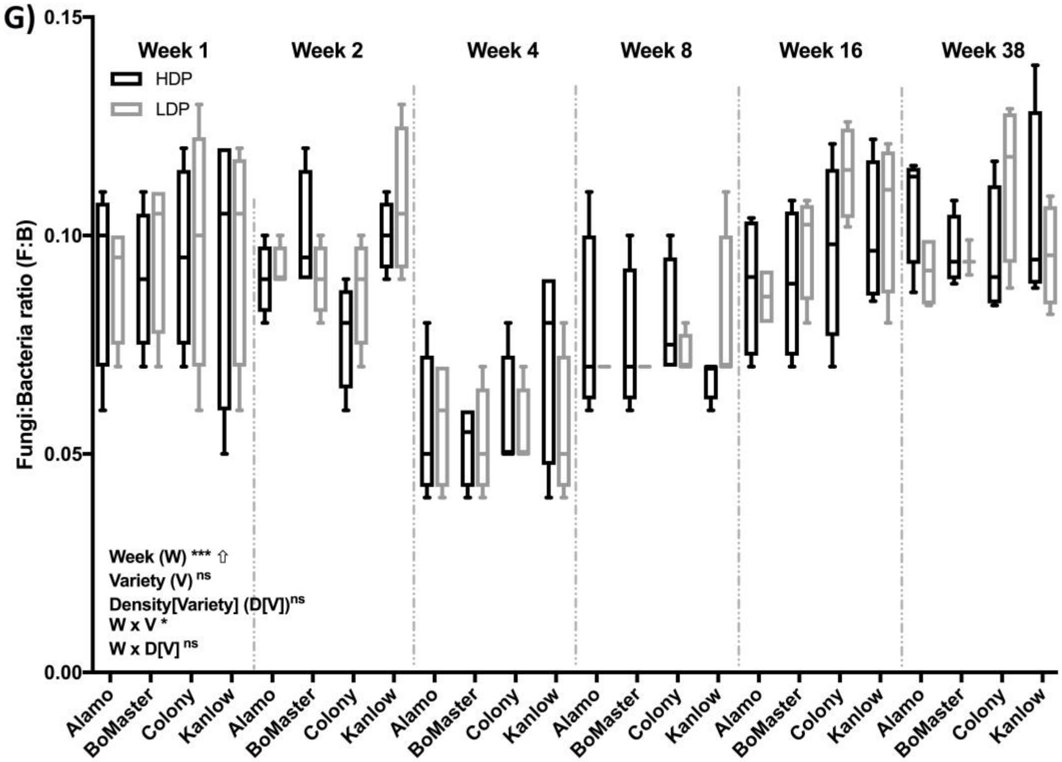
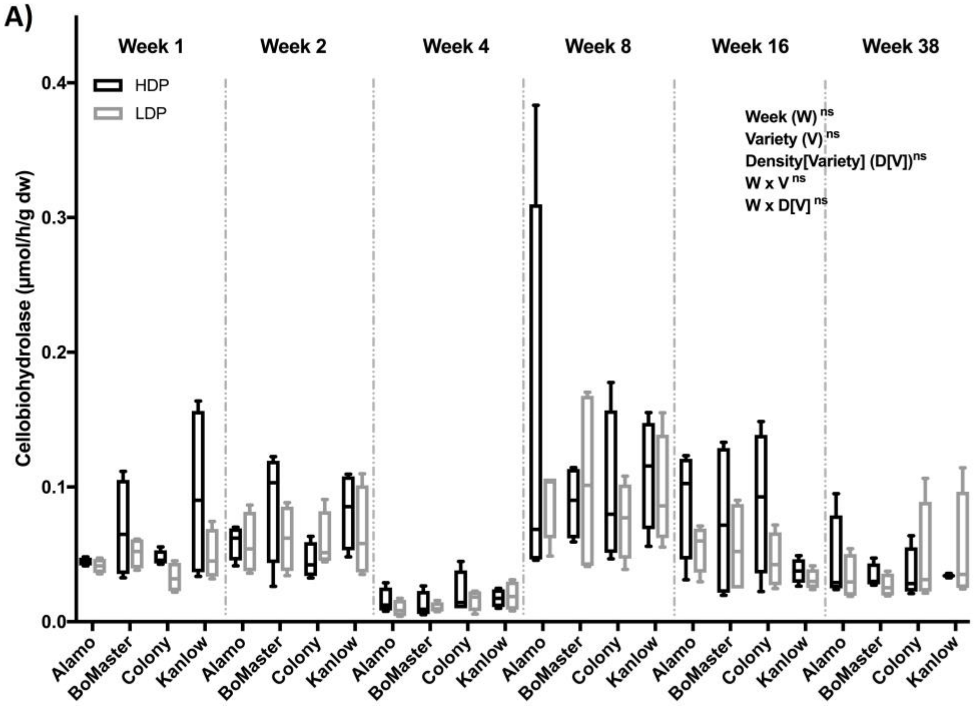

G)
Fungi:Bacteria ratio (F:B)
0.15
0.10
0.05
0.00
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇧
Variety (V) ns
Density[Variety] (D[V])ns
W x V *
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

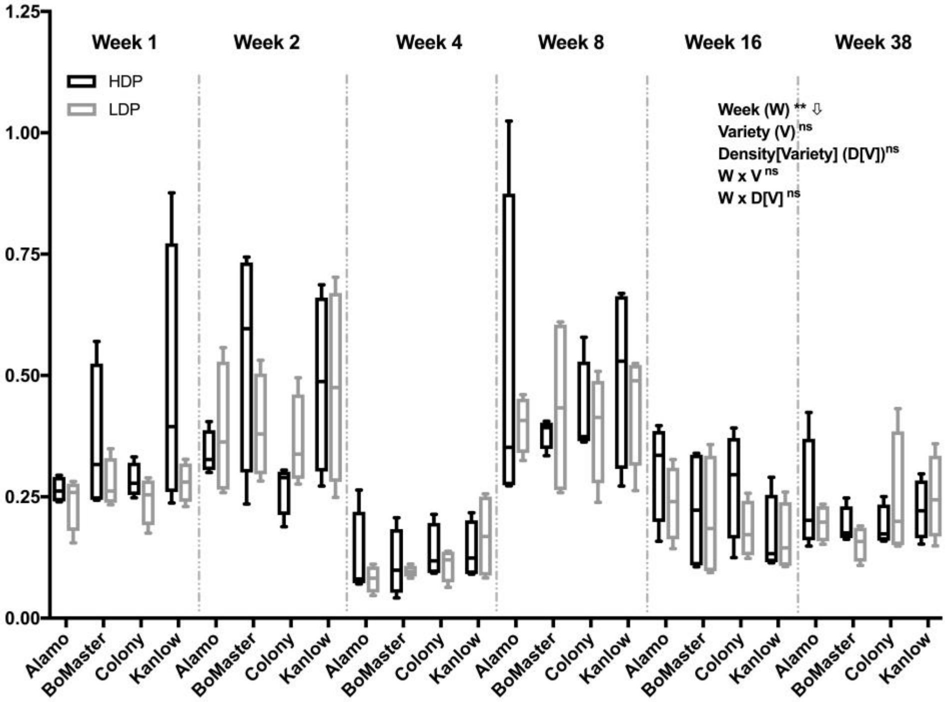
Figure 3.4.

EEAs Dynamics over the Growing Season

Temporal dynamics of extracellular enzyme activities (µmol h^{-1} g^{-1} dw) in soils of four Panicum virgatum cultivars (Alamo, Bomaster, Colony, and Kanlow) The parameters (A) Cellobiohydrolase (CBH), (B) β-glucosidase (βG), (C) N-acetylglucosaminadase (NAG), (D) Phosphatase (Phos) were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects “Variety” (V) “Density[Variety]” D[V] interactions and “Block” as a random effect ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

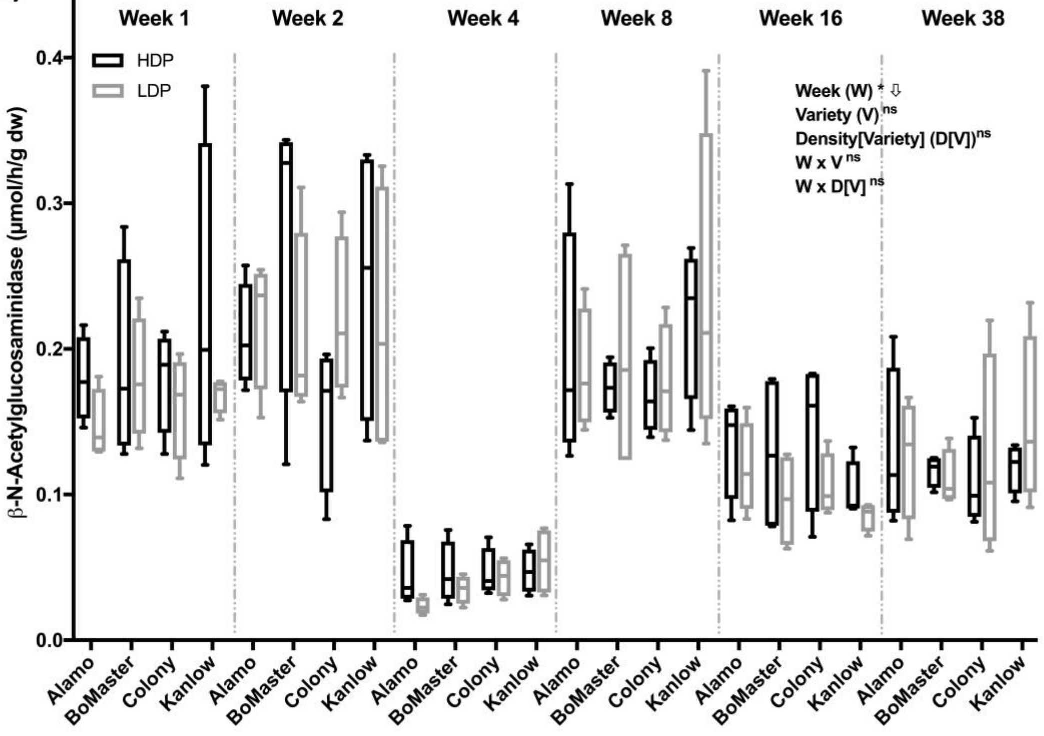


B)



1.25
1.00
0.75
0.50
0.25
0.00
β-Glucosidase (μmol/h/g dw)
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) ** ⇩
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

C)



0.4
0.3
0.2
0.1
0.0
β-N-Acetylglucosaminidase (μmol/h/g dw)
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) * ⇩
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

D) There is a significant categorical Week effect F5,141 = 154.90; P < 0.0001

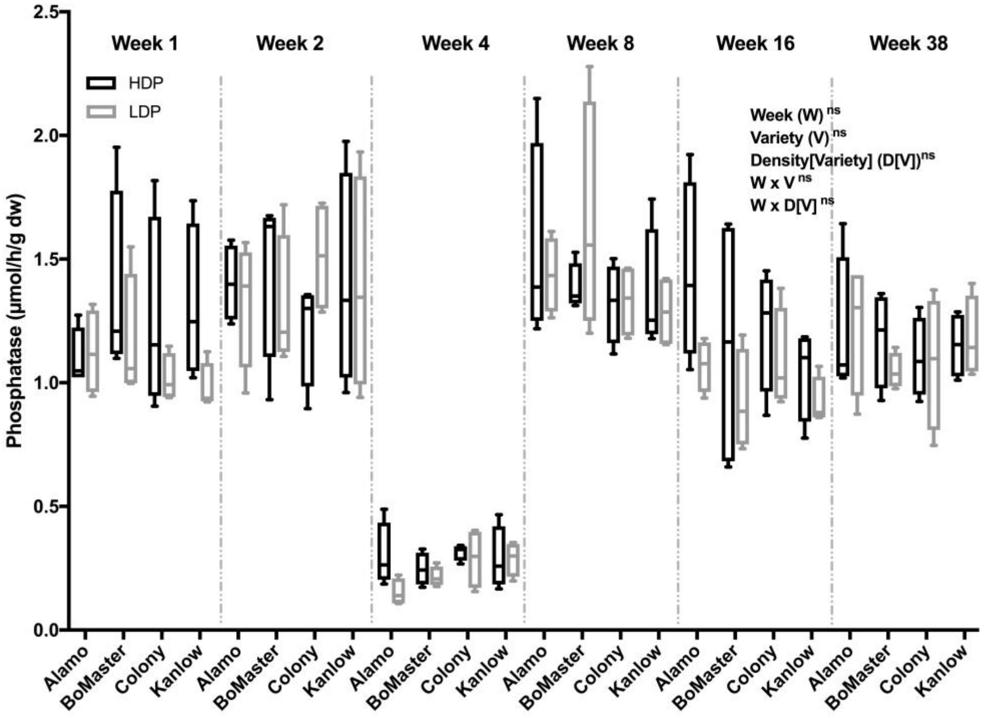


Table 3.4.

***Bacterial Alpha Diversity*.**

Bacterial observed (S_{Obs}) and extrapolative (Chao 1) richness, diversity (Shannon's H') and evenness (E_H) in roots and soils of four Panicum virgatum cultivars (Alamo, Bomaster, Colony, and Kanlow) grown under conservation agriculture management after being sown in high or low seeding densities (mean ± standard deviation). The parameters were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects "Variety" (V) "Density[Variety]" D[V] and "Block" as a random effect with 3 degrees freedom for numerator for "Variety" and 4 degrees freedom for numerator for "Density[Variety]" with 21 degrees of freedom for the denominator. For each estimate, the upper case letters indicate pairwise Student's t-test comparisons of cultivars, the lower case letters identify differences in planting densities for that cultivar. ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$.

	Alamo		**Bomaster**		**Colony**		**Kanlow**	
	HDP	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**
Roots - Week 1								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.76±0.11 $^{A\ a}$	0.68±0.01 $^{A\ a}$	0.75±0.1 $^{A\ a}$	0.68±0.03 $^{A\ a}$	0.69±0.02 $^{A\ a}$	0.65±0.04 $^{A\ a}$	0.71±0.09 $^{A\ a}$	0.75±0.08 $^{A\ a}$
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	1030.68±408.73 $^{A\ a}$	1275.36±74.53 $^{A\ a}$	1016.45±355.01 $^{A\ a}$	1282.25±111 $^{A\ a}$	1211.51±108.74 $^{A\ a}$	1409.89±143.12 $^{A\ a}$	1190.94±360.15 $^{A\ a}$	1037.52±290.71 $^{A\ a}$
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	2389.06±1113.97 $^{A\ a}$	3229.8±86.75 $^{A\ a}$	2477.62±1002.95 $^{A\ a}$	3268.5±189.42 $^{A\ a}$	3106.94±156.83 $^{A\ a}$	3472.61±333.51 $^{A\ a}$	2905.71±854.13 $^{A\ a}$	2560.96±767.61 $^{A\ a}$
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	5.86±1.07 $^{A\ a}$	6.42±0.26 $^{A\ a}$	5.76±0.84 $^{A\ a}$	6.32±0.35 $^{A\ a}$	6.07±0.52 $^{A\ a}$	6.73±0.32 $^{A\ a}$	6.38±0.73 $^{A\ a}$	5.85±0.66 $^{A\ a}$

Evenness(E_H) ***V(ns) D[V] (ns)***	0.85±0.1 $^{\text{A a}}$	0.9±0.03 $^{\text{A a}}$	0.83±0.09 $^{\text{A a}}$	0.88±0.04 $^{\text{A a}}$	0.86±0.06 $^{\text{A a}}$	0.93±0.03 $^{\text{A a}}$	0.9±0.06 $^{\text{A a}}$	0.84±0.06 $^{\text{A a}}$
Roots - Week 2								
Coverage ***V(ns) D[V] (ns)***	0.71±0.1 $^{\text{A a}}$	0.67±0.01 $^{\text{A a}}$	0.67±0.03 $^{\text{A a}}$	0.67±0.03 $^{\text{A a}}$	0.69±0.03 $^{\text{A a}}$	0.67±0.02 $^{\text{A a}}$	0.75±0.08 $^{\text{A a}}$	0.68±0.01 $^{\text{A a}}$
S_{Obs} $^{\textit{V(ns) D[V]}}$ ***(ns)***	1187.66±342.79 $^{\text{A a}}$	1318.61±62.69 $^{\text{A a}}$	1323.8±116.84 $^{\text{A a}}$	1327.99±153.71 $^{\text{A a}}$	1269.89±96.85 $^{\text{A a}}$	1336.01±109.12 $^{\text{A a}}$	1091.67±280.58 $^{\text{A a}}$	1310.73±51.85 $^{\text{A a}}$
Chao 1 $^{\textit{V(ns)}}$ ***D[V] (ns)***	2846.46±1029.1 $^{\text{A a}}$	3252.27±131.98 $^{\text{A a}}$	3289.94±247.17 $^{\text{A a}}$	3331.37±230.76 $^{\text{A a}}$	3139.62±305.16 $^{\text{A a}}$	3384.5±100.09 $^{\text{A a}}$	2437.78±788.81 $^{\text{A a}}$	3239.9±148.11 $^{\text{A a}}$
Diversity (H') $^{\textit{V(ns) D[V]}}$ ***(ns)***	6.38±0.62 $^{\text{A a}}$	6.61±0.15 $^{\text{A a}}$	6.58±0.28 $^{\text{A a}}$	6.53±0.44 $^{\text{A a}}$	6.53±0.18 $^{\text{A a}}$	6.64±0.25 $^{\text{A a}}$	6.27±0.53 $^{\text{A a}}$	6.59±0.13 $^{\text{A a}}$
Evenness (E_H) $^{\textit{V(ns) D[V]}}$ ***(ns)***	0.9±0.05 $^{\text{A a}}$	0.92±0.02 $^{\text{A a}}$	0.92±0.03 $^{\text{A a}}$	0.91±0.05 $^{\text{A a}}$	0.91±0.02 $^{\text{A a}}$	0.92±0.02 $^{\text{A a}}$	0.9±0.04 $^{\text{A a}}$	0.92±0.01 A a
Roots - Week 4								
Coverage ***V(ns) D[V] (ns)***	0.71±0.1 A a	0.75±0.07 A a	0.73±0.12 A a	0.7±0.1 A a	0.72±0.09 A a	0.72±0.11 A a	0.73±0.11 A a	0.76±0.04 A a
S_{Obs} $^{\textit{V(ns) D[V]}}$ ***(ns)***	1219.05±330.17 A a	1068.17±223.67 A a	1144.16±435.54 A a	1225.84±378.09 A a	1170.58±295.74 A a	1158.67±354.17 A a	1120.3±392.04 A a	1049.62±145.94 A a

Chao 1 $^{V(ns)\ D[V]\ (ns)}$	2782.91±1031.36 A a	2403.52±686.5 A a	2683.35±1148.07 A a	2911.89±922.65 A a	2757.09±864.61 A a	2711.27±1035.77 A a	2607.45±1025.68 A a	2385.27±456.23 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.52±0.46 A a	6.19±0.4 A a	6.13±1.11 A a	6.12±1.33 A a	6.29±0.54 A a	6.32±0.59 A a	6.23±0.86 A a	6.22±0.32 A a
Evenness $(E_H)^{V(ns)\ D[V]\ (ns)}$	0.92±0.03 A a	0.89±0.03 A a	0.87±0.11 A a	0.86±0.15 A a	0.89±0.04 A a	0.9±0.05 A a	0.89±0.08 A a	0.89±0.03 A a
Roots - Week 8								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.79±0.04 A a	0.82±0.04 A a	0.84±0.05 A a	0.79±0.02 A a	0.8±0.04 A a	0.79±0.03 A a	0.81±0.05 A a	0.81±0.05 A a
$S_{Obs}^{V(ns)\ D[V]\ (ns)}$	941.21±137.21 A a	821.15±181.78 A a	764.5±247.64 A a	960.73±74.64 A a	918.06±175.45 A a	920.92±153.72 A a	869.25±232.23 A a	864.34±224.61 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	1976.67±373.05 A a	1788.1±386.88 A a	1530.42±444.19 A a	2012.87±163.93 A a	1919.77±278.32 A a	1979.86±298.4 A a	1766.87±485.77 A a	1783.49±463.42 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	5.94±0.5 A a	5.65±0.5 A a	5.38±1.14 A a	6.05±0.2 A a	5.92±0.55 A a	5.77±0.72 A a	5.78±0.77 A a	5.79±0.72 A a
Evenness $(E_H)^{V(ns)\ D[V]\ (ns)}$	0.87±0.06 A a	0.84±0.05 A a	0.81±0.13 A a	0.88±0.02 A a	0.87±0.06 A a	0.85±0.09 A a	0.86±0.08 A a	0.86±0.07 A a

Roots - Week 16								
Coverage ***V(ns) D[V] (ns)***	0.81±0.03 A a	0.8±0.02 A a	0.8±0.01 A a	0.8±0.02 A a	0.81±0.04 A a	0.82±0.03 A a	0.82±0.03 A a	0.77±0.02 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	893.26±136.48 A a	933.51±93.6 A a	959±34.02 A a	920.51±81.62 A a	898±212.3 A a	873.04±116.88 A a	852.39±138.78 A a	1043.87±67.58 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	1777.94±310.27 A a	1896.88±195.9 A a	1917.25±90.56 A a	1878.16±206.24 A a	1777.2±396.04 A a	1761.14±317.35 A a	1677.85±256.39 A a	2179.46±167.35 A a
Diversity (H') $^{V(ns)\ D[V]}$ ***(ns)***	6.02±0.36 A a	6.02±0.27 A a	6.13±0.13 A a	6.02±0.32 A a	5.73±1.06 A a	5.96±0.26 A a	5.95±0.41 A a	6.31±0.15 A a
Evenness (E_H) $^{V(ns)\ D[V]}$ ***(ns)***	0.89±0.03 A a	0.88±0.03 A a	0.89±0.02 A a	0.88±0.04 A a	0.84±0.13 A a	0.88±0.02 A a	0.88±0.04 A a	0.91±0.01 A a

Roots - Week 38								
Coverage ***V(ns) D[V] (ns)***	0.82±0.03 A a	0.82±0.02 A a	0.81±0.05 A a	0.83±0.02 A a	0.81±0.02 A a	0.83±0.02 A a	0.79±0.1 A a	0.8±0.05 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	814.89±130.53 A a	807.7±74.66 A a	832.96±205.53 A a	776.37±84.09 A a	869.67±115.1 A a	774.15±115.17 A a	917.36±359.15 A a	936.31±205.53 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	1749.37±218.35 A a	1758.17±140.94 A a	1843.16±496.41 A a	1650.52±203.48 A a	1820.11±219.04 A a	1671.85±244.85 A a	2016.6±913.62 A a	1921.95±427.46 A a

Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	5.45±0.66 A a	5.44±0.49 A a	5.47±1 A a	5.45±0.33 A a	5.82±0.38 A a	5.31±0.59 A a	5.67±0.83 A a	5.9±0.55 A a
Evenness ***(*** E_H ***)*** $^{V(ns)\ D[V]\ (ns)}$	0.81±0.08 A a	0.81±0.06 A a	0.81±0.12 A a	0.82±0.04 A a	0.86±0.04 A a	0.8±0.07 A a	0.83±0.08 A a	0.86±0.05 A a
Soil - Week 1								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.64±0.04 A a	0.62±0.01 A a	0.62±0.01 A a	0.61±0.01 A a	0.62±0.01 A a	0.62±0.02 A a	0.62±0.03 A a	0.62±0 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	1451.84±118.15 A a	1521.75±45.77 A a	1511.93±31.21 A a	1558.84±26.68 A a	1524.3±45.57 A a	1504.9±76.96 A a	1513.48±93.22 A a	1520.58±22.07 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	3412.14±474.84 A a	3663.42±129.14 A a	3589.7±78.2 A a	3774.54±103.64 A a	3743.2±79.83 A a	3628.19±218.39 A a	3681.51±254.33 A a	3653.31±116.67 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.85±0.14 A a	6.95±0.09 A a	6.94±0.07 A a	6.99±0.06 A a	6.94±0.1 A a	6.93±0.12 A a	6.93±0.17 A a	6.95±0.07 A a
Evenness ***(*** E_H ***)*** $^{V(ns)\ D[V]\ (ns)}$	0.94±0.01 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0.01 A a
Soil - Week 2								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.62±0.01 A a	0.62±0.01 A a	0.63±0.02 A a	0.62±0 A a	0.63±0.01 A a	0.62±0.01 A a	0.64±0.01 A a	0.63±0.01 A a

S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	1507.35±41.84 A a	1507.14±26.62 A a	1474.6±60.97 A a	1514.76±16.49 A a	1481.45±12.86 A a	1515.87±14.24 A a	1471.1±33.66 A a	1467.6±42.13 A a
Chao 1 $^{V(*)\ D[V]\ (ns)}$	3721.48±191.77 B a	3674.49±46.94 B a	3548.85±195.44 AB a	3668.52±59.81 AB a	3591.05±72.82 AB a	3754.56±114.23 AB a	3506.93±92.1 A a	3543.67±116.34 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.91±0.08 A a	6.94±0.06 A a	6.87±0.12 A a	6.94±0.03 A a	6.89±0.03 A a	6.93±0.02 A a	6.89±0.06 A a	6.88±0.05 A a
Evenness (E_H) $^{V(ns)\ D[V]\ (ns)}$	0.94±0.01 A a	0.95±0.01 A a	0.94±0.01 A a	0.95±0 A a	0.94±0 A a	0.95±0 A a	0.94±0.01 A a	0.94±0 A a
Soil - Week 4								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.61±0.01 A a	0.61±0 A a	0.62±0.01 A a	0.61±0 A a	0.61±0.01 A a	0.61±0.01 A a	0.62±0.01 A a	0.62±0.01 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	1562.62±18.22 A a	1540.81±8.67 A a	1511.34±37.02 A a	1543.83±17.01 A a	1561.55±18.3 A a	1561.01±21.38 A a	1518.15±30.28 A a	1529.04±46.66 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	3812.3±126.9 A a	3771.15±85.77 A a	3641.99±137.2 A a	3765.31±45.4 A a	3819.38±70.17 A a	3772.1±104.99 A a	3706.34±167.02 A a	3689.13±147.02 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	7.02±0.02 A a	6.99±0.02 A a	6.93±0.08 A a	6.97±0.09 A a	7.02±0.03 A a	7.02±0.03 A a	6.96±0.03 A a	6.98±0.06 A a
Evenness (E_H) $^{V(ns)\ D[V]\ (ns)}$	0.95±0 A a	0.95±0 A a	0.95±0.01 A a	0.95±0.01 A a	0.95±0 A a	0.95±0 A a	0.95±0 A a	0.95±0 A a

Soil - Week 8								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.64±0.02 A a	0.62±0.01 A a	0.62±0.02 A a	0.63±0 A a	0.62±0 A a	0.62±0.01 A a	0.64±0.03 A a	0.63±0.03 A a
$S_{Obs}^{V(ns)\ D[V]\ (ns)}$	1461.85±55.96 A a	1501.52±41.37 A a	1527.11±82.48 A a	1502.12±10.94 A a	1522.41±4.29 A a	1510.84±47.32 A a	1460.91±89.97 A a	1485.43±100.34 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	3555.25±194.8 A a	3705.52±128.97 A a	3734.64±198.81 A a	3649.74±52.53 A a	3764.41±74.15 A a	3744.86±163.53 A a	3548.32±248.42 A a	3679.1±261.09 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.88±0.08 A a	6.92±0.05 A a	6.92±0.17 A a	6.93±0.02 A a	6.96±0.01 A a	6.92±0.1 A a	6.87±0.15 A a	6.89±0.16 A a
Evenness $(E_H)^{V(ns)\ D[V]\ (ns)}$	0.94±0.01 A a	0.95±0 A a	0.94±0.02 A a	0.95±0 A a	0.95±0 A a	0.94±0.01 A a	0.94±0.01 A a	0.94±0.01 A a
Soil - Week 16								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.66±0.02 A a	0.65±0 A a	0.65±0.01 A a	0.65±0.01 A a	0.65±0.02 A a	0.66±0.01 A a	0.64±0.01 A a	0.65±0.02 A a
$S_{Obs}^{V(ns)\ D[V]\ (ns)}$	1410.5±57.31 A a	1461.13±17.9 A a	1455.61±33 A a	1453.07±32 A a	1460.77±59.59 A a	1431.31±31.08 A a	1465.43±33.46 A a	1431.94±65.3 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	3193.04±178.89 A a	3367.69±25.35 A a	3304.42±119.62 A a	3295.06±142.08 A a	3335.82±171.84 A a	3270.97±110.44 A a	3377.95±47.79 A a	3276.91±188.73 A a

Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.84±0.1 A a	6.92±0.03 A a	6.9±0.04 A a	6.91±0.04 A a	6.88±0.15 A a	6.88±0.05 A a	6.92±0.06 A a	6.85±0.11 A a
Evenness (E_H) $^{V(ns)\ D[V]\ (ns)}$	0.94±0.01 A a	0.95±0 A a	0.95±0 A a	0.95±0 A a	0.94±0.02 A a	0.95±0 A a	0.95±0.01 A a	0.94±0.01 A a

Soil - Week 38								
Coverage $^{V(ns)\ D[V]\ (ns)}$	0.71±0.04 A a	0.69±0.04 A a	0.71±0.09 A a	0.73±0.07 A a	0.68±0.03 A a	0.68±0.02 A a	0.69±0.04 A a	0.68±0.03 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	1249.03±147.07 A a	1304.41±139.2 A a	1199.48±348.97 A a	1168.64±252.29 A a	1346.2±94.45 A a	1336.26±75.38 A a	1321.74±104.5 A a	1338.45±72.79 A a
Chao 1 $^{V(ns)\ D[V]\ (ns)}$	2713.96±391.25 A a	2999.26±377.9 A a	2747.46±811.78 A a	2513.44±605.74 A a	3005±313.13 A a	2987.71±244.7 A a	2917.52±369.72 A a	2968.48±275.16 A a
Diversity (H') $^{V(ns)\ D[V]\ (ns)}$	6.62±0.21 A a	6.64±0.19 A a	6.32±0.89 A a	6.38±0.6 A a	6.75±0.11 A a	6.73±0.1 A a	6.73±0.13 A a	6.73±0.09 A a
Evenness (E_H) $^{V(ns)\ D[V]\ (ns)}$	0.93±0.01 A a	0.93±0.01 A a	0.89±0.09 A a	0.9±0.06 A a	0.94±0.01 A a	0.94±0.01 A a	0.94±0.01 A a	0.94±0.01 A a

Table 3.5.

Fungal Alpha Diversity.

Fungal observed (SObs) and extrapolative (Chao 1) richness, diversity (Shannon's H') and evenness (E_H) in roots and soils of four Panicum virgatum cultivars (Alamo, Bomaster, Colony, and Kanlow) grown under conservation agriculture management after being sown in high or low seeding densities (mean ± standard deviation). The parameters were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects "Variety" (V) "Density[Variety]" D[V] and "Block" as a random effect with 3 degrees freedom for numerator for "Variety" and 4 degrees freedom for numerator for "Density[Variety]" with 21 degrees of freedom for the denominator. For each estimate, the uppercase letters indicate pairwise Student's t-test comparisons of cultivars, the lowercase letters identify differences in planting densities for that cultivar. ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

	Alamo		**Bomaster**		**Colony**		**Kanlow**	
	HDP	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**	**HDP**	**LDP**
Roots - Week 1								
Coverage $^{V(ns)}$ ***D[V] (ns)***	0.99±0.00 A a	0.98±0.00 A a	0.98±0.00 A a	0.98±0.00 A a	0.99±0.00 A a	0.99±0.00 A a	0.98±0.00 A a	0.98±0.00 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	111.78±15.36 A a	109.83±15.48 A a	109.16±14.36 A a	104.59±24.36 A a	103.21±13.42 A a	92.82±33.89 A a	120.56±23.04 A a	105.52±19.33 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	168.73±18.57 A a	165.22±19.33 A a	165.9±31.94 A a	172.11±30.83 A a	164.39±28.2 A a	141.4±50.67 A a	190.42±29.01 A a	161±27.2 A a
Diversity (H') ***V(ns) D[V] (ns)***	3.02±0.22 A a	2.89±0.32 A a	2.87±0.08 A a	2.75±0.42 A a	2.7±0.16 A a	2.58±0.65 A a	2.88±0.32 A a	2.64±0.32 A a

Evenness (E_H) *V(ns) D[V] (ns)*	0.64±0.03 A a	0.62±0.05 A a	0.61±0.02 A a	0.59±0.06 A a	0.58±0.03 A a	0.57±0.1 A a	0.6±0.04 A a	0.57±0.07 A a
Roots - Week 2								
Coverage $^{V(**)}$ *D[V] (ns)*	0.98±0.00 A a	0.97±0.00 A a	0.98±0.00 A a	0.97±0.01 A a	0.98±0.00 AB a	0.98±0.01 AB a	0.99±0.01 B a	0.98±0.01 B a
S_{Obs} $^{V(**)\ D[V]\ (ns)}$	137.45±27.02 B a	160.72±21.17 B a	159.98±34.18 B a	165.83±24.46 B a	145.09±23.81 B a	112.82±37.61 B a	86.49±27.05 A a	120.54±38.29 A a
Chao 1 $^{V(**)}$ *D[V] (ns)*	242.76±44.6 B a	270.63±45.57 B a	258.05±50.42 B a	266.33±46.16 B a	238.79±40.48 AB a	180.06±58.44 AB a	154.03±63.64 A a	197.36±58.92 A a
Diversity (H') *V(*) D[V] (ns)*	2.83±0.4 AB a	3.25±0.31 AB a	3.09±0.54 B a	3.03±0.33 B a	3.1±0.16 B a	2.67±0.36 B a	2.14±0.7 A a	2.59±0.86 A a
Evenness (E_H) *V(ns) D[V] (ns)*	0.58±0.06 A a	0.64±0.05 A a	0.61±0.08 A a	0.59±0.05 A a	0.62±0.03 A a	0.57±0.04 A a	0.48±0.12 A a	0.54±0.15 A a
Roots - Week 4								
Coverage $^{V(ns)}$ *D[V] (ns)*	0.98±0.01 A a	0.98±0.00 A a	0.98±0.00 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.00 A a	0.98±0.00 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	134.61±39.36 A a	140±44.6 A a	125.96±9.64 A a	130.91±44.9 A a	153.96±34.33 A a	143.23±36.44 A a	122.71±19.45 A a	105.37±15.74 A a

Chao 1 $^{V(ns)}$ ***D[V] (ns)***	215.55±60.99 A a	224.13±56.01 A a	218.01±12.45 A a	225.65±77.11 A a	250.28±54.55 A a	243.7±50.74 A a	199.64±39.11 A a	186.62±19.6 A a
Diversity (H') ***V(ns) D[V] (ns)***	2.84±0.31 A a	2.6±1.39 A a	2.79±0.18 A a	2.78±0.42 A a	3.03±0.25 A a	2.72±0.58 A a	2.91±0.25 A a	2.43±0.54 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.58±0.03 A a	0.52±0.25 A a	0.58±0.03 A a	0.57±0.05 A a	0.6±0.03 A a	0.55±0.09 A a	0.61±0.04 A a	0.52±0.1 A a
Roots - Week 8								
Coverage $^{V(*)}$ ***D[V] (*)***	0.98±0.01 A b	0.98±0.01 A ab	0.98±0.01 AB ab	0.97±0.01 AB a	0.98±0.01 AB ab	0.98±0.00 AB ab	0.98±0.01 B ab	0.99±0.00 B ab
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	147.22±33.19 A a	112.75±58.63 A a	113.58±48.41 A a	164.29±35.93 A a	140.97±31.7 A a	146.19±23.12 A a	109.25±36.03 A a	93.28±29.41 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	249.78±51.91 A a	196.89±93.49 A a	189.81±72.08 A a	285.17±50.26 A a	231.28±49.29 A a	241.6±24.26 A a	190.61±58.73 A a	158.97±46.74 A a
Diversity (H') ***V(ns) D[V] (ns)***	2.71±0.57 A a	2.2±0.77 A a	2.8±0.69 A a	2.92±0.51 A a	2.9±0.31 A a	2.9±0.28 A a	2.72±0.46 A a	2.16±0.46 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.54±0.09 A a	0.47±0.11 A a	0.59±0.09 A a	0.57±0.08 A a	0.59±0.04 A a	0.58±0.04 A a	0.58±0.06 A a	0.48±0.07 A a
Roots - Week 16								

Coverage $^{V(ns)}$ ***D[V] (ns)***	0.98±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.00 A a	0.98±0.00 A a	0.97±0.01 A a
S_{Obs} ***V(ns) D[V] (ns)***	121.17±29.14 A a	120.15±89.01 A a	132.41±25.09 A a	130.3±39.28 A a	118.37±51.87 A a	144.01±24.41 A a	128.57±12.45 A a	161.96±52.68 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	205.99±60.03 A a	211.51±127.17 A a	235.52±56.73 A a	228.64±52.7 A a	205.75±72.5 A a	253.69±46.38 A a	227.08±17.8 A a	267.44±64.85 A a
Diversity (H') ***V(ns) D[V] (ns)***	2.45±0.22 A a	2.15±1.32 A a	2.68±0.43 A a	2.58±0.65 A a	2.5±0.52 A a	2.93±0.19 A a	2.82±0.45 A a	2.82±0.67 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.51±0.03 A a	0.45±0.21 A a	0.55±0.07 A a	0.53±0.11 A a	0.53±0.06 A a	0.59±0.03 A a	0.58±0.08 A a	0.56±0.12 A a

Roots - Week 38								
Coverage $^{V(ns)}$ ***D[V] (ns)***	0.97±0.00 A a	0.97±0.00 A a	0.97±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.98±0.01 A a	0.97±0.02 A a	0.97±0.02 A a
S_{Obs} ***V(ns) D[V] (ns)***	175.58±32.18 A a	165.27±21.15 A a	186.31±37.13 A a	105.71±54.06 A a	131.66±41.26 A a	149.13±63.25 A a	204.39±131.8 A a	188.08±121.75 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	288.69±32.13 A a	283.81±32.73 A a	321.76±68.14 A a	190.39±85.18 A a	222.28±63.05 A a	244.8±90.05 A a	352.21±221.42 A a	299.37±158.66 A a
Diversity (H') ***V(ns) D[V] (ns)***	3.46±0.39 A a	3.4±0.08 A a	3.29±0.25 A a	2.55±0.65 A a	2.62±0.67 A a	2.71±0.64 A a	3.21±1.04 A a	3.27±0.69 A a

Evenness (E_H) ***V(ns) D[V] (ns)***	0.67±0.06 A a	0.67±0.02 A a	0.63±0.03 A a	0.55±0.09 A a	0.54±0.11 A a	0.55±0.09 A a	0.61±0.15 A a	0.64±0.06 A a
Soil - Week 1								
Coverage $^{V(ns)}$ ***D[V] (ns)***	0.92±0.01 A a	0.92±0.01 A a	0.92±0.00 A a	0.91±0.01 A a	0.91±0.00 A a	0.92±0.01 A a	0.92±0.01 A a	0.92±0.00 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	483.85±26.1 A a	496.25±105.04 A a	493.69±15.75 A a	511.72±33.65 A a	530.2±17.87 A a	501.51±45.62 A a	436.89±60.35 A a	462.94±44.2 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	773.52±64.7 A a	790.67±114.65 A a	794.83±15.47 A a	831.06±61.21 A a	842.04±30.21 A a	794.27±71.81 A a	728.03±76.13 A a	763.76±43.3 A a
Diversity (H') ***V(ns) D[V] (ns)***	4.98±0.03 A a	4.79±0.92 A a	4.97±0.18 A a	4.98±0.1 A a	5.14±0.13 A a	4.92±0.52 A a	4.59±0.42 A a	4.76±0.36 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.81±0.01 A a	0.77±0.12 A a	0.8±0.03 A a	0.8±0.01 A a	0.82±0.02 A a	0.79±0.07 A a	0.76±0.05 A a	0.78±0.05 A a
Soil - Week 2								
Coverage $^{V(*)}$ ***D[V] (ns)***	0.92±0.01 A a	0.92±0.01 A a	0.92±0.01 A a	0.92±0.01 A a	0.92±0.00 AB a	0.92±0.00 AB a	0.94±0.01 B a	0.92±0.01 B a
S_{Obs} $^{V(***)\ D[V]}$ ***(ns)***	467.96±98.81 B a	501.38±56.16 B a	423.42±52.99 AB a	464.6±43.15 AB a	483.44±42.87 B a	491.73±11.82 B a	351.75±52.17 A a	445.14±64.58 A a

Chao 1 $^{V(***)}$ ***D[V] (ns)***	779.4±117.28 B a	809.51±54.91 B a	727.87±66.64 B a	783.51±53.92 B a	779.7±36.27 B a	793.63±32.13 B a	622.82±73.76 A a	752.78±94.17 A a
Diversity (H') ***V(ns) D[V] (ns)***	4.57±0.69 A a	5.01±0.33 A a	4.28±0.62 A a	4.73±0.34 A a	4.88±0.3 A a	4.86±0.18 A a	4.28±0.35 A a	4.68±0.3 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.74±0.09 A a	0.81±0.04 A a	0.71±0.09 A a	0.77±0.05 A a	0.79±0.04 A a	0.78±0.03 A a	0.73±0.04 A a	0.77±0.04 A a
Soil - Week 4								
Coverage $^{V(ns)}$ ***D[V] (ns)***	0.93±0.03 A a	0.92±0.01 A a	0.92±0.00 A a	0.92±0.01 A a	0.92±0.00 A a	0.92±0.01 A a	0.92±0.02 A a	0.93±0.01 A a
S_{Obs} $^{V(ns)\ D[V]\ (ns)}$	455.5±49.8 A a	476.05±83.3 A a	434.1±35.24 A a	460.37±64.03 A a	463.24±40.09 A a	428.63±57 A a	478.47±105.35 A a	400.48±39.55 A a
Chao 1 $^{V(ns)}$ ***D[V] (ns)***	727.04±187.91 A a	799.99±85.71 A a	772.27±29.88 A a	792.03±45.12 A a	782.48±44.07 A a	735.34±46.65 A a	801.83±144.59 A a	689.44±70.85 A a
Diversity (H') ***V(ns) D[V] (ns)***	4.84±0.26 A a	4.71±0.56 A a	4.32±0.47 A a	4.71±0.41 A a	4.72±0.41 A a	4.52±0.51 A a	4.72±0.68 A a	4.47±0.07 A a
Evenness (E_H) ***V(ns) D[V] (ns)***	0.79±0.04 A a	0.76±0.07 A a	0.71±0.07 A a	0.77±0.05 A a	0.77±0.06 A a	0.75±0.07 A a	0.76±0.08 A a	0.75±0.01 A a
Soil - Week 8								

Coverage $^{V (ns)}$ D[V] (ns)	0.93±0.01 A a	0.91±0.01 A a	0.91±0.00 A a	0.92±0.01 A a	0.92±0.01 A a	0.92±0.01 A a	0.93±0.02 A a	0.92±0.01 A a
S_{Obs} $^{V (ns)\ D[V]\ (ns)}$	360.41±102.71 A a	530.66±44.65 A a	492.85±12.54 A a	442.79±61.11 A a	462.35±62.8 A a	467.82±36.45 A a	419.57±83.07 A a	443.3±46.28 A a
Chao 1 $^{V (ns)}$ D[V] (ns)	648.56±133.21 A a	898.5±119.29 A a	818.06±22.38 A a	745.18±55 A a	767.25±79.7 A a	761.54±48.95 A a	715.43±135.81 A a	761.47±55.95 A a
Diversity (H') V(ns) D[V] (ns)	3.88±0.82 A a	4.93±0.27 A a	4.87±0.2 A a	4.52±0.47 A a	4.59±0.4 A a	4.72±0.4 A a	4.53±0.46 A a	4.51±0.27 A a
Evenness (E_H) V(ns) D[V] (ns)	0.66±0.11 A a	0.79±0.05 A a	0.79±0.03 A a	0.74±0.06 A a	0.75±0.05 A a	0.77±0.06 A a	0.75±0.06 A a	0.74±0.04 A a
Soil - Week 16								
Coverage $^{V (ns)}$ D[V] (ns)	0.93±0.01 A a	0.93±0.01 A a	0.93±0.01 A a	0.93±0.01 A a	0.93±0.00 A a	0.94±0.01 A a	0.93±0.01 A a	0.94±0.00 A a
S_{Obs} $^{V (ns)\ D[V]\ (ns)}$	403.31±57.49 A a	438.99±44.96 A a	423.34±36.04 A a	393.01±66.63 A a	451.14±22.97 A a	369.11±111.51 A a	415.19±60.01 A a	400.11±10.25 A a
Chao 1 $^{V (ns)}$ D[V] (ns)	655.48±61.4 A a	699.43±47.18 A a	688.64±43 A a	649.13±60.28 A a	708.83±24.64 A a	607.98±134.19 A a	666.95±84.83 A a	637.9±21.56 A a
Diversity (H') V(ns) D[V] (ns)	4.52±0.66 A a	4.7±0.39 A a	4.66±0.31 A a	4.02±0.97 A a	4.93±0.13 A a	4.24±0.87 A a	4.58±0.39 A a	4.63±0.25 A a

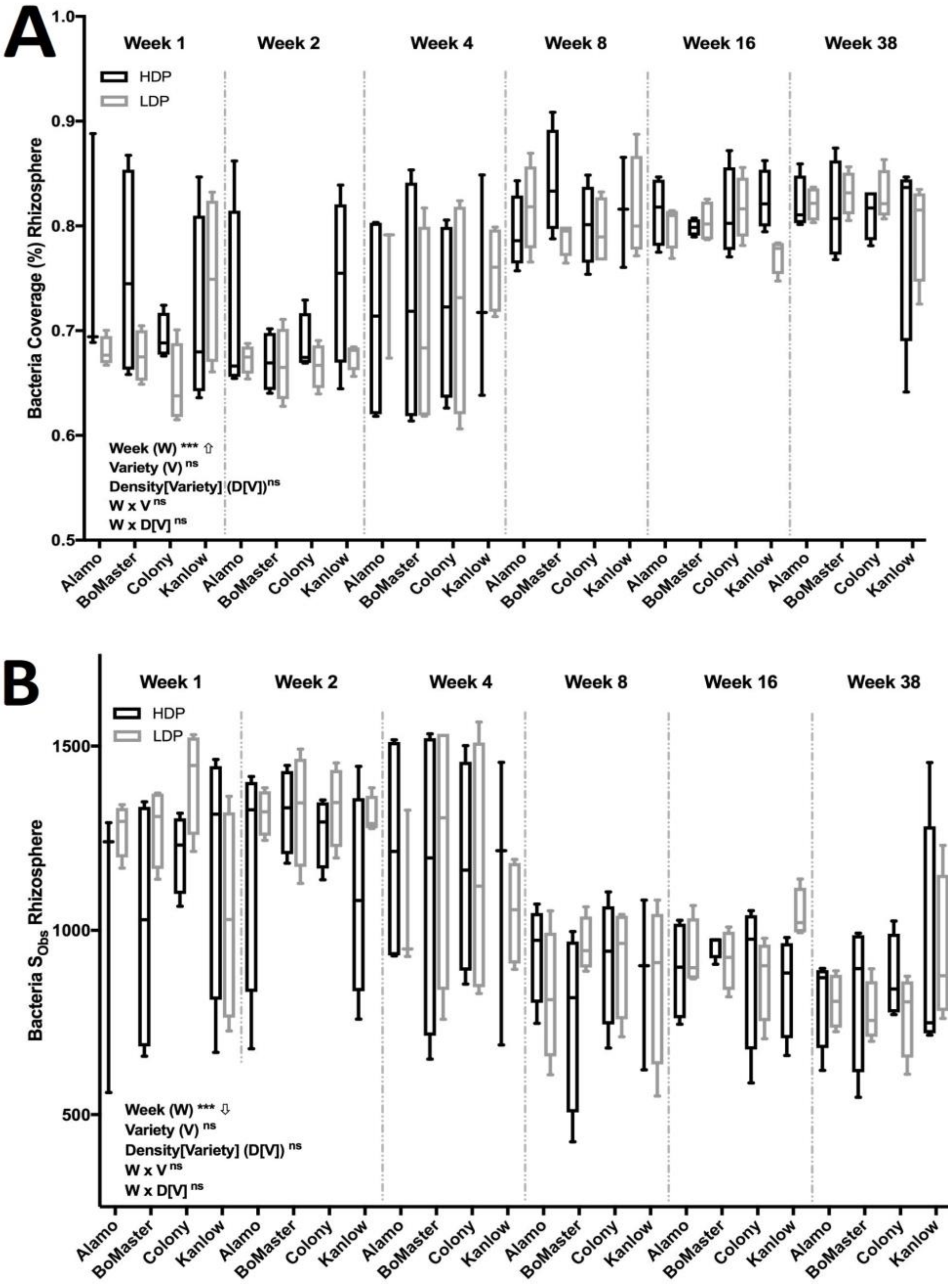
Evenness (E_H) *V(ns) D[V] (ns)*	0.75±0.1 A a	0.77±0.05 A a	0.77±0.05 A a	0.67±0.14 A a	0.81±0.02 A a	0.72±0.11 A a	0.76±0.05 A a	0.77±0.04 A a

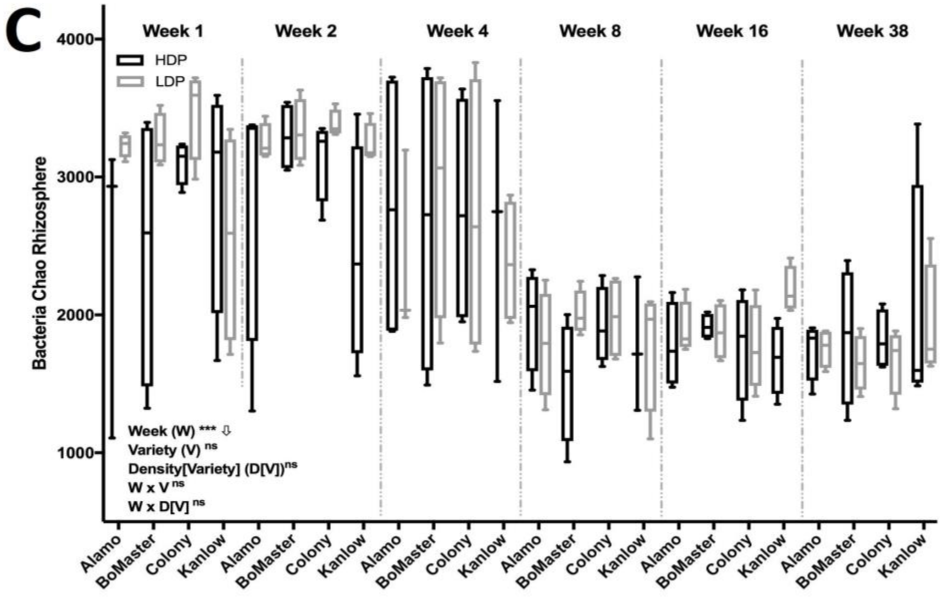
Soil - Week 38								
Coverage $^{V(ns)}$ *D[V] (ns)*	0.94±0.01 A a	0.93±0.01 A a	0.94±0.02 A a	0.95±0.02 A a	0.94±0.01 A a	0.94±0.01 A a	0.94±0.01 A a	0.94±0.01 A a
S_{Obs} *V(ns) D[V] (ns)*	342.59±66.36 A a	418.58±57.84 A a	349.74±155.21 A a	328.61±115.38 A a	375.44±109.8 A a	389.08±49.81 A a	417.69±47.56 A a	352.5±27.14 A a
Chao 1 $^{V(ns)}$ *D[V] (ns)*	535.07±93.29 A a	643.02±87.86 A a	555.21±228.78 A a	498.47±160.73 A a	575.73±120.32 A a	599.04±76.24 A a	616.38±84.83 A a	536.58±45.77 A a
Diversity (H') *V(ns) D[V] (ns)*	4.04±0.77 A a	4.7±0.36 A a	3.9±1.14 A a	4.18±0.64 A a	4.17±1.34 A a	4.47±0.47 A a	4.79±0.23 A a	4.13±0.28 A a
Evenness (E_H) *V(ns) D[V] (ns)*	0.69±0.12 A a	0.78±0.04 A a	0.67±0.15 A a	0.73±0.07 A a	0.7±0.2 A a	0.75±0.06 A a	0.79±0.03 A a	0.71±0.04 A a

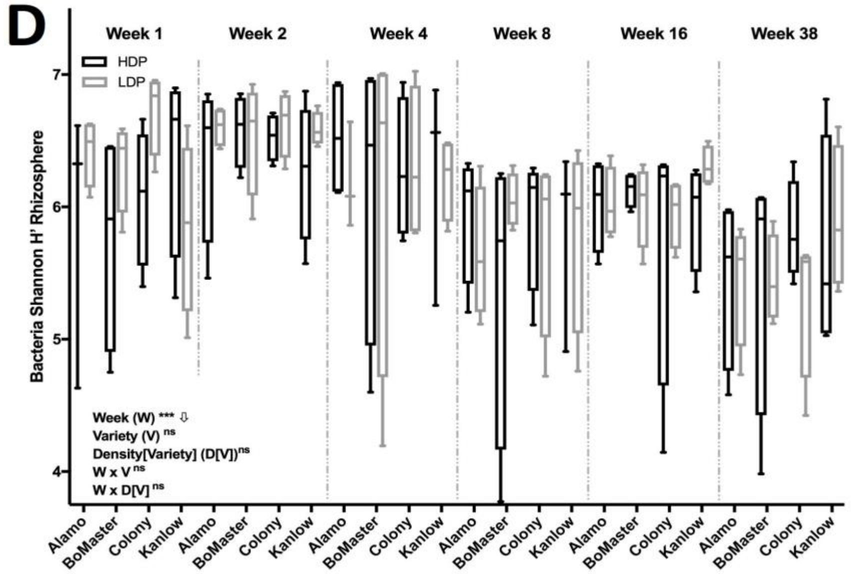
Figure 3.5.

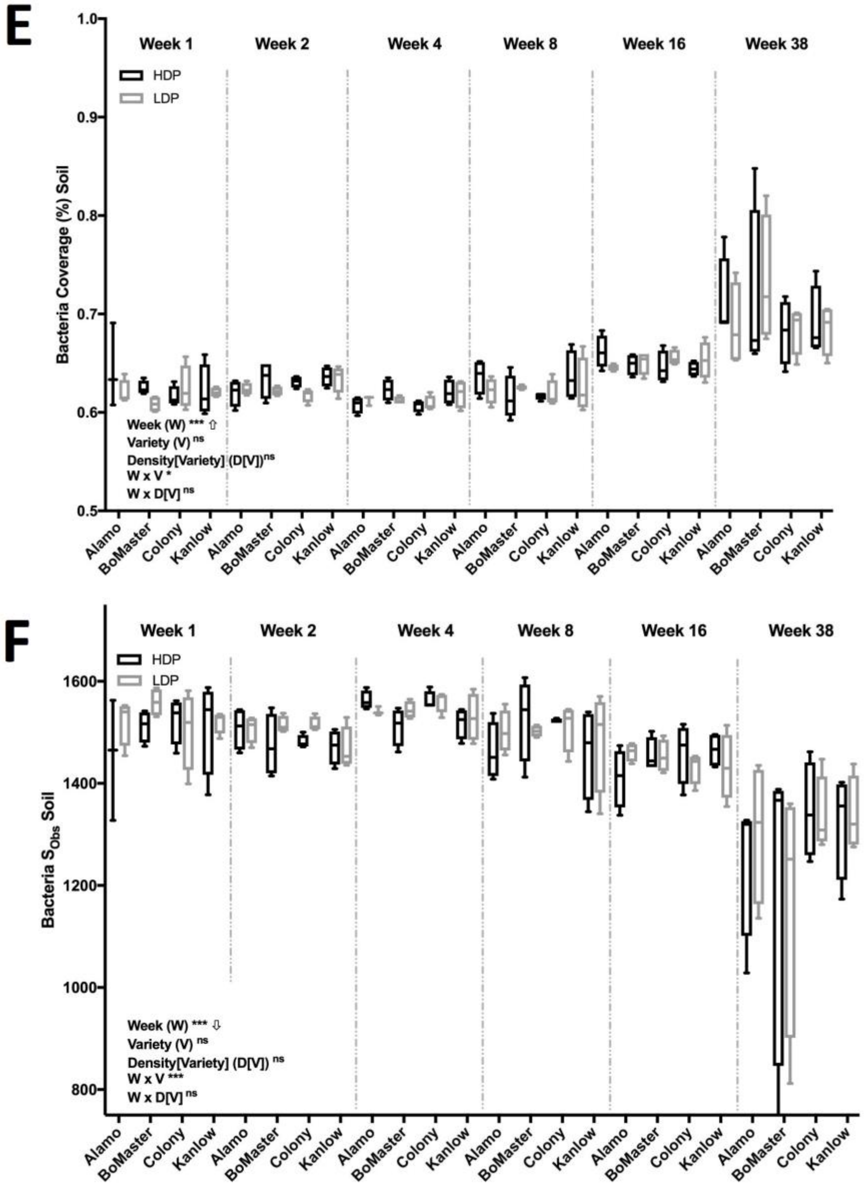
Temporal Dynamics of Bacterial Alpha Diversity Metrics

The parameters: Coverage, S_{Obs}, Chao 1, Shannon $_{H'}$ and Shannon E_H were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects “Week” (W) “Variety” (V) “Density[Variety]” D[V] interactions and “Block” as a random effect ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

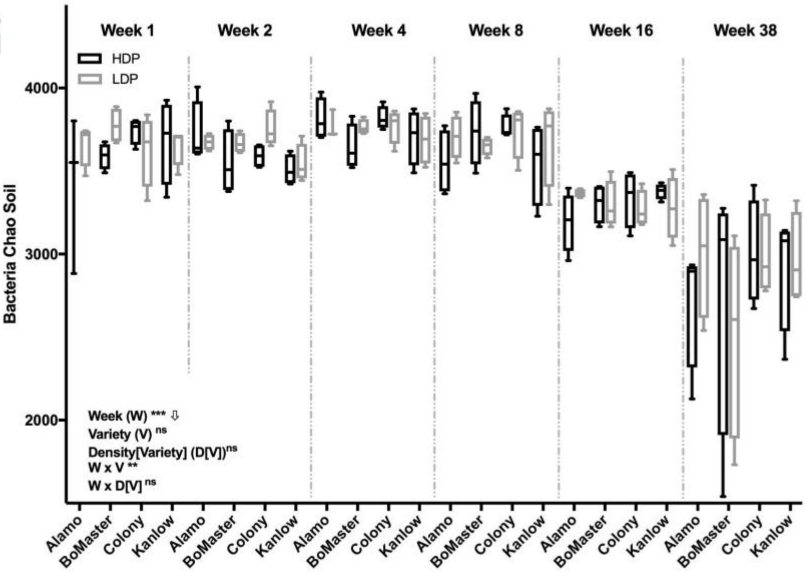



C
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Bacteria Chao Rhizosphere
4000
3000
2000
1000
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow


D
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Bacteria Shannon H' Rhizosphere
7
6
5
4
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

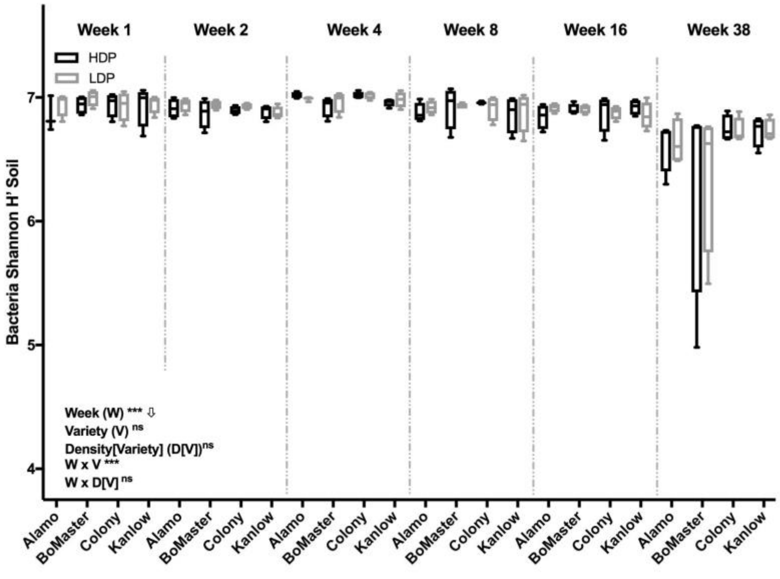

E
Bacteria Coverage (%) Soil
1.0
0.9
0.8
0.7
0.6
0.5
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇧
Variety (V) ns
Density[Variety] (D[V]) ns
W x V *
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
F
Bacteria S_Obs Soil
1600
1400
1200
1000
800
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ***
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow

G



Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Bacteria Chao Soil
4000
3000
2000
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V **
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

J

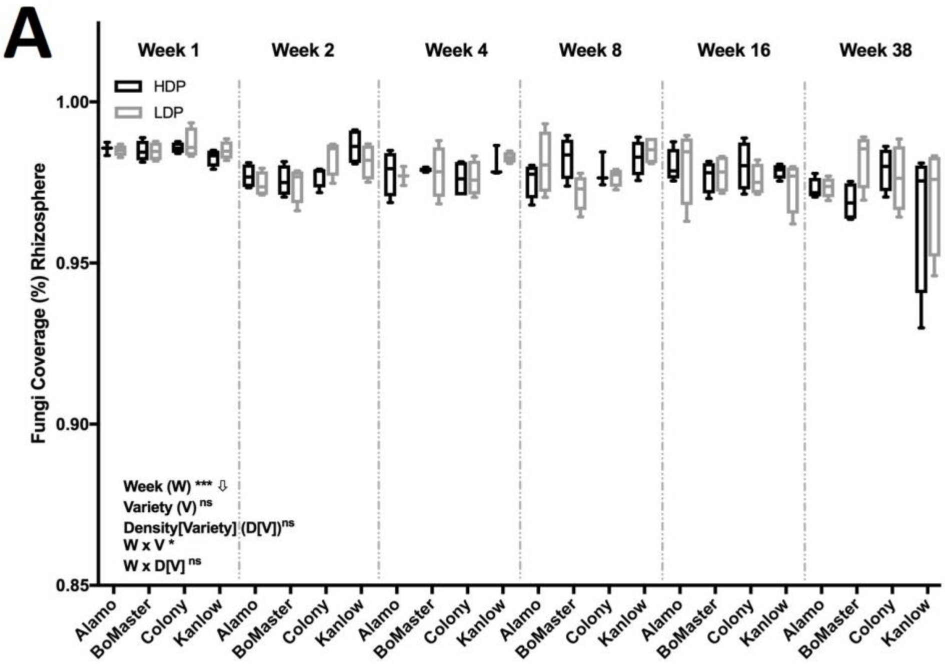


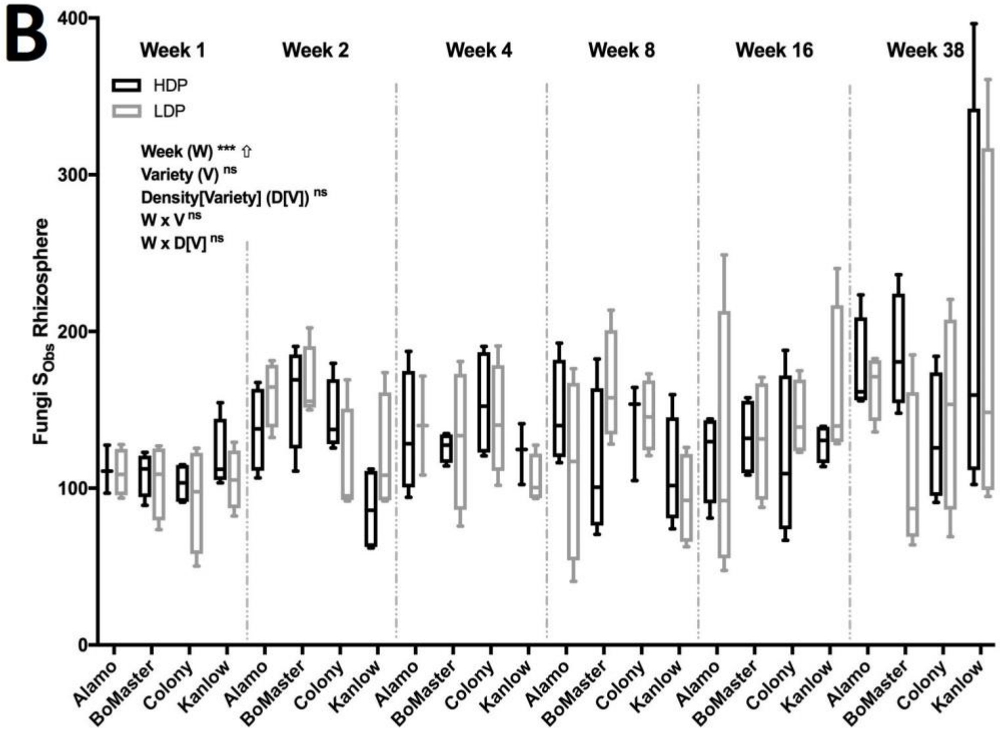
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Bacteria Shannon H' Soil
7
6
5
4
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ***
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

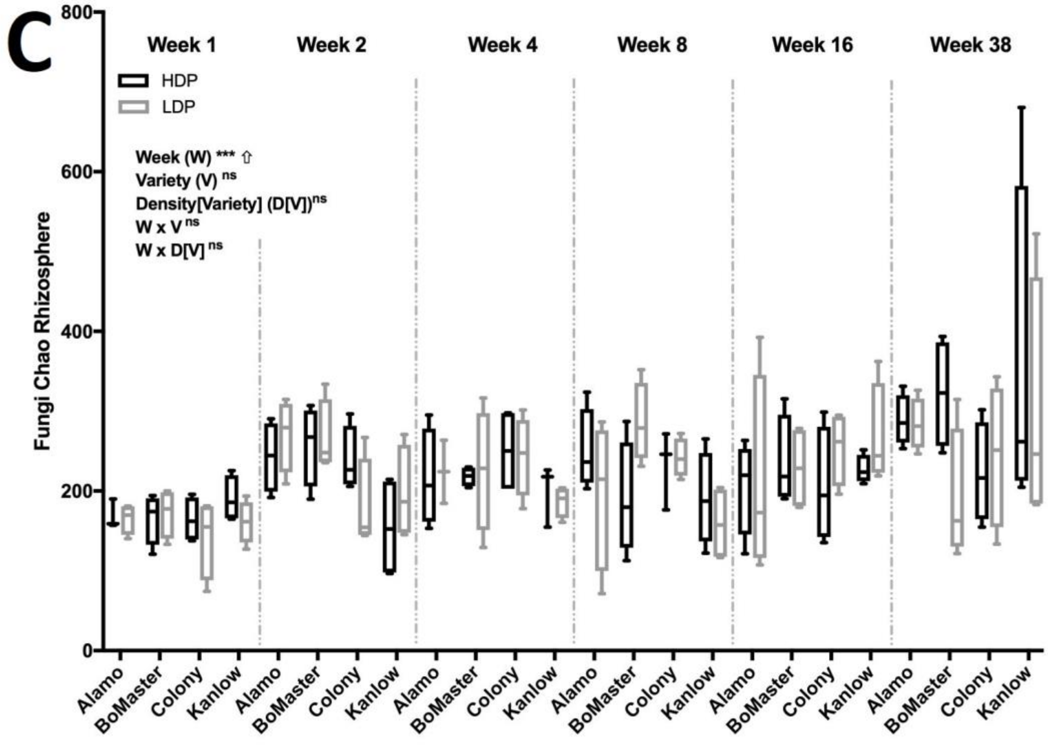
Figure 3.6.

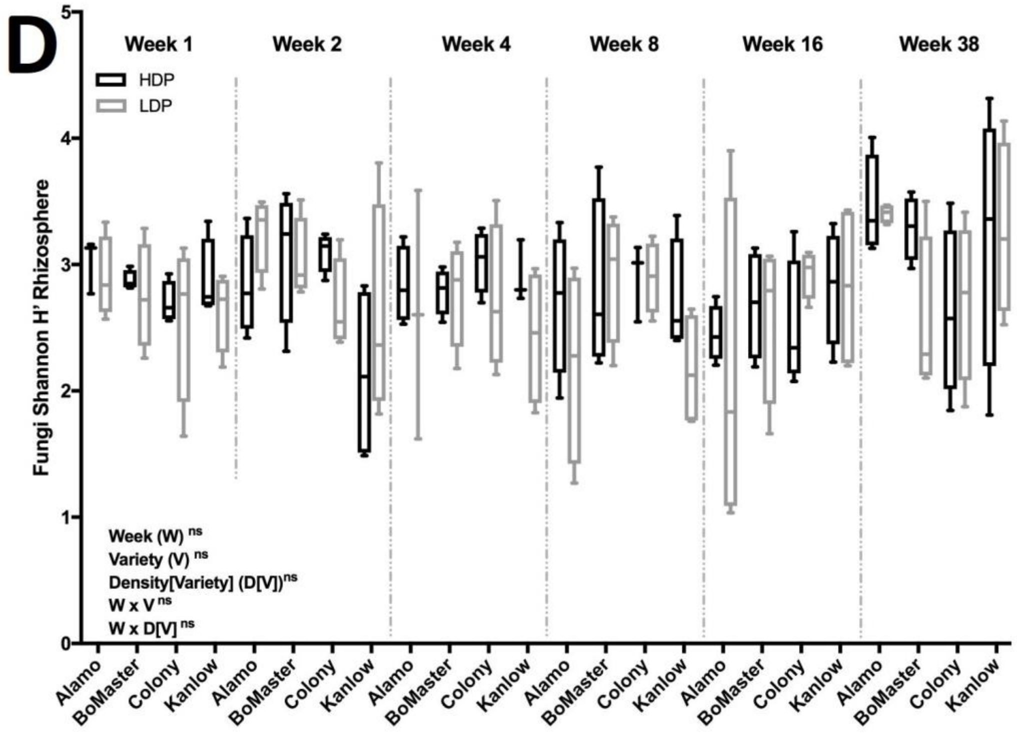
Temporal Dynamics of Fungal Alpha Diversity Metrics

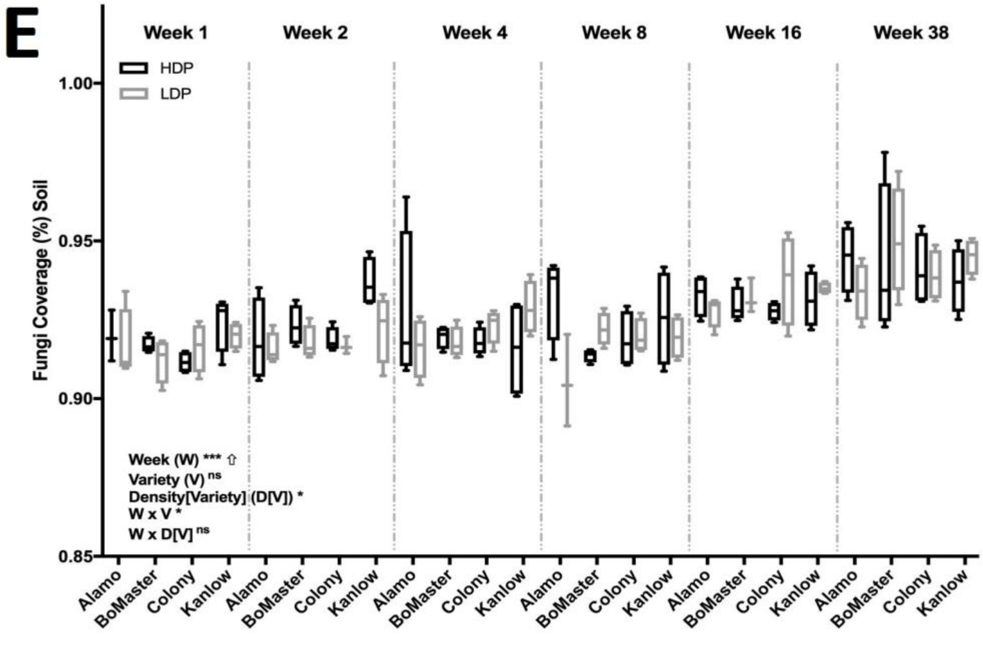
The parameters: Coverage, S_{Obs}, Chao 1, Shannon $_{H'}$ and Shannon E_H were followed from one week after the first leaf emergence to the end of the growing season for a total of 38 weeks. The superscript following each estimator summarizes the mixed effects ANOVA results for a model with fixed effects “Week” (W) “Variety” (V) “Density[Variety]” D[V] interactions and “Block” as a random effect ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

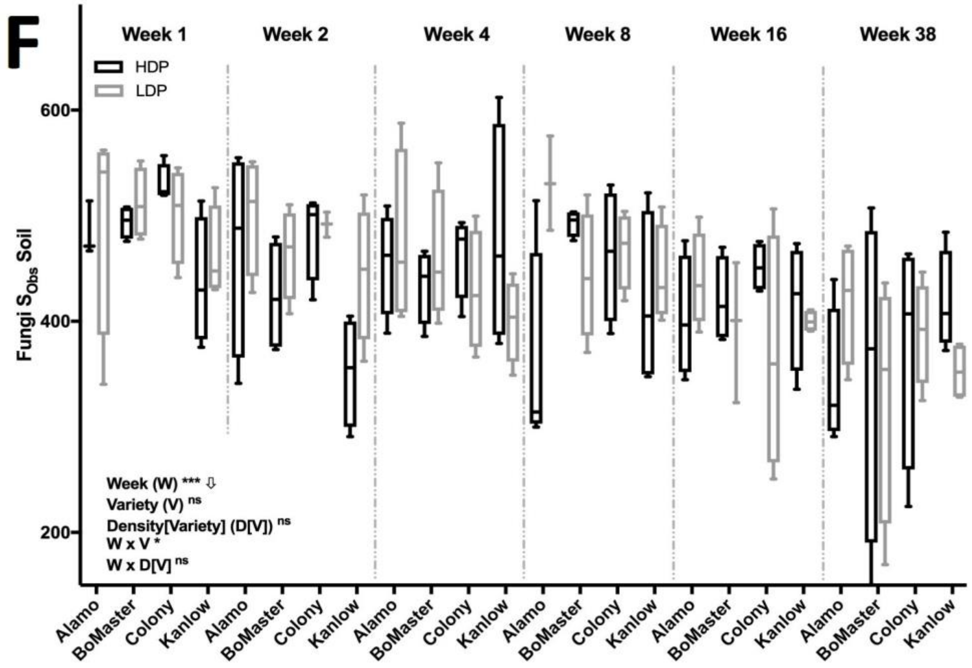


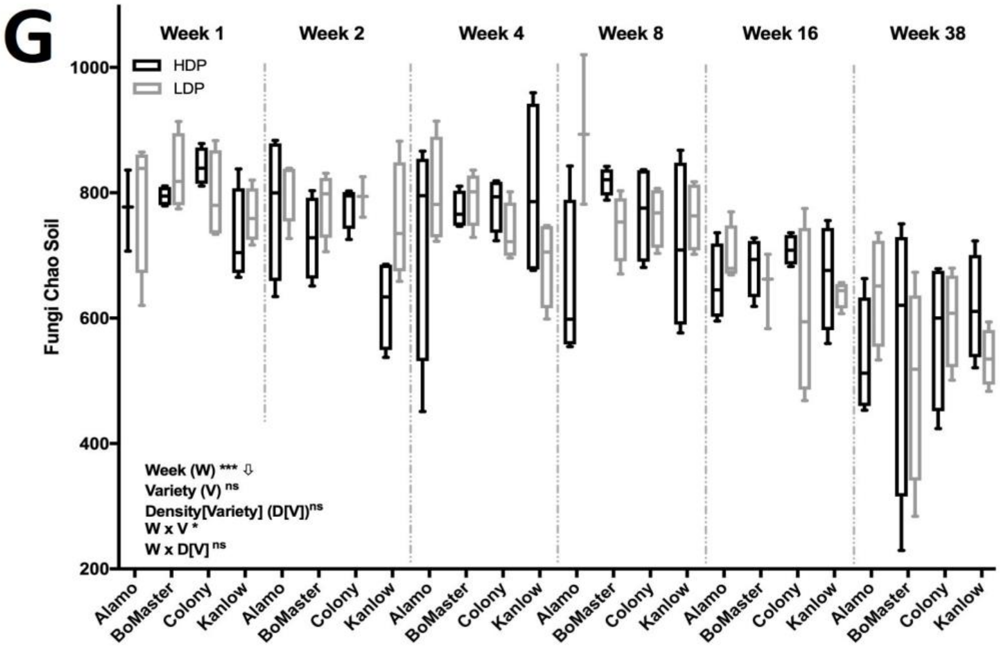

B
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇧
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ns
W x D[V] ns
Fungi S_Obs Rhizosphere
400
300
200
100
0
Alamo
BoMaster
Colony
Kanlow

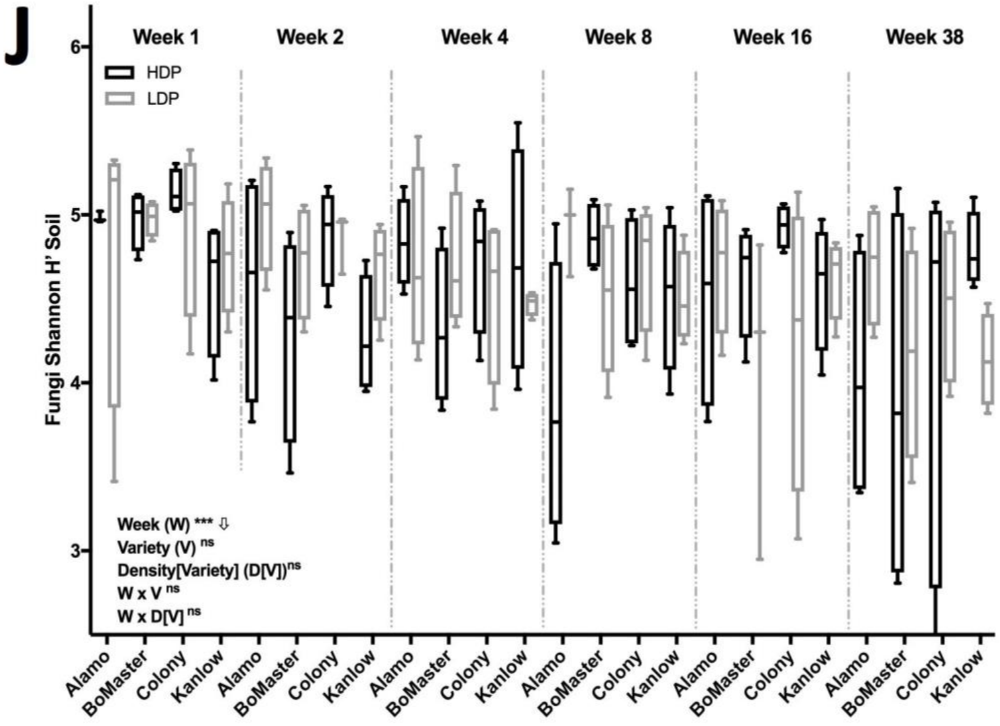

C
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇧
Variety (V) ns
Density[Variety] (D[V]) ns
W x V ns
W x D[V] ns
Fungi Chao Rhizosphere
800
600
400
200
0
Alamo
BoMaster
Colony
Kanlow


D
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Fungi Shannon H' Rhizosphere
0
1
2
3
4
5
Week (W) ^{ns}
Variety (V) ^{ns}
Density[Variety] (D[V])^{ns}
W x V ^{ns}
W x D[V] ^{ns}
Alamo
BoMaster
Colony
Kanlow


E
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Fungi Coverage (%) Soil
0.85
0.90
0.95
1.00
Week (W) *** ⇧
Variety (V) ^{ns}
Density[Variety] (D[V]) *
W x V *
W x D[V] ^{ns}
Alamo
BoMaster
Colony
Kanlow


F
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Fungi S_{Obs} Soil
600
400
200
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V]) ns
W x V *
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow


G
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Fungi Chao Soil
1000
800
600
400
200
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V *
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow


J
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
6
5
4
3
Fungi Shannon H' Soil
Week (W) *** ⇩
Variety (V) ns
Density[Variety] (D[V])ns
W x V ns
W x D[V] ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

Chapter 4 - Conclusion

Plant microbiome has been a topic of interest for many scientists who discovered that mindful plant microbiome manipulation has a potential to promote plant growth, health, and overall fitness (Kim et al. 2012; Ray et al. 2015). There has also been a number of studies describing that a range of biotic and abiotic factors can rapidly change microbiome composition, diversity, and functionality (e.g., Chen et al 2019; Grady et al. 2019; Ghimire et al. 2011; Rodrigues et al. 2017). Conservation agriculture management regimes limit the amount of active management, but instead aim to promote the use of practical tools as plant variety or cultivar choices and planting densities to achieve sustainable production and/or conservation goals (Hoorman et al 2009). To better understand the effects of these tools as factors affecting plant microbiome and soil chemistry, we repeatedly sampled roots and soils of four Panicum virgatum (a.k.a switchgrass) varieties growing under two planning densities in southeastern Mississippi. In addition, to specifically test the effect of seasonal dynamics we repeated sampling starting at leaf emergence and approximating a log2 time series until the end of the growing season for a total of six times. We then dissected the switchgrass-associated microbiomes in soils and roots and measured soil chemistry characteristics.

The first chapter of this thesis compared Next-Generation Sequencing (NGS) data produced by a direct DNA extraction and amplification system with a more commonly used PowerSoil kits extraction system. In this study, I found that, although the direct extraction and amplification kits provide a fast and cost-effective alternative to the more commonly used PowerSoil kits, the generated microbial data was compatible in richness/diversity metrics among roots, but not leaves. The low community richness in leaves can be a result of the low tissue homogenization and we recommend extraction protocol modification to include bead beating step to achieve higher DNA quantities and greater microbial diversity and richness among different plant tissues (Cheng et al. 2016, Griffiths et al. 2006, Ueno et al. 2011). Findings of this study highlight the importance of consistency in the research methods and awareness of potential biases among various studies.

The second chapter of this thesis focused on better understanding the factors that shape switchgrass-associated microbiomes in soil switchgrass roots. These analyses revealed that seasonal dynamics is the strongest driver impacting the assembly of the switchgrass microbiome

and soil chemistry. In contrast, switchgrass planting densities or choice of switchgrass varieties had little or no overall effect on soil chemistry and the switchgrass microbiome richness/diversity or its composition. However, although switchgrass varieties had minimal or no effect on the microbiomes in general, we observed that varieties affected soil chemistry and microbial communities differently in the beginning of the season. In the early growing season, the switchgrass varieties differed in the community composition and indicator analyses identified a number of potential plant mutualists and putative pathogen suggesting a potential for microbiome manipulation through informed variety choices to better meet conservation agriculture objectives. Again, these plant-associated microbial communities were temporally dynamic and shifted during the growing season. The results of this study strongly indicate that seasonal dynamics overwhelm the effects of conservation agriculture management choices, as shown here for the choice of switchgrass variety and planting density.

Overall, we conclude that microbial community changes are driven by the temporal dynamics rather than management choices. Our results and conclusions are important in understanding interactions within the plant-microbiome systems and factors influencing these systems. Despite the small impact of switchgrass varieties highlighted in the course of these studies, this thesis shows that management choices bear a promise as a potential tool for the informed plant microbiome manipulation to promote the sustainability in conservation agriculture, particularly so early in the stand establishment and early growing season.

References

Chen, H., Yang, Z. K., Yip, D., Morris, R. H., Lebreux, S. J., Cregger, M. A., . . . Schadt, C. W. (2019). One-time nitrogen fertilization shifts switchgrass soil microbiomes within a context of larger spatial and temporal variation. Plos One, 14(6), Article e0211310. https://doi.org/10.1371/journal.pone.0211310

Cheng, F., Hou, L., Woeste, K., Shang, Z., Peng, X., Zhao, P., & Zhang, S. (2016). Soil pretreatment and fast cell lysis for direct polymerase chain reaction from forest soils for terminal restriction fragment length polymorphism analysis of fungal communities. Brazilian Journal of Microbiology, 47(4), 817-827. https://doi.org/https://doi.org/10.1016/j.bjm.2016.06.007

Ghimire, S. R., & Craven, K. D. (2011). Enhancement of Switchgrass (Panicum virgatum L.) Biomass Production under Drought Conditions by the Ectomycorrhizal Fungus Sebacina vermifera. Applied and Environmental Microbiology, 77(19), 7063-7067. https://doi.org/10.1128/aem.05225-11

Grady, K. L., Sorensen, J. W., Stopnisek, N., Guittar, J., & Shade, A. (2019). Assembly and seasonality of core phyllosphere microbiota on perennial biofuel crops. Nature Communications, 10, Article 4135. https://doi.org/10.1038/s41467-019-11974-4

Griffiths, L. J., Anyim, M., Doffman, S. R., Wilks, M., Millar, M. R., & Agrawal, S. G. (2006). Comparison of DNA extraction methods for Aspergillus fumigatus using real-time PCR. J Med Microbiol, 55(Pt 9), 1187-1191. https://doi.org/10.1099/jmm.0.46510-0

Hoorman, J., Sundermeier, Islam, R., & Reeder, R. (2009). Using Cover Crops to Convert to No-till. Crops and Soils, 42, 9-13.

Kim, S., Lowman, S., Hou, G., Nowak, J., Flinn, B., & Mei, C. (2012). Growth promotion and colonization of switchgrass (Panicum virgatum) cv. Alamo by bacterial endophyte Burkholderia phytofirmans strain PsJN. Biotechnol Biofuels, 5(1), 37. https://doi.org/10.1186/1754-6834-5-37

Ray, P., Ishiga, T., Decker, S., Turner, G., & Craven, K. (2015). A Novel Delivery System for the Root Symbiotic Fungus, Sebacina vermifera, and Consequent Biomass Enhancement of Low Lignin COMT Switchgrass Lines. BioEnergy Research, 8. https://doi.org/10.1007/s12155-015-9636-8

Rodrigues, R. R., Moon, J., Zhao, B., & Williams, M. A. (2017). Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. Global Change Biology Bioenergy, 9(6), 1057-1070. https://doi.org/10.1111/gcbb.12396

Appendix A - Supplemental materials for chapter 3

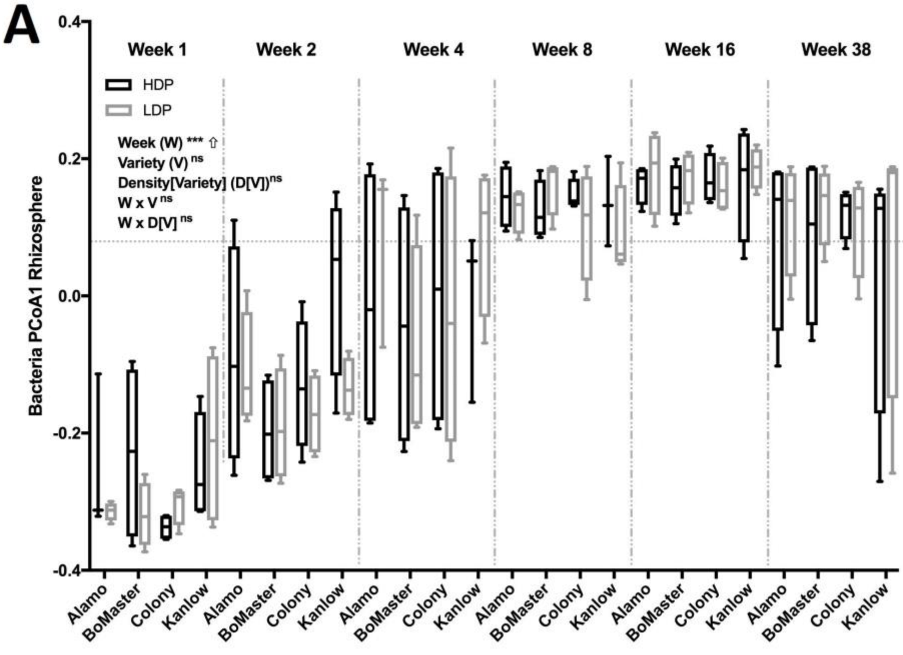
Figures

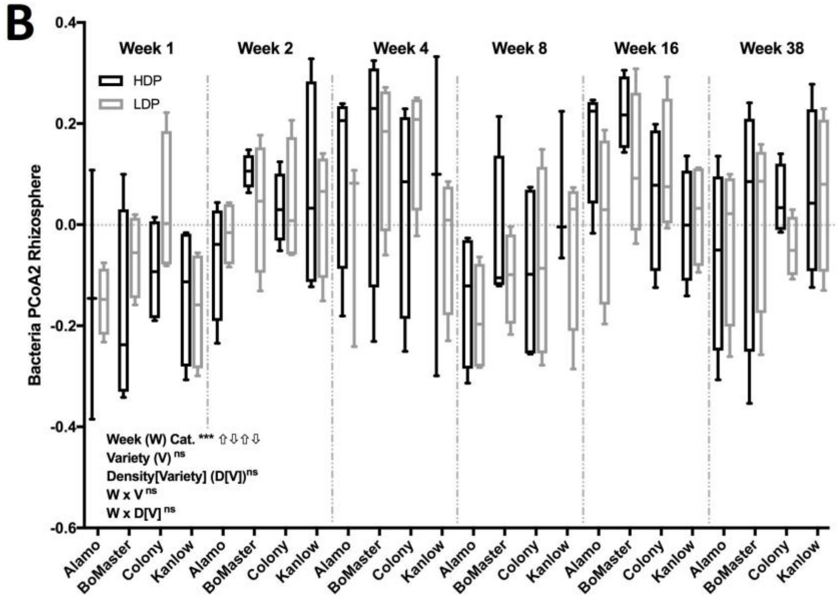
PCoA axis analysis

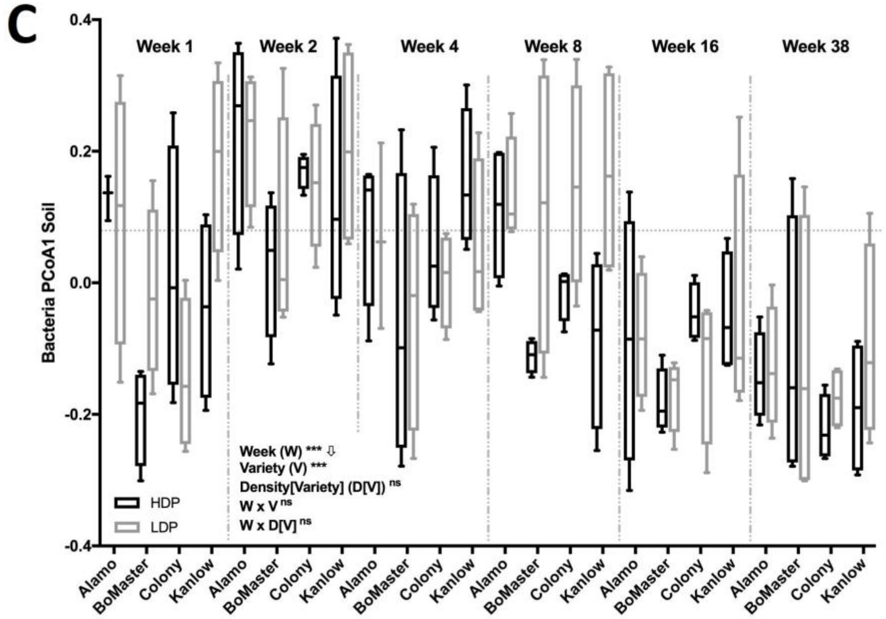
Figure A.1.

Principal Component Axis Analysis of Temporal Dynamics of Root and Soil Bacterial Communities.

Temporal dynamics of bacterial communities for (A),(B) rhizosphere and (C), (D) soil for all 6 sample collection time points during the growing season. Gradual change in the axis scores in Principle Component Axis Analysis indicated the change bacterial communities over time. ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$




B
Bacteria PCoA2 Rhizosphere
0.4
0.2
0.0
-0.2
-0.4
-0.6
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) Cat. *** ⇧⇩⇧⇩
Variety (V) ^{ns}
Density[Variety] (D[V])^{ns}
W x V ^{ns}
W x D[V] ^{ns}
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow


C
Bacteria PCoA1 Soil
0.4
0.2
0.0
-0.2
-0.4
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
Week (W) *** ⇩
Variety (V) ***
Density[Variety] (D[V]) ^{ns}
W x V ^{ns}
W x D[V] ^{ns}
HDP
LDP
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

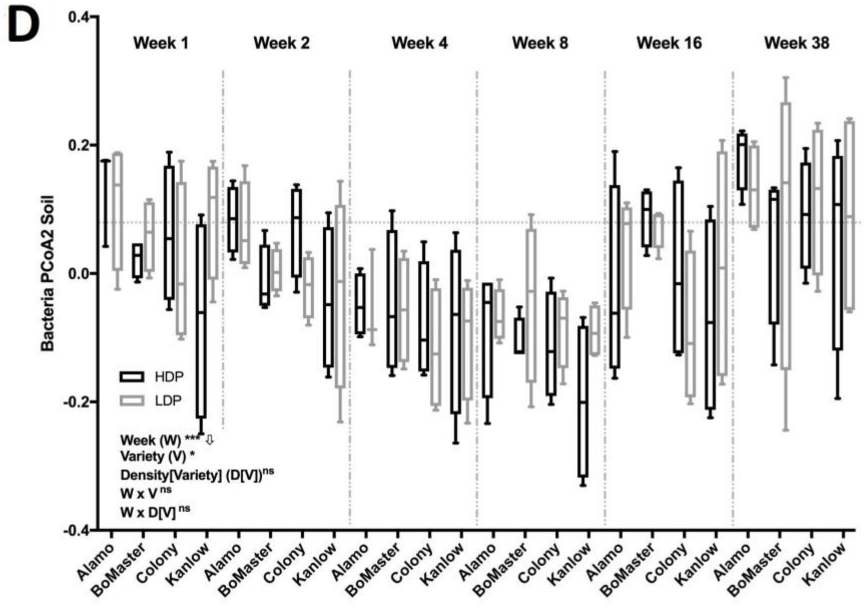
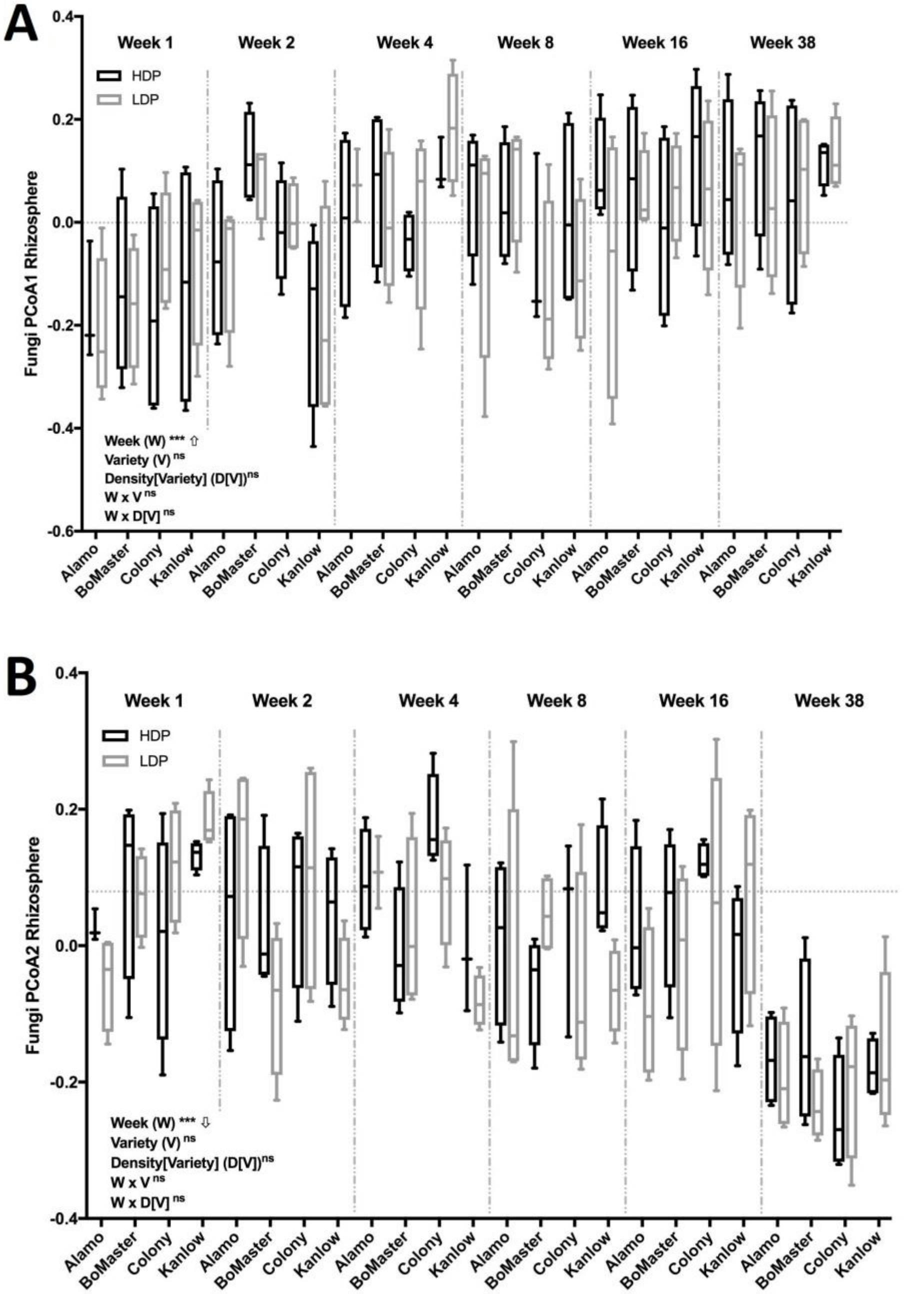

D
Bacteria PCoA2 Soil
0.4
0.2
0.0
-0.2
-0.4
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇩
Variety (V) *
Density[Variety] (D[V])^ns
W x V ^ns
W x D[V] ^ns
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

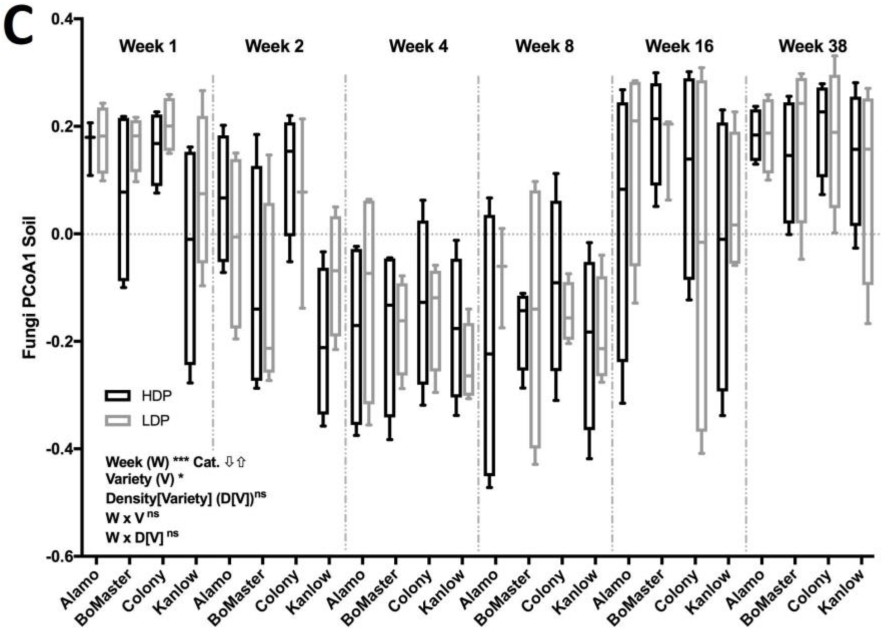
Figure A.2.

Principal Component Axis Analysis of Temporal Dynamics of Root and Soil Fungal Communities.

Temporal dynamics of fungal communities for (A),(B) rhizosphere and (C), (D) soil for all 6 sample collection time points during the growing season. Gradual change in the axis scores in Principle Component Axis Analysis indicated the change bacterial communities over time. ns = $P \geq 0.05$; * = $0.05 > P \geq 0.01$; ** = $0.01 > P \geq 0.001$; *** = $0.001 > P$

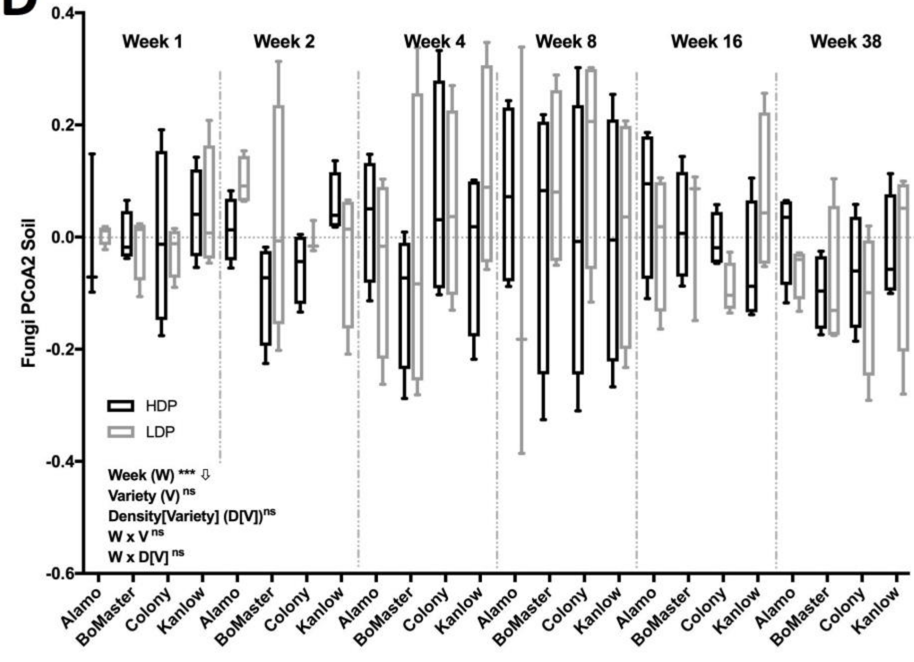


C



Fungi PCoA1 Soil
0.4
0.2
0.0
-0.2
-0.4
-0.6
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** Cat. ⇩⇧
Variety (V) *
Density[Variety] (D[V])^{ns}
W x V ^{ns}
W x D[V] ^{ns}
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

D



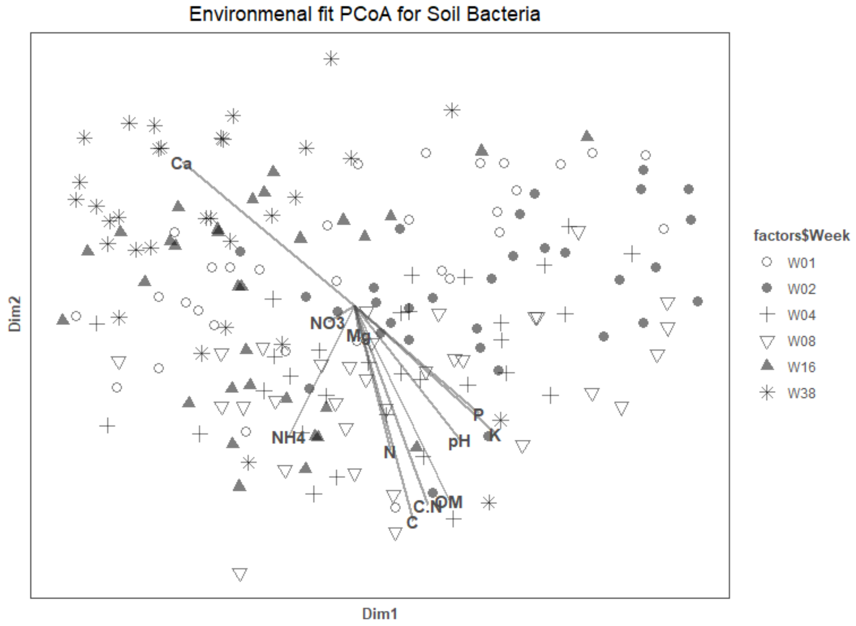
Fungi PCoA2 Soil
0.4
0.2
0.0
-0.2
-0.4
-0.6
Week 1
Week 2
Week 4
Week 8
Week 16
Week 38
HDP
LDP
Week (W) *** ⇩
Variety (V) ^{ns}
Density[Variety] (D[V])^{ns}
W x V ^{ns}
W x D[V] ^{ns}
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow
Alamo
BoMaster
Colony
Kanlow

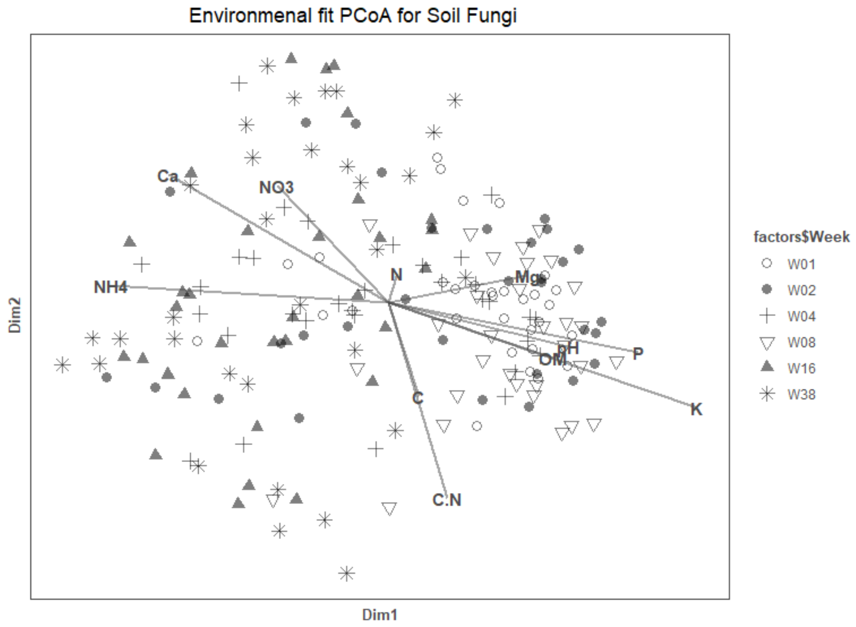
Environmental fit PCoA for microbial communities

Figure A.3.

Environmental Fit PCoA for Soil Associated Bacteria and Fungi

Environmental vectors (Ca, NH_4^+, NO_3^-, Mg, N, C, C:N. OM, pH, P) fit for microbial communities associated with *Panicum virgatum* soil for all 6 sample collection time points during the growing season. The projection of points on the soil chemistry vectors has a maximum correlation with corresponding weeks.





Tables

Microbial indicators for overall analysis

Table A.1.

A list of Bacterial Indicators in Soil Associated with Panicum virgatum for Varieties in Overall Analysis

OTU	Phylum	Class	Order	Family	Genus
BOMASTER					
Otu0000306	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0001699	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001840	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0008326	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002406	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0001641	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
Otu0000261	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002213	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu0001049	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0005528	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000334	unclassified	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004635	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Nitrosospira
Otu0002009	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	unclassified
Otu0002519	Actinobacteria	unclassified	unclassified	unclassified	unclassified
Otu0001098	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0002636	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0005178	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0002351	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0001321	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0002423	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000462	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002234	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002542	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified

Otu0000456	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000467	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0006619	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000231	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0000859	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001847	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0002838	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0003269	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0000362	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Rhizomicrobium	unclassified
Otu0001966	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002163	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0004898	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0002766	Acidobacteria	Acidobacteria_Gp13	Gp13	unclassified	unclassified
Otu0002922	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0004776	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0003836	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0006863	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0001948	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0004483	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0005216	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0000327	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000658	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0000172	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001190	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001173	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002242	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0002427	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0003817	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008147	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Anaeromyxobacter
Otu0002808	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu0000110	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003187	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0002282	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified

Otu0000920	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0003574	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001022	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007486	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus
Otu0002118	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0000354	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001069	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000065	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0005173	Acidobacteria	unclassified	unclassified	unclassified	unclassified
Otu0002237	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002256	Acidobacteria	Acidobacteria_Gp22	Gp22	unclassified	unclassified
Otu0001309	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Anaeromyxobacter
Otu0000603	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0001673	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001853	Acidobacteria	Acidobacteria_Gp1	Granulicella	unclassified	unclassified
Otu0000393	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002284	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0003257	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001479	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003998	Proteobacteria	Deltaproteobacteria	Myxococcales	Kofleriaceae	Kofleria
Otu0001435	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0004729	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0003950	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu0000597	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Hamadaea
Otu0007822	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008514	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005049	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0005655	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0002739	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0001045	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004884	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001070	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0001017	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0005657	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

Otu0002953	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0002642	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0002108	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001944	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0002850	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Aquisphaera
Otu0003856	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0001512	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001605	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000116	unclassified	unclassified	Bacteria_unclassified	unclassified	unclassified
Otu0007104	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001525	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	unclassified	unclassified
Otu0001549	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004152	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000313	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001450	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000348	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000747	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001545	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006288	Acidobacteria	Acidobacteria_Gp15	Gp15	unclassified	unclassified
Otu0005819	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0009017	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0001887	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0002127	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004868	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003766	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000368	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004957	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0002454	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002944	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000711	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002865	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007983	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0003126	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004060	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004797	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified

Otu0004067	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0001143	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001752	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0002116	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007225	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000856	Acidobacteria	Acidobacteria_Gp18	Gp18	unclassified	unclassified
Otu0000921	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0000840	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007136	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002241	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006736	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus
Otu0007204	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	unclassified
Otu0002364	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002304	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002918	Acidobacteria	Acidobacteria_Gp12	Gp12	unclassified	unclassified
Otu0001627	Acidobacteria	Acidobacteria_Gp22	Gp22	unclassified	unclassified
Otu0000039	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007781	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0000274	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0000114	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008195	unclassified	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0004004	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001313	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0008777	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002192	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0006308	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001621	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Brevibacillus
Otu0004487	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0000759	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000477	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	unclassified
Otu0008562	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004284	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007342	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0000707	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0008149	Verrucomicrobia	Subdivision3	Limisphaera	unclassified	unclassified

Otu0002877	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004414	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002268	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001719	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000590	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0007965	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004050	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008032	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000526	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0007832	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000629	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001896	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0000577	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0008062	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000949	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0001851	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000945	unclassified	unclassified	Bacteria_unclassified	unclassified	unclassified
Otu0001941	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0006387	Acidobacteria	Acidobacteria_Gp17	Gp17	unclassified	unclassified
Otu0005612	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	unclassified
Otu0000637	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0007328	unclassified	unclassified	Bacteria_unclassified	unclassified	unclassified
Otu0008182	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	unclassified
Otu0002087	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004072	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001915	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008278	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0000963	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006366	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000683	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Anaeromyxobacter
Otu0000511	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0005203	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0004796	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000210	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

Otu0004199	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001014	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0006814	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002033	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001345	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0005449	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004074	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0005803	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001367	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000696	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003810	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001655	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0001625	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0001319	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0008915	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001558	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0002226	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004313	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006167	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001165	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000967	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0002674	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0003500	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001074	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0002591	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0003703	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0002208	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000803	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005163	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005675	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004512	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007722	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0006795	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002481	Proteobacteria	Proteobacteria_unclassified	unclassified	unclassified	unclassified

Otu0004537	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0007784	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005120	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0007185	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001294	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000307	Candidate _division_WPS-2	unclassified	unclassified	unclassified	unclassified
Otu0000167	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0005743	unclassified	Bacteria_unclassified	unclassified	unclassified	unclassified
Otu0000308	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001984	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0001587	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005205	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000541	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000600	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	unclassified
Otu0001392	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000752	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008557	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002148	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001404	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella
Otu0002022	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0004658	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000184	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Permianibacter
Otu0008678	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0000634	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0005755	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006671	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002340	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0002044	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	Ktedonobacter
Otu0006430	Planctomycetes	Planctomycetia	Planctomycetales	unclassified	unclassified
Otu0001526	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000687	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	unclassified
Otu0002245	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella

Otu0006026	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000964	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0000989	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000713	Acidobacteria	Acidobacteria_Gp16	unclassified	unclassified	unclassified
Otu0003575	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004458	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006507	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000109	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001702	Acidobacteria	Acidobacteria_Gp13	Gp13	unclassified	unclassified
Otu0002826	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001161	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000266	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0002457	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000885	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0007622	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0007371	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000987	Acidobacteria	Acidobacteria_Gp13	Gp13	unclassified	unclassified
Otu0007547	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000241	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006423	Candidate_division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0005047	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0004906	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0003612	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu0006145	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006984	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003843	Latescibacteria	unclassified	unclassified	unclassified	unclassified
COLONY					
Otu0004233	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0003999	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001188	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000722	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0002238	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0006058	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified

Otu0008448	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006791	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0006002	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000863	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006048	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001957	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001579	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0009220	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001485	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0000794	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0004652	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006790	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008427	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0002794	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004348	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0007919	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Cystobacter
Otu0003534	Verrucomicrobia	unclassified	unclassified	unclassified	unclassified
Otu0007292	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0008393	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008207	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003685	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002961	unclassified	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0000163	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006004	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009357	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003626	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia
Otu0008020	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000884	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0004173	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0005030	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001115	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000844	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001408	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000677	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella
Otu0000670	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified

Otu0002184	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005315	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001092	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007360	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002335	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0009320	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0008592	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003993	Armatimonadetes	Armatimonadetes_gp4	unclassified	unclassified	unclassified
Otu0004484	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001335	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobineae_incertae_sedis	Aciditerrimonas
Otu0004024	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005740	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
KANLOW					
Otu0005983	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0005601	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0003364	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007430	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0006533	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified
Otu0008994	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000833	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0009524	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0006078	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0007585	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	unclassified
Otu0002248	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0002717	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007089	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001024	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005725	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007248	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0007933	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0008188	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0007261	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008762	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified

Otu0001311	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	Peredibacter
Otu0005295	Acidobacteria	Acidobacteria_Gp10	unclassified	unclassified	unclassified
Otu0002554	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0007147	Acidobacteria	Acidobacteria_Gp4	unclassified	unclassified	unclassified
Otu0005640	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0003359	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006029	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0004536	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0007903	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0006087	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0007303	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001814	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	unclassified
Otu0005079	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002765	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007467	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007567	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0004594	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0004895	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0009026	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0009255	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia
Otu0003953	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0002390	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006537	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0002920	Acidobacteria	Acidobacteria_Gp4	Blastocatella	unclassified	unclassified
Otu0007679	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0006996	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006611	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0008635	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Flavisolibacter
Otu0000475	Bacteroidetes	Cytophagia	Cytophagales	Ohtaekwangia	unclassified
Otu0003561	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0006517	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Povalibacter
Otu0005603	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0002630	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified

Otu0007995	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0004591	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008570	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0006373	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002274	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0002448	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0005559	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009221	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000253	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002521	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0006300	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0002999	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0007692	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005039	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0006209	Verrucomicrobia	unclassified	unclassified	unclassified	unclassified
Otu0007549	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005157	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005900	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007470	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0009381	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0006804	Bacteroidetes	Sphingobacteriia	unclassified	Sphingobacteriaceae	Solitalea
Otu0005735	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella
Otu0008966	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0004327	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified

Table A.2.

A list of Bacterial Indicators in Associated with Panicum virgatum Roots in for Varieties in Overall Analysis

OTU	Phylum	Class	Order	Family	Genus
ALAMO					
Otu0005700	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	unclassified
BOMASTER					
Otu0000172	Acidobacteria	unclassified	Gp2	Gp2_unclassified	unclassified
Otu0001810	Acidobacteria	Acidobacteria_Gp1	unclassified	unclassified	unclassified
Otu0008725	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu0000340	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Kitasatospora
Otu0002095	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0009038	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisoma
Otu0003505	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006378	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007547	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002097	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006863	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
COLONY					
Otu0001953	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0002869	Acidobacteria	Acidobacteria_Gp17	Gp17	unclassified	unclassified
Otu0003654	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
Otu0002180	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0002463	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0004003	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella
Otu0004036	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified

Otu0004345	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0006505	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria _incertae_sedis	Geminicoccus	unclassified
Otu0008786	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0002184	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002191	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003629	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005180	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005586	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006199	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003306	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0008631	Verrucomicrobia	Spartobacteria	Terrimicrobium	unclassified	unclassified
Otu0008659	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
KANLOW					
Otu0007261	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0006315	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008097	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	unclassified
Otu0008120	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified

Table A.3.

A list of Fungal Indicators in Soil associated with Panicum virgatum in for Varieties in Overall Analysis

OTU	Phylum	Class	Order	Family	Genus
ALAMO					
Otu01807	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01930	Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Cyphellophora
Otu02010	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02364	Ascomycota	Sordariomycetes	Hypocreales	unclassified	unclassified
BOMASTER					
Otu00601	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Paecilomyces
Otu01116	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified
Otu01160	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified
Otu01756	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus
Otu01788	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02459	unclassified	unclassified	unclassified	unclassified	unclassified
COLONY					
Otu00086	unclassified	unclassified	unclassified	Fungi_unclassified	unclassified
Otu00235	Ascomycota	Sordariomycetes	Xylariales	Xylariales_family _Incertae_sedis	Microdochium
Otu00276	Chytridiomycota	unclassified	unclassified	unclassified	unclassified
Otu00323	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Stagonospora
Otu00700	Ascomycota	Sordariomycetes	unclassified	Nectriaceae	Cylindrocarpon
Otu00823	Ascomycota	unclassified	unclassified	unclassified	unclassified

Otu00952	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01321	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01627	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01763	Glomeromycota	unclassified	unclassified	unclassified	unclassified
Otu02015	unclassified	unclassified	unclassified	unclassified	unclassified
KANLOW					
Otu00118	Zygomycota	unclassified	Mortierellales	Mortierellaceae	Mortierella
Otu00313	Basidiomycota	Agaricomycetes	Auriculariales	unclassified	unclassified
Otu00561	Basidiomycota	Agaricomycetes	Cantharellales	Tulasnellaceae	Epulorhiza
Otu00897	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Phaeosphaeria
Otu01312	Ascomycota	Sordariomycetes	Microascales	Halosphaeriaceae	unclassified
Otu02131	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	unclassified
Otu02162	Ascomycota	Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	Cyphellophora
Otu02220	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified
Otu02285	unclassified	unclassified	unclassified	unclassified	unclassified

Table A.4.

A list of Fungal Indicators Associated with Panicum virgatum Roots in for Varieties in Overall Analysis

OTU	**Phylum**	**Class**	**Order**	**Family**	**Genus**
BOMASTER					
Otu00217	Ascomycota	unclassified	unclassified	unclassified	unclassified
Otu00303	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified
Otu00708	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00717	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Cosmospora
Otu00928	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01020	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified
Otu01689	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	unclassified
Otu01702	Ascomycota	unclassified	unclassified	unclassified	unclassified

Microbial indicators for management choices analysis

Table A.5.

A List of Bacterial Indicators in Soil Associated with Panicum virgatum with their Taxonomic Associations for Varieties in by Week Analysis

OTU	Phylum	Class	Order	Family	Genus
WEEK 8					
HDP					
Otu0004068	Acidobacteria	Acidobacteria_Gp17	Gp17	unclassified	unclassified
Otu0007713	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000174	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000180	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000377	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000579	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000691	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000737	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu0002119	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
Otu0002448	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	unclassified
Otu0000471	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000623	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001719	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002430	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004146	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007104	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000056	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
Otu0000616	Bacteroidetes	Cytophagia	Cytophagales	Chryseolinea	unclassified
Otu0000793	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0005599	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium

Otu0003175	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004264	candidate_division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000444	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus
Otu0002715	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0001789	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0002211	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000018	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000052	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000109	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000303	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000354	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified
Otu0000461	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0000827	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000950	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001340	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0001826	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0003985	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0006184	Proteobacteria	unclassified	unclassified	unclassified	unclassified

Table A.6.

A List of Fungal Indicators Associated with Panicum virgatum roots with their Taxonomic Associations for Varieties in by Week Analysis

OTU	Phylum	Class	Order	Family	Genus	Species
WEEK 2						
BOMASTER						
Otu01441	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00869	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus_custos
WEEK 4						
KANLOW						
Otu00039	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00055	Ascomycota	Sordariomycetes	Hypocreales	Hypocreales _family_Incertae_sedis	Sarocladium	Sarocladium_strictum

Microbial indicators for temporal dynamics

Table A.7.

A list of Bacterial Indicators in Soil Associated with Panicum virgatum for Temporal Dynamics Analysis

OTU	**Phylum**	**Class**	**Order**	**Family**	**Genus**
WEEK 1					
Otu0000440	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0001273	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001971	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0002128	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0002335	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0004083	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0008418	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001676	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0003837	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	Fimbriimonas
Otu0000495	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001188	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002238	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002314	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002596	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002772	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003130	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003907	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004758	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005074	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005278	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005834	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006215	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0006875	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007552	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007673	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007800	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008907	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00086	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009507	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006868	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0008282	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003419	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000781	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Parachlamydia
Otu0002130	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0007058	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0003582	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Leptolinea
Otu0001186	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0004965	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0006427	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0000135	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0000264	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0005673	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0006778	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0007400	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0008832	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0000215	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu00002	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0000422	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000911	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0001408	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0002283	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Anaeromyxobacter

Otu0002306	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002518	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0002544	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0002621	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0003529	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004050	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0005083	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0005192	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0005532	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0005612	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0005683	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0005848	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0006133	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0009343	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000601	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0001763	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002614	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003318	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003552	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0005043	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

WEEK 2					
Otu0002223	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified
Otu0002253	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Chitinimonas
Otu0007944	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	unclassified

WEEK 4					
Otu0001461	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0004355	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified

Otu0000380	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0000562	Actinobacteria	Actinobacteria	Actinomycetales	Demequinaceae	Demequina
Otu0000602	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Nakamurella
Otu0000606	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000673	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
Otu0000773	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0001000	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0001001	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Nakamurella
Otu0001021	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001428	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Herbiconiux
Otu0001748	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Cellulomonas
Otu0002597	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0002864	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Phycicoccus
Otu0002906	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agromyces
Otu0002927	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Aquihabitans
Otu0003092	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0003518	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0004222	Actinobacteria	unclassified	unclassified	unclassified	unclassified
Otu0005386	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0005943	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agromyces
Otu0006637	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Gordonia
Otu0007348	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0003135	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/Armatimonadetes_gp3
Otu0001141	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00018	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003334	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003957	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008958	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001033	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified

Otu0002142	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002156	Bacteroidetes	Cytophagia	Cytophagales	Ohtaekwangia	unclassified
Otu0002415	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0002472	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
Otu0002726	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0002942	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003123	Bacteroidetes	Cytophagia	Cytophagales	unclassified	unclassified
Otu0003319	Bacteroidetes	Cytophagia	Cytophagales	unclassified	unclassified
Otu0003324	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0004139	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Sediminibacterium
Otu0004817	Bacteroidetes	Cytophagia	Cytophagales	Ohtaekwangia	unclassified
Otu0005437	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0005648	Bacteroidetes	Flavobacteriia	Flavobacteriales	unclassified	unclassified
Otu0008126	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0008780	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0002106	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	unclassified
Otu0002806	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	unclassified
Otu0005421	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	unclassified
Otu0000388	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0002275	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0006710	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0007068	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008800	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008948	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Blastopirellula
Otu0000089	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Povalibacter
Otu0000132	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000394	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter
Otu0000705	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis
Otu0000761	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000827	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified

Otu0000926	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	unclassified
Otu0000958	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0001419	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0002386	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0002507	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales _incertae_sedis	Alsobacter
Otu0002510	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0002610	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0002857	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia
Otu0003567	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
Otu0003606	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	unclassified
Otu0003684	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu00040	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0004876	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Oceanospirillaceae	unclassified
Otu0005458	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	unclassified
Otu0005587	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	unclassified
Otu0005806	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0006242	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	unclassified
Otu0006319	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Uliginosibacterium
Otu0006354	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0006509	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0006684	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	unclassified
Otu0007194	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0008259	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu00093	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0005374	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
Otu0007665	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
Otu0000175	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0001191	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0005777	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified

WEEK 8					
Otu0000652	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0003701	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0005486	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0006370	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0007155	Acidobacteria	Acidobacteria_Gp4	Gp4	Gp4_unclassified	unclassified
Otu0007751	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0000934	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Catellatospora
Otu0001260	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frondihabitans
Otu0001348	Actinobacteria	Actinobacteria	Actinomycetales	Cryptosporangiaceae	Cryptosporangium
Otu0001548	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Amnibacterium
Otu0001852	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes
Otu0002475	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Smaragdicoccus
Otu0002501	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	unclassified
Otu0002910	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0003838	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineosporia
Otu0005151	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Geodermatophilus
Otu0005623	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus
Otu0005802	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium
Otu0006709	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	unclassified
Otu0007151	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	unclassified
Otu0007200	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobineae _incertae_sedis	Aciditerrimonas
Otu0007829	Armatimonadetes	Armatimonadetes_gp5	unclassified	unclassified	unclassified
Otu0002041	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003470	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004644	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006407	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0006516	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000134	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Chryseobacterium
Otu0000684	Bacteroidetes	Cytophagia	Cytophagales	Chryseolinea	unclassified
Otu0000739	Bacteroidetes	Cytophagia	Cytophagales	unclassified	unclassified
Otu0000787	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium
Otu0002020	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola
Otu0002490	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0002916	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0002926	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu0003012	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0003113	Bacteroidetes	Cytophagia	Cytophagales	Chryseolinea	unclassified
Otu0003353	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0003438	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0003472	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu0003572	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0003902	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
Otu0004322	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
Otu0004683	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0004966	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
Otu0006864	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0007251	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0005619	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0005639	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0007293	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0000298	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0000913	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0001216	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0002039	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Otu0003227	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc
Otu0005268	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Leuconostoc

Otu0005849	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0006763	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified
Otu0002604	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0008626	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0002870	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003589	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003695	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004613	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000034	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Pseudoduganella
Otu0000045	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0000048	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia
Otu0000075	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000079	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0000082	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Rhizobacter
Otu0000106	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
Otu0000144	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter
Otu0000200	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000360	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax
Otu0000378	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Otu0000410	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000485	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000624	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	unclassified
Otu0000672	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter
Otu0000702	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
Otu0000783	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas
Otu0000876	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000979	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0001006	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0001052	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0001148	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified

Otu0001377	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001413	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Otu0001536	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales _incertae_sedis	Aquabacterium
Otu0001583	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0001683	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001728	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0001844	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu00017	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas
Otu0002260	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas
Otu0002286	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0002318	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0002435	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0002516	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0002556	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0002557	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	unclassified
Otu0002688	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0002729	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia
Otu0002929	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter
Otu0002939	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002974	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified
Otu0003169	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu0003189	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0003195	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Otu0003307	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0003416	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter
Otu0003508	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	unclassified
Otu0003686	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Noviherbaspirillum
Otu0003689	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Otu0003741	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Alkanibacter

Otu0003813	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
Otu00038	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0004206	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia
Otu0004285	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
Otu0004298	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0004409	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0004771	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004803	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0005052	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Gluconobacter
Otu0005141	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0005305	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
Otu0005539	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0005672	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
Otu0005692	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0006000	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0006220	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Salmonella
Otu0007228	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0007396	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Povalibacter
Otu0007454	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Belnapia
Otu0007827	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0008007	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Lacibacterium
Otu0008170	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0008347	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Geminicoccus	unclassified
Otu0008685	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Silvimonas
Otu0000269	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
Otu0000556	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
Otu0001595	Spirochaetes	Spirochaetia	Spirochaetales	Leptospiraceae	Turneriella
Otu0001106	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0001134	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus

Otu0001969	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0004265	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0004402	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu00048	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Luteolibacter
Otu0006569	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007720	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Luteolibacter
Otu0008253	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
WEEK 16					
Otu0000046	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000064	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu0000066	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000102	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu00001	Acidobacteria	Acidobacteria_Gp1	Terriglobus	unclassified	unclassified
Otu0000203	Acidobacteria	Acidobacteria_Gp1	unclassified	unclassified	unclassified
Otu0000305	Acidobacteria	Acidobacteria_Gp1	Terriglobus	unclassified	unclassified
Otu0000310	Acidobacteria	Acidobacteria_Gp1	unclassified	unclassified	unclassified
Otu0000454	Acidobacteria	Acidobacteria_Gp1	Acidicapsa	unclassified	unclassified
Otu0000470	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000482	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000489	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu0000543	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000583	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000618	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu0000665	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu00006	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000736	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000757	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu0000801	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000912	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified

Otu0001015	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001020	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001032	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0001162	Acidobacteria	Acidobacteria_Gp4	unclassified	unclassified	unclassified
Otu0001606	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0001669	Acidobacteria	Acidobacteria_Gp12	Gp12	unclassified	unclassified
Otu0001706	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001800	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001910	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001948	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002109	Acidobacteria	Acidobacteria_Gp2	Gp2	unclassified	unclassified
Otu0002192	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002300	Acidobacteria	Acidobacteria_Gp1	Edaphobacter	unclassified	unclassified
Otu0002333	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0002817	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0003003	Acidobacteria	Acidobacteria_Gp1	Terriglobus	unclassified	unclassified
Otu0003085	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0003234	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0003281	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0003610	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0004612	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0004726	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0004827	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0005049	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0006249	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0006335	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0006822	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0007031	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007475	Acidobacteria	Acidobacteria_Gp3	Candidatus_Solibacter	unclassified	unclassified
Otu0008677	Acidobacteria	Acidobacteria_Gp1	Candidatus_Koribacter	unclassified	unclassified

Otu0000073	Actinobacteria	Actinobacteria	Actinomycetales	Thermomonosporaceae	unclassified
Otu0000121	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0000122	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0000202	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Dactylosporangium
Otu0000227	Actinobacteria	Actinobacteria	Actinomycetales	Thermomonosporaceae	Actinomadura
Otu0000371	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Kutzneria
Otu0000493	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu0000498	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Kribbella
Otu0000569	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0000896	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu00004	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001031	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001133	Actinobacteria	Actinobacteria	Actinomycetales	Cryptosporangiaceae	Jatrophihabitans
Otu0001283	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001294	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Hamadaea
Otu0001364	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0001577	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001636	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001895	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002392	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	unclassified
Otu0002522	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0002609	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0002924	Actinobacteria	Actinobacteria	Actinomycetales	Actinospicaceae	Actinospica
Otu0003061	Actinobacteria	unclassified	unclassified	unclassified	unclassified
Otu0003192	Actinobacteria	unclassified	unclassified	unclassified	unclassified
Otu0003259	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Hamadaea
Otu0003481	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	unclassified
Otu0003863	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiacea	unclassified
Otu0003871	Actinobacteria	Actinobacteria	Actinomycetales	Catenulisporaceae	Catenulispora
Otu0004127	Actinobacteria	Actinobacteria	Actinomycetales	Catenulisporaceae	Catenulispora

Otu0004180	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Aquihabitans
Otu0005390	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0005508	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0005774	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0006541	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Aquihabitans
Otu0006928	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0007774	Actinobacteria	unclassified	unclassified	unclassified	unclassified
Otu0008081	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0008917	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0009522	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Amycolatopsis
Otu0001977	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonas/ Armatimonadetes_gp1
Otu0002002	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0003620	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0004241	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0000342	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000358	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000363	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000387	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000542	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000585	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000717	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000902	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000972	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001028	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001316	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001325	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001358	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0001510	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001596	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001787	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001900	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00020	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002105	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002147	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002171	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002208	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002251	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002305	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002424	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002618	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002691	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002704	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002776	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002905	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002918	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003053	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003126	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003154	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003264	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004116	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004147	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004292	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005320	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006070	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006139	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006264	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006333	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0006556	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006823	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006846	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006977	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006980	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006985	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007337	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007762	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007882	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00084	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009272	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000267	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
Otu0000285	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0000474	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0000591	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0000930	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0002011	Bacteroidetes	Bacteroidia	Bacteroidales	unclassified	unclassified
Otu0002090	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0002533	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0004911	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Chitinophaga
Otu0007208	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0007539	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0000140	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000806	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000982	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0001566	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0002056	Candidate	unclassified	unclassified	unclassified	unclassified

	_division_WPS-1				
Otu0002937	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0003549	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0004978	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0000336	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000413	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000778	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0000804	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	unclassified
Otu0000849	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0000918	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001178	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001286	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001400	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001420	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001421	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001720	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002048	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002291	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002302	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002328	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002523	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002570	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002629	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002640	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002867	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0003150	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0003487	Chloroflexi	unclassified	unclassified	unclassified	unclassified

Otu0003631	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0004538	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0006743	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0008882	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0000752	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0001219	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0001401	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0002075	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0004386	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0008013	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	unclassified
Otu0000726	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0000760	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001073	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001160	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001182	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0001780	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002312	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002583	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003236	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003452	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004163	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0006809	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0000029	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000152	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000159	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0000161	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0000165	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dokdonella
Otu0000171	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000209	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000226	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Blastochloris

Otu0000229	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
Otu0000281	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Labrys
Otu0000293	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000330	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000359	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0000415	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Reyranella	unclassified
Otu0000427	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0000505	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisoma
Otu0000514	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Vampirovibrio
Otu0000530	Proteobacteria	Alphaproteobacteria	unclassified	Rhizomicrobium	unclassified
Otu0000531	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000535	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Rhizomicrobium	unclassified
Otu0000561	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
Otu0000627	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000642	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	unclassified
Otu0000661	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000719	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	unclassified
Otu0000733	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unclassified	unclassified
Otu0000734	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0000742	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000768	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000808	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000817	Proteobacteria	Gammaproteobacteria	Chromatiales	unclassified	unclassified
Otu0000822	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000887	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000950	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000961	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	unclassified
Otu0001153	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea
Otu0001179	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified

Otu0001221	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	unclassified
Otu0001227	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001244	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
Otu0001318	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001418	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
Otu0001449	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Vampirovibrio
Otu0001472	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0001514	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Rhizobacter
Otu0001555	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
Otu0001637	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001738	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0001782	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0001784	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	unclassified
Otu0001790	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0001822	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified
Otu0002073	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0002154	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002160	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002361	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	unclassified
Otu0002531	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unclassified	unclassified
Otu0002595	Proteobacteria	Alphaproteobacteria	unclassified	Rhizomicrobium	unclassified
Otu0002722	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0002809	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	unclassified
Otu0003166	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	unclassified
Otu0003247	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Nevskia
Otu0003253	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0003326	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0003557	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0003623	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Chondromyces
Otu0003739	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	unclassified

Otu0003753	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0003782	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0003794	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unclassified	unclassified
Otu0003848	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0003968	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0004089	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0004158	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004195	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0004368	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004497	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0004694	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004979	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0004986	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unclassified	unclassified
Otu0005177	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
Otu0005223	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0005253	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0005576	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0005678	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0005898	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Nevskia
Otu0006321	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unclassified	unclassified
Otu0006708	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0007495	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0008521	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0008708	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000167	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000257	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0000400	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000744	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000851	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu00000	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

Otu0001056	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001078	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001429	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001434	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0001587	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001714	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001891	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001909	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002004	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002013	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002097	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003242	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003370	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004219	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004278	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0005286	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0005681	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0005782	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006523	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006649	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007056	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007111	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0008294	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
WEEK 38					
Otu0000017	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0000032	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000044	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000147	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0000164	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified

Otu0000194	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000198	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0000239	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000242	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0000270	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0000283	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0000345	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000366	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000368	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000435	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000476	Acidobacteria	Acidobacteria_Gp25	Gp25	unclassified	unclassified
Otu0000516	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0000525	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000528	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0000532	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0000593	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000612	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000655	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000660	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000667	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000731	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000775	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000871	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0000874	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0000880	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0000939	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0000940	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000966	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000977	Acidobacteria	Acidobacteria_Gp25	Gp25	unclassified	unclassified
Otu0000984	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified

Otu00001	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001002	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001077	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001228	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified
Otu0001371	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001388	Acidobacteria	Acidobacteria_Gp7	Gp7	unclassified	unclassified
Otu0001390	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001487	Acidobacteria	Acidobacteria_Gp10	Gp10	unclassified	unclassified
Otu0001518	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001519	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0001535	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001565	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0001624	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001680	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0001698	Acidobacteria	Acidobacteria_Gp4	unclassified	unclassified	unclassified
Otu0001731	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0001877	Acidobacteria	Acidobacteria_Gp25	Gp25	unclassified	unclassified
Otu0001883	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002114	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002138	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002319	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0002330	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0002372	Acidobacteria	Acidobacteria_Gp25	Gp25	unclassified	unclassified
Otu0002628	Acidobacteria	Acidobacteria_Gp3	unclassified	unclassified	unclassified
Otu0002932	Acidobacteria	Acidobacteria_Gp25	Gp25	unclassified	unclassified
Otu0003127	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0003223	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0003225	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0003248	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0003502	Acidobacteria	Acidobacteria_Gp16	Gp16	unclassified	unclassified

Otu0003600	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0003613	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0004114	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0004427	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0004519	Acidobacteria	Acidobacteria_Gp17	Gp17	unclassified	unclassified
Otu0004762	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0004775	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0005060	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0005264	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0005281	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0005465	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0005757	Acidobacteria	Acidobacteria_Gp5	Gp5	unclassified	unclassified
Otu0005869	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0006781	Acidobacteria	Acidobacteria_Gp1	Gp1	unclassified	unclassified
Otu0006943	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007273	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007413	Acidobacteria	Acidobacteria_Gp3	Gp3	unclassified	unclassified
Otu0007530	Acidobacteria	Holophagae	Holophagales	Holophagaceae	unclassified
Otu0008362	Acidobacteria	Acidobacteria_Gp4	Gp4	unclassified	unclassified
Otu0009465	Acidobacteria	Acidobacteria_Gp6	Gp6	unclassified	unclassified
Otu0000180	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000213	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000234	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0000438	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000509	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0000579	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000654	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0001004	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0001427	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0001521	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Aquihabitans

Otu0001578	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0002232	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002815	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0002883	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0003156	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0003180	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0003325	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0003415	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0004858	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0004901	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	unclassified
Otu0005107	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0005935	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0006605	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0006824	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0007023	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0008176	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobineae _incertae_sedis	Aciditerrimonas
Otu0000907	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0001263	Armatimonadetes	Armatimonadetes _gp4	unclassified	unclassified	unclassified
Otu0001564	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0002606	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0002644	Armatimonadetes	Armatimonadetes _gp4	unclassified	unclassified	unclassified
Otu0002880	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0003374	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0004931	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/

					Armatimonadetes_gp3
Otu0005036	Armatimonadetes	Armatimonadetes_gp4	unclassified	unclassified	
Otu0006831	Armatimonadetes	Armatimonadetes_gp4	unclassified	unclassified	
Otu0007401	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0007653	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0007842	Armatimonadetes	Armatimonadetes_gp4	unclassified	unclassified	
Otu0009060	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0000108	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000133	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000186	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000292	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000346	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00004	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000533	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000614	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000770	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000795	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000870	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000891	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00009	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001180	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001539	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001586	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001739	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001759	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001821	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001849	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0002131	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002140	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002353	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002379	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002387	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002388	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002943	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002958	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003043	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003059	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003412	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003485	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003577	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003584	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004105	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004129	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004166	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004468	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004558	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004681	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005010	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005878	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005976	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006014	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006034	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006051	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006052	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006855	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007971	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008428	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0008516	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009115	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008785	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008829	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0009008	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Sporocytophaga
Otu0005416	BRC1	unclassified	unclassified	unclassified	unclassified
Otu0001201	candidate_division _WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0003035	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0008138	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	unclassified
Otu0008732	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0000192	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0002829	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0004390	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0001053	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Aquisphaera
Otu0005004	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Aquisphaera
Otu0000640	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001379	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0002537	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0004212	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0004290	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0004840	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0004887	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0005109	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0006165	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0005510	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0003972	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0009437	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001154	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0002887	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata

Otu0008561	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0003723	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0004154	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0008809	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0002563	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0000423	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0000557	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0001265	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0002174	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0002512	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0003387	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
Otu0001737	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctopirus
Otu0001349	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu00034	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0003543	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0004420	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0005663	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0006390	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0003446	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0001306	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0002935	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0001920	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu00007	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0001409	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0003636	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Thermogutta
Otu0000090	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000433	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000730	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000956	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000986	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified

Otu0001158	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001206	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001491	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001497	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001570	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001604	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001633	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001650	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001762	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001846	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001951	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu00011	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002038	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002100	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002198	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002220	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002346	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002377	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003060	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003117	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003272	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003625	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003803	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003935	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004205	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004232	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004250	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004353	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004372	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0004560	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified

Otu0004801	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0005312	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0006495	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0007690	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008071	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008157	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008669	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0009226	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000852	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0000941	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0001795	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0002375	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0002832	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0003168	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0003275	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0004625	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0005482	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0001423	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0005756	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0003854	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0003132	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0006733	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0000041	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes
Otu0000063	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified
Otu0000139	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000154	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0000160	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0000168	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0000437	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0000486	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified

Otu0000659	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000680	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0001081	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0001103	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0001116	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0001671	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Reyranella	unclassified
Otu0001696	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0001845	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002301	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0002381	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0002580	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella
Otu00027	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Nitrosospira
Otu0003760	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0004286	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0004397	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0004464	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0004508	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu00045	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Aquicella
Otu0005263	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0005632	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	unclassified	unclassified
Otu0007694	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0007811	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0007841	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0008243	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0009327	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0009477	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000332	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0000723	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0000816	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0001091	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

Otu0001171	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0001338	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0001563	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0001827	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002396	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0002683	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003133	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0003460	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified
Otu0004226	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified

Table A.8.

A list of Bacterial Indicators Panicum virgatum Roots for Temporal Dynamics Analysis

OTU	**Phylum**	**Class**	**Order**	**Family**	**Genus**
WEEK 1					
Otu0003981	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Catellatospora
Otu0001687	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0000174	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000279	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000568	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000621	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000639	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000922	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0001444	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0001676	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0002687	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0005102	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0004310	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Modestobacter

Otu0009216	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus
Otu0000502	Acidobacteria	Acidobacteria	Gp5	unclassified	unclassified
Otu0000597	Acidobacteria	Acidobacteria	Gp13	unclassified	unclassified
Otu0000831	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0001011	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0001730	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0001917	Acidobacteria	Acidobacteria	Gp11	unclassified	unclassified
Otu0002335	Acidobacteria	Acidobacteria	Gp5	unclassified	unclassified
Otu0002582	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0002608	Acidobacteria	Acidobacteria	Gp12	unclassified	unclassified
Otu0002724	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0003015	Acidobacteria	Acidobacteria	Gp22	unclassified	unclassified
Otu0003212	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0003263	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0007212	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0007577	Acidobacteria	Acidobacteria	Gp5	unclassified	unclassified
Otu0000496	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0000578	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0000701	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0001129	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0001346	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0002236	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002441	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0002965	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0003378	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0005565	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0000118	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000206	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000220	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000430	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0000614	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000644	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000656	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000759	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000835	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000863	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001049	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001063	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001108	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001188	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001202	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001268	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001448	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001480	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001574	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001711	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001719	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001786	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001925	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001967	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002238	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002309	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002314	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002368	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002403	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002404	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002596	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002635	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002655	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002950	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0003062	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003130	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003137	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003229	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003240	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003300	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003315	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003316	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003560	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003569	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003616	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003907	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004688	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004697	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005020	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005203	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005380	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005593	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006128	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006493	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006767	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006830	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007229	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007559	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007879	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008337	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008679	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009128	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000143	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0000201	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter

Otu0000611	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0000638	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0000866	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0001168	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0001200	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0001275	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0001433	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0001524	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0001638	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0001874	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002068	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0002129	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0002133	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0002136	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Taibaiella
Otu0002366	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002393	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002409	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002756	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002781	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002787	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002975	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0002979	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0003101	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003174	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003265	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003295	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0003363	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0003367	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003537	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0003850	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium

Otu0004779	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0004913	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0004982	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0005279	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0005324	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0005335	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0005459	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	Fluviicola
Otu0006126	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0006213	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	unclassified
Otu0006322	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0006360	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0006827	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0006856	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0007033	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	unclassified
Otu0007060	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0007177	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0007251	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0007523	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0007662	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0007906	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0008269	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0008363	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0008421	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Chryseobacterium
Otu0009032	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0009061	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0009062	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter
Otu0009169	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
Otu0009298	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0009442	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Otu0009516	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium

Otu0000140	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002693	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003663	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004351	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004622	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005138	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005515	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000276	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000794	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0002790	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0003010	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0006926	Chlamydiae	Chlamydiia	Chlamydiales	Simkaniaceae	Simkania
Otu0000740	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0000878	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0001867	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002082	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0002477	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0002532	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002570	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0003150	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0003257	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0003280	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Thermomarinilinea
Otu0004686	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0006580	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0007269	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0007737	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0001507	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0003450	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0003581	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0007656	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus

Otu0000370	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0001579	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0002882	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0004112	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0004965	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0005860	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0001045	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0002026	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0004182	Latescibacteria	unclassified	unclassified	unclassified	unclassified
Otu0002316	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0005673	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Otu0004405	Parcubacteria	unclassified	unclassified	unclassified	unclassified
Otu0004747	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Blastopirellula
Otu0005541	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0006948	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0008897	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0000013	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0000072	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000101	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000215	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000243	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000247	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000262	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0000365	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas

Otu0000439	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
Otu0000522	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000588	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax
Otu0000607	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0000625	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0000635	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
Otu0000676	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0000703	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0000728	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0000996	Proteobacteria	Gamma proteobacteria	unclassified	unclassified	unclassified
Otu0001087	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0001223	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0001276	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0001277	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0001279	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001391	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0001407	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0001580	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
Otu0001620	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0001666	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0001691	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0001792	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0001797	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0001854	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified

Otu0001868	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	Bacteriovorax
Otu0002237	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002289	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0002347	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Undibacterium
Otu0002408	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0002701	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu0002865	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0003116	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	Bacteriovorax
Otu0003131	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0003139	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0003244	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0003246	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0003357	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0003394	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0003595	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Herbaspirillum
Otu0003598	Proteobacteria	Gamma proteobacteria	unclassified	unclassified	unclassified
Otu0003777	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0003866	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Undibacterium
Otu0003910	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0003919	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0004050	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0004076	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0004444	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0004544	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas

Otu0004576	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0004780	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	Yersinia
Otu0004903	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0005003	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0005255	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0005923	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0005932	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0005975	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
Otu0006032	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0006055	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0006133	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0006175	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0006193	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0006367	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0007010	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu0007052	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0007366	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0007695	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Otu0007697	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0007715	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
Otu0007770	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacterium
Otu0007944	Proteobacteria	Betaproteobacteria	Gallionellales	Gallionellaceae	unclassified
Otu0008018	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0008175	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas

Otu0008203	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0008260	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0008289	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0008938	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0009247	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000551	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0000663	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001473	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001763	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001862	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0001988	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0002029	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002221	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002614	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0002642	Verrucomicrobia	Subdivision3	Limisphaera	unclassified	unclassified
Otu0002739	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004082	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004188	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004302	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0004354	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0005674	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006329	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0007211	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0009236	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
WEEK 2					
Otu0000385	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Geothrix

Otu0000592	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0008500	Acidobacteria	Acidobacteria	Gp13	unclassified	unclassified
Otu0009112	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0005460	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0005974	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
Otu0008717	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0001858	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002578	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008616	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0001431	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002760	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004044	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008279	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007049	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0000068	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0000298	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0000322	Firmicutes	Bacilli	Bacillales	Planococcaceae	Bhargavaea
Otu0000388	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0000450	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified
Otu0000577	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0000712	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0000829	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0000877	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0000913	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0001192	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0001216	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0001278	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0001576	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Brevibacillus
Otu0001640	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified
Otu0001661	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified

Otu0001713	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus
Otu0002030	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0002275	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0002370	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0002382	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0002775	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0003033	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0003069	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus
Otu0003483	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0003513	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0004040	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0004081	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus (80)
Otu0004739	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0005055	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0005564	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0005631	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Cohnella
Otu0005641	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0005805	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0005901	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0006196	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0006896	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0007591	Firmicutes	Bacilli	Bacillales	Planococcaceae	Bhargavaea
Otu0008069	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified
Otu0008471	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0009012	Firmicutes	Bacilli	Bacillales	unclassified	unclassified
Otu0009138	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0009162	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	unclassified
Otu0009266	Firmicutes	Bacilli	Bacillales	Bacillaceae_1	Bacillus
Otu0003232	Gemmatimonadetes	Gemma timonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas

Otu0000316	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000587	Proteobacteria	Alpha proteobacteria	Rhizobiales	unclassified	unclassified
Otu0001989	Proteobacteria	Beta proteobacteria	unclassified	unclassified	unclassified
Otu0002253	Proteobacteria	Beta proteobacteria	Burkholderiales	Burkholderiaceae	Chitinimonas
Otu0002560	Proteobacteria	Beta proteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu0004048	Proteobacteria	Alpha proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
Otu0005170	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0005273	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0006594	Proteobacteria	Beta proteobacteria	unclassified	unclassified	unclassified
Otu0007380	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0008038	Proteobacteria	Delta proteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio
Otu0008265	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
WEEK 4					
Otu0000943	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0002240	Acidobacteria	Acidobacteria	Gp16	unclassified	unclassified
Otu0003064	Acidobacteria	Acidobacteria	Gp16	unclassified	unclassified
Otu0004247	Acidobacteria	Acidobacteria	Gp17	unclassified	unclassified
Otu0007758	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0000076	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides

Otu0000105	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0000124	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0000380	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0000447	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0000691	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0000805	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0001000	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0001021	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001197	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0001241	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0001672	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes
Otu0001748	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Cellulomonas
Otu0001886	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0001939	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0004121	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Aquihabitans
Otu0005197	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0005487	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0005911	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus
Otu0006511	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Conexibacter
Otu0006831	Armatimonadetes	Armatimonadetes	unclassified	unclassified	unclassified
Otu0001141	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003036	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004607	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006661	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008066	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008602	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000596	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
Otu0001242	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Sediminibacterium
Otu0002156	Bacteroidetes	Cytophagia	Cytophagales	Ohtaekwangia	unclassified
Otu0002397	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified

Otu0002876	Bacteroidetes	Cytophagia	Cytophagales	Chryseolinea	unclassified
Otu0002926	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Ferruginibacter
Otu0004002	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0004342	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0004817	Bacteroidetes	Cytophagia	Cytophagales	Ohtaekwangia	unclassified
Otu0008024	Candidate _division_WPS-1	unclassified	unclassified	unclassified	unclassified
Otu0002034	Chlamydiae	Chlamydiia	Chlamydiales	unclassified	unclassified
Otu0002106	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	unclassified
Otu0002806	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	unclassified
Otu0005784	Chloroflexi	Thermomicrobia	unclassified	unclassified	unclassified
Otu0007847	Firmicutes	Bacilli	Bacillales	Planococcaceae	unclassified
Otu0008037	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0005251	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0005761	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000228	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000394	Proteobacteria	Gamma proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter
Otu0000580	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0000926	Proteobacteria	Alpha proteobacteria	Sphingomonadales	Erythrobacteraceae	unclassified
Otu0000958	Proteobacteria	Beta proteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0001111	Proteobacteria	Beta proteobacteria	unclassified	unclassified	unclassified
Otu0001419	Proteobacteria	Beta proteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0001534	Proteobacteria	Beta proteobacteria	unclassified	unclassified	unclassified
Otu0001659	Proteobacteria	Alpha proteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0002386	Proteobacteria	Delta	unclassified	unclassified	unclassified

		proteobacteria			
Otu0002513	Proteobacteria	Gamma proteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas
Otu0002679	Proteobacteria	Alpha proteobacteria	Rhizobiales	unclassified	unclassified
Otu0002713	Proteobacteria	Alpha proteobacteria	Rhizobiales	unclassified	unclassified
Otu0002833	Proteobacteria	Alpha proteobacteria	Rhizobiales	unclassified	unclassified
Otu0003528	Proteobacteria	Beta proteobacteria	unclassified	unclassified	unclassified
Otu0004482	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0004876	Proteobacteria	Gamma proteobacteria	Oceanospirillales	Oceanospirillaceae	unclassified
Otu0004945	Proteobacteria	Delta proteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0005084	Proteobacteria	Beta proteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0005337	Proteobacteria	Gamma proteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified
Otu0005429	Proteobacteria	Alpha proteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
Otu0006319	Proteobacteria	Beta proteobacteria	Rhodocyclales	Rhodocyclaceae	Uliginosibacterium
Otu0006988	Proteobacteria	Delta proteobacteria	Myxococcales	unclassified	unclassified
Otu0007409	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0008158	Proteobacteria	Beta proteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0008263	Proteobacteria	Delta proteobacteria	Myxococcales	Polyangiaceae	Chondromyces
Otu0008341	Proteobacteria	Gamma proteobacteria	unclassified	unclassified	unclassified

WEEK 8					
Otu0005623	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus
Otu0007151	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	unclassified
Otu0005125	Armatimonadetes	Armatimonadetes	unclassified	unclassified	unclassified
Otu0004966	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Hymenobacter
Otu0003589	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0002514	Proteobacteria	Alpha proteobacteria	Rhizobiales	Rhizobiaceae	Kaistia
Otu0002557	Proteobacteria	Alpha proteobacteria	Rhizobiales	Beijerinckiaceae	unclassified
Otu0006375	Proteobacteria	Delta proteobacteria	Myxococcales	unclassified	unclassified
Otu0007074	Proteobacteria	Alpha proteobacteria	Sneathiellales	Sneathiellaceae	Taonella
Otu0007411	Proteobacteria	Alpha proteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0008007	Proteobacteria	Alpha proteobacteria	Rhodospirillales	Rhodospirillaceae	Lacibacterium
Group W16					
Otu0000066	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000102	Acidobacteria	Acidobacteria	Gp2	unclassified	unclassified
Otu0000113	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000172	Acidobacteria	Acidobacteria	Gp2	unclassified	unclassified
Otu0000199	Acidobacteria	Acidobacteria	Terriglobus	unclassified	unclassified
Otu0000221	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0000222	Acidobacteria	Acidobacteria	Gp2	unclassified	unclassified
Otu0000305	Acidobacteria	Acidobacteria	Terriglobus	unclassified	unclassified
Otu0000310	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified

Otu0000326	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000441	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0000470	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0000482	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000489	Acidobacteria	Acidobacteria	Candidatus_Solibacter	unclassified	unclassified
Otu0000543	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000583	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0000626	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000665	Acidobacteria	Acidobacteria	Candidatus_Solibacter	unclassified	unclassified
Otu0000736	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0000912	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0000959	Acidobacteria	Acidobacteria	Candidatus_Solibacter	unclassified	unclassified
Otu0001032	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0001162	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0001320	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0001606	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0001697	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0001706	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0001800	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0001830	Acidobacteria	Acidobacteria	Gp7	unclassified	unclassified
Otu0001910	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0002300	Acidobacteria	Acidobacteria	Edaphobacter	unclassified	unclassified
Otu0002496	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0002817	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0002830	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0003225	Acidobacteria	Acidobacteria	Gp6	unclassified	unclassified
Otu0003610	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified

Otu0003853	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0004202	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0004726	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0005184	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0006249	Acidobacteria	Acidobacteria	Gp3	unclassified	unclassified
Otu0006575	Acidobacteria	Acidobacteria	unclassified	unclassified	unclassified
Otu0006933	Acidobacteria	Acidobacteria	Gp10	unclassified	unclassified
Otu0008853	Acidobacteria	Acidobacteria	Gp4	unclassified	unclassified
Otu0000091	Actinobacteria	Actinobacteria	Gaiellales	unclassified	Gaiella
Otu0000121	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0000371	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Kutzneria
Otu0000493	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu0000569	Actinobacteria	Actinobacteria	Solirubrobacterales	unclassified	unclassified
Otu0000840	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces
Otu0000896	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0001047	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0001283	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0001294	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Hamadaea
Otu0001332	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0001364	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0001381	Actinobacteria	Actinobacteria	Actinomycetales	Streptosporangiaceae	Nonomuraea
Otu0001768	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0001895	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002088	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0002448	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae (59)	unclassified
Otu0002609	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0002653	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0002788	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0002924	Actinobacteria	Actinobacteria	Actinomycetales	Actinospicaceae	Actinospica
Otu0003259	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Hamadaea

Otu0003481	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	unclassified
Otu0003735	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0003871	Actinobacteria	Actinobacteria	Actinomycetales	Catenulisporaceae	Catenulispora
Otu0004000	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0004127	Actinobacteria	Actinobacteria	Actinomycetales	Catenulisporaceae	Catenulispora
Otu0004207	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella
Otu0005635	Actinobacteria	Actinobacteria	Acidimicrobiales	unclassified	unclassified
Otu0005774	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0006080	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia
Otu0007835	Actinobacteria	Actinobacteria	unclassified	unclassified	unclassified
Otu0007843	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	Sporichthya
Otu0008249	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	unclassified
Otu0008599	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	unclassified
Otu0008705	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides
Otu0009522	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Amycolatopsis
Otu0001642	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0002002	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0003400	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0003949	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0006331	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Chthonomonas/ Armatimonadetes_gp3
Otu0000358	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000363	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000542	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000585	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000717	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000902	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0001028	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001163	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001358	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001544	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001596	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0001900	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002099	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002171	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002196	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002246	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002305	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002691	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002704	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002776	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0003154	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004116	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004238	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0004292	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005232	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0005839	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006333	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006846	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006985	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007213	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007391	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0007762	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008316	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008499	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008970	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009046	unclassified	unclassified	unclassified	unclassified	unclassified

Otu0009308	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000267	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
Otu0000930	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0003296	Chlamydiae	Chlamydiia	Chlamydiales	Parachlamydiaceae	Neochlamydia
Otu0000778	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0000804	Chloroflexi	Ktedonobacteria	Ktedonobacterales	unclassified	unclassified
Otu0001178	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001286	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001400	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002629	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0002867	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0003096	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	unclassified
Otu0004538	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0005414	Chloroflexi	unclassified	unclassified	unclassified	unclassified
Otu0001219	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0001401	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0002075	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0004386	Firmicutes	unclassified	unclassified	unclassified	unclassified
Otu0004632	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Otu0000507	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0000726	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
Otu0001073	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001160	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0001182	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0001712	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0001737	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctopirus
Otu0002100	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0003110	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0003251	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera

Otu0003452	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0005364	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0005696	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0006557	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	unclassified
Otu0006748	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0000029	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000103	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0000131	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000159	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0000161	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Minicystis
Otu0000171	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000209	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000265	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000281	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Labrys
Otu0000287	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified
Otu0000289	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria _incertae_sedis	Rhizomicrobium	unclassified
Otu0000293	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000325	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium
Otu0000330	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000361	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Reyranella	unclassified
Otu0000373	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0000381	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000415	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Reyranella	unclassified
Otu0000427	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0000472	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria _incertae_sedis	Rhizomicrobium	unclassified
Otu0000514	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Vampirovibrio
Otu0000530	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria _incertae_sedis	Rhizomicrobium	unclassified

Otu0000531	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000535	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Rhizomicrobium	unclassified
Otu0000561	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
Otu0000627	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0000661	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000719	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	unclassified
Otu0000734	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0000742	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000774	Proteobacteria	Deltaproteobacteria	unclassified	unclassified	unclassified
Otu0000808	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0000817	Proteobacteria	Gammaproteobacteria	Chromatiales	unclassified	unclassified
Otu0000887	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0000946	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0000950	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0000961	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	unclassified
Otu0001149	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0001153	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rudaea
Otu0001203	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001236	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Rhizomicrobium	unclassified
Otu0001318	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0001486	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0001514	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Rhizobacter
Otu0001581	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001649	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	unclassified
Otu0001755	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0001784	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	unclassified
Otu0001820	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0001916	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified

Otu0002160	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0002259	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0002744	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0002809	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	unclassified
Otu0003326	Proteobacteria	Gammaproteobacteria	unclassified	unclassified	unclassified
Otu0003459	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0003554	Proteobacteria	unclassified	unclassified	unclassified	unclassified
Otu0003623	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Chondromyces
Otu0003755	Proteobacteria	Deltaproteobacteria	Myxococcales	Kofleriaceae	Kofleria
Otu0003782	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0003818	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0003848	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0003968	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0004089	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0004158	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0004323	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
Otu0004489	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Chondromyces
Otu0004690	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
Otu0004713	Proteobacteria	Alphaproteobacteria	Rhodospirillales	unclassified	unclassified
Otu0004979	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0005223	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0005253	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0005576	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0005588	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0005665	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified	unclassified
Otu0006000	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0006578	Proteobacteria	Gamma proteobacteria	Xanthomonadales	Sinobacteraceae	Povalibacter
Otu0007169	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007479	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium

Otu0007689	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0007934	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0008011	Proteobacteria	Alphaproteobacteria	unclassified	unclassified	unclassified
Otu0008654	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Byssovorax
Otu0001434	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0003054	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0003159	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
Otu0006649	Verrucomicrobia	Subdivision3	unclassified	unclassified	unclassified
WEEK 38					
Otu0002483	Acidobacteria	Acidobacteria	Gp1	unclassified	unclassified
Otu0004075	Acidobacteria	Acidobacteria	Gp2	unclassified	unclassified
Otu0004571	Acidobacteria	Holophagae	Holophagales	Holophagaceae	Holophaga
Otu0000295	Actinobacteria	Actinobacteria	Actinomycetales	unclassified	unclassified
Otu0004575	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	unclassified
Otu0000125	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0002517	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0006843	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0008505	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0009445	unclassified	unclassified	unclassified	unclassified	unclassified
Otu0000620	Bacteroidetes	unclassified	unclassified	unclassified	unclassified
Otu0001102	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Niastella
Otu0002444	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0004705	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	unclassified
Otu0008492	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
Otu0002719	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium _sensu_stricto
Otu0003617	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Sporomusa
Otu0004078	Firmicutes	Bacilli	Bacillales	Paenibacillaceae_1	Paenibacillus
Otu0006598	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium

					_sensu_stricto
Otu0002935	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
Otu0003432	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
Otu0000034	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Pseudoduganella
Otu0000040	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu0000079	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
Otu0000081	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	unclassified
Otu0000099	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	unclassified
Otu0000271	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu0000367	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000595	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0000674	Proteobacteria	Betaproteobacteria	unclassified	unclassified	unclassified
Otu0000678	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Chitinimonas
Otu0000683	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	Geobacter
Otu0001085	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Azonexus
Otu0001189	Proteobacteria	Gamma proteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
Otu0001217	Proteobacteria	Deltaproteobacteria	Myxococcales	unclassified	unclassified
Otu0001472	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	unclassified
Otu0001631	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu0002087	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0002094	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Vogesella
Otu0002331	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0002334	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Chitinimonas
Otu0003348	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	unclassified	unclassified
Otu0003437	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0003463	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	unclassified
Otu0003833	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	unclassified
Otu0003851	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Chromobacterium

Otu0003974	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0004161	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0004449	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0004573	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_unclassified	unclassified
Otu0004628	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
Otu0004897	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0005033	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0005142	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu0005283	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
Otu0005362	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	unclassified
Otu0005376	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu0005453	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0005634	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified	unclassified
Otu0005719	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Propionivibrio
Otu0005720	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia
Otu0006172	Proteobacteria	Gamma proteobacteria	unclassified	unclassified	unclassified
Otu0006220	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	Salmonella
Otu0006295	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Jeongeupia
Otu0006313	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0006518	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
Otu0006758	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	unclassified
Otu0006819	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	Desulfobulbus
Otu0006956	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0007106	Proteobacteria	Gamma proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
Otu0007148	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Pseudoduganella

Otu0007168	Proteobacteria	Gamma proteobacteria	Enterobacteriales	Enterobacteriaceae	unclassified
Otu0007521	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Pseudoduganella
Otu0007661	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0008169	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
Otu0008522	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	unclassified
Otu0009188	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
Otu0009256	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
Otu0009427	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
Otu0001632	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaeta
Otu0001468	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Otu0006043	Verrucomicrobia	Spartobacteria	unclassified	unclassified	unclassified

Table A.9.

A list of Fungal Indicators in Soil Associated with Panicum virgatum for Temporal Dynamics Analysis

OTU	Phylum	Class	Order	Family	Genus	Species
WEEK 1						
Otu00804	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00166	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	unclassified
Otu00377	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	unclassified	Chaetomiaceae_sp
Otu01963	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	unclassified	unclassified
Otu00178	Ascomycota	Sordariomycetes	Hypocreales	Hypocreales	Stachybotrys	unclassified
Otu01307	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Neocosmospora	Neocosmospora _vasinfecta
Otu00682	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01621	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00416	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00022	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00086	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00128	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00135	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00273	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00480	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00573	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00750	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00916	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01526	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02403	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01539	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01294	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

WEEK 2						
Otu00350	Ascomycota	Dothideomycetes	Pleosporales	Cucurbitariaceae	Pyrenochaetopsis	Pyrenochaetopsis_sp_NRRL_62966
Otu01119	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Exophiala	Exophiala_moniliae
Otu00407	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae	unclassified	unclassified
Otu00332	Ascomycota	Sordariomycetes	Hypocreales	Hypocreales	Stachybotrys	unclassified
Otu01653	Ascomycota	Sordariomycetes	Hypocreales	unclassified	unclassified	unclassified
Otu00185	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	Mortierella_sp_18_M_4
Otu02041	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	unclassified
Otu00579	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales	Periconia	Periconia_sp_CY137
Otu00164	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu00043	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu01163	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Protrudomycetaceae	Protrudomyces	Protrudomyces_lateralis
Otu00239	Chytridiomycota	Chytridiomycetes	Rhizophydiales	Rhizophydiaceae	Rhizophydium	Rhizophydium
Otu00999	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu00222	Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	unclassified	unclassified
Otu00781	Ascomycota	Lecanoromycetes	Ostropales	Stictidaceae	unclassified	unclassified
Otu00140	Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriales	unclassified	Trichosphaeriales
Otu00691	Chytridiomycota	unclassified	unclassified	unclassified	unclassified	Chytridiomycota
WEEK 4						
Otu00784	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00512	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus_flavus
Otu01183	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00492	Ascomycota	Leotiomycetes	unclassified	unclassified	unclassified	unclassified

Otu00054	Ascomycota	Dothideomycetes	Pleosporales	Montagnulaceae	unclassified	Montagnulaceae_sp
Otu00029	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	Gibberella_intricans
Otu00026	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	unclassified	unclassified
Otu00972	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Powellomyces	Powellomyces_sp
Otu01063	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Powellomyces	unclassified
Otu01905	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Powellomyces	unclassified
Otu00577	Basidiomycota	Tremellomycetes	Tremellales	Tremellales	Bulleromyces	Bulleromyces_albus
Otu02039	Basidiomycota	Tremellomycetes	unclassified	unclassified	unclassified	unclassified
Otu00123	Ascomycota	Dothideomycetes	Pleosporales	Tubeufiaceae	unclassified	Tubeufiaceae_sp
WEEK 8						
Otu00537	Glomeromycota	Glomeromycetes	Diversisporales	Acaulosporaceae	Acaulospora	unclassified
Otu00585	Glomeromycota	Glomeromycetes	Diversisporales	Acaulosporaceae	unclassified	unclassified
Otu00454	Basidiomycota	Agaricomycetes	Agaricales	unclassified	unclassified	unclassified
Otu00186	Basidiomycota	Tremellomycetes	Cystofilobasidiales	Cystofilobasidiaceae	Cystofilobasidium	Cystofilobasidium_macerans
Otu01941	Basidiomycota	Tremellomycetes	Filobasidiales	Filobasidiaceae	Cryptococcus	Cryptococcus_chernovii
Otu01522	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Articulospora	Articulospora_sp
Otu02155	Ascomycota	Leotiomycetes	Helotiales	Helotiales	Tetracladium	Tetracladium_marchalianum
Otu00683	Zygomycota	Zygomycota	Mucorales	Mucoraceae	Mucor	Mucor_hiemalis
Otu00165	Ascomycota	Dothideomycetes	Pleosporales	Phaeosphaeriaceae	Stagonospora	Stagonospora_pseudocaricis
Otu01663	Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporidiobolus	Sporidiobolus_aff_pararoseus_1_MCA_3691
Otu00383	Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolales)	Rhodotorula	Rhodotorula_nothofagi
Otu00896	Basidiomycota	Tremellomycetes	Tremellales	Tremellales	Cryptococcus	Cryptococcus

						_dimennae
Otu01704	Basidiomycota	Tremellomycetes	Tremellales	Tremellales	Tremellales	unclassified
Otu02076	Basidiomycota	Tremellomycetes	Tremellales	Tremellales	Cryptococcus	Cryptococcus _paraflavus
WEEK 16						
Otu00253	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00393	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00469	Glomeromycota	Glomeromycetes	Archaeosporales	Archaeosporaceae	u unclassified	Archaeosporaceae
Otu00442	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	unclassified
Otu00190	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	unclassified
Otu00352	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	unclassified
Otu00031	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00103	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00209	Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Conocybe	unclassified
Otu02304	Ascomycota	Dothideomycetes	Capnodiales	unclassified	unclassified	unclassified
Otu00225	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	Ceratobasidium_sp
Otu02221	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium	Ceratobasidium_sp
Otu00296	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	unclassified
Otu00397	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00413	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00545	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00662	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00879	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01672	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01904	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01744	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00935	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp
Otu01116	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp
Otu01170	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp

Otu01195	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp
Otu01417	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp
Otu01994	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae_sp
Otu00159	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00680	Ascomycota	Sordariomycetes	Hypocreales	Hypocreales	Acremonium	Acremonium _sp_24_OA_2013
Otu00265	Ascomycota	Dothideomycetes	Pleosporales	Montagnulaceae	unclassified	unclassified
Otu01211	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	unclassified	unclassified
Otu00243	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _brasilianum
Otu00247	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _brasilianum
Otu00709	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _occultum
Otu01198	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus_occultum
Otu01257	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus_occultum
Otu00544	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	unclassified
Otu00981	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	unclassified
Otu00237	Glomeromycota	Glomeromycetes	Paraglomerales	unclassified	unclassified	unclassified
Otu01970	Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae	Zygophiala	Zygophiala_sp_FS2
Otu00137	Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Trichosporon	Trichosporon _moniliiforme
Otu00303	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	Archaeosporales_sp
Otu00316	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	Archaeosporales_sp
Otu00962	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	unclassified
Otu00379	Glomeromycota	Glomeromycetes	Archaeosporales	unclassified	unclassified	unclassified
Otu00535	Glomeromycota	Glomeromycetes	Glomerales	unclassified	unclassified	Glomerales_sp
Otu00177	Glomeromycota	unclassified	unclassified	unclassified	unclassified	Glomeromycota_sp
Otu00250	Glomeromycota	unclassified	unclassified	unclassified	unclassified	Glomeromycota_sp

Otu00421	Glomeromycota	unclassified	unclassified	unclassified	unclassified	Glomeromycota_sp
Otu01229	Glomeromycota	Glomeromycetes	Paraglomerales	unclassified	unclassified	Paraglomerales_sp
WEEK 38						
Otu02182	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00101	Ascomycota	Dothideomycetes	Jahnulales	Aliquandostipitaceae	Xylomyces	Xylomyces_sp
Otu00072	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00245	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01134	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00616	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00154	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00635	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02441	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01537	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01723	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00027	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	unclassified
Otu00124	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	Chaetomium _jatrophae
Otu00105	Ascomycota	Dothideomycetes	Pleosporales	Didymosphaeriaceae	Didymosphaeria	Didymosphaeria_sp
Otu00953	Glomeromycota	Glomeromycetes	Diversisporales	Diversisporaceae	Diversispora	Diversispora _epigaea
Otu00205	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00229	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00242	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00251	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00252	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00277	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00311	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Otu00317	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00410	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00446	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00477	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00478	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00514	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00660	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00671	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00678	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00679	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00740	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00830	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00842	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00850	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00854	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00892	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00933	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01093	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01104	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01117	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01126	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01128	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01148	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01208	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01239	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01290	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01300	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01318	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01367	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01429	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Otu01459	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01472	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01602	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01611	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01740	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01852	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01935	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02140	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02181	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02356	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00991	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00769	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01080	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01465	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00799	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01568	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02088	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02090	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01042	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00997	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01076	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01678	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00794	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02301	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00220	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00299	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00079	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00701	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01241	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00468	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified

Otu00556	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus_sp
Otu00800	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus_sp
Otu00908	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00957	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00966	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu01184	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu01097	Glomeromycota	Glomeromycetes	Glomerales	unclassified	unclassified	unclassified
Otu01007	Glomeromycota	Glomeromycetes	Glomerales	unclassified	unclassified	unclassified
Otu00076	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tricladium	Tricladium_splendens
Otu00036	Ascomycota	Leotiomycetes	Helotiales	unclassified	Scytalidium	Scytalidium_sp_2013
Otu00023	Ascomycota	Sordariomycetes	Sordariomycetes	Magnaporthaceae	unclassified	Magnaporthaceae
Otu00373	Basidiomycota	Agaricomycetes	Polyporales	Meruliaceae	Hyphoderma	Hyphoderma_obtusiforme
Otu00307	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Viridispora	Viridispora
Otu00617	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu00122	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu01333	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu00343	Chytridiomycota	Chytridiomycetes	Rhizophydiales	unclassified	unclassified	unclassified
Otu02428	Basidiomycota	Agaricomycetes	Russulales	unclassified	unclassified	unclassified
Otu01006	Chytridiomycota	Chytridiomycetes	Spizellomycetales	Spizellomycetaceae	Spizellomyces	Spizellomyces_dolichospermus
Otu00032	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	Chaetothyriales

Table A.10.

A list of Fungal Indicators Panicum virgatum Roots for Temporal Dynamics Analysis

OTU	Phylum	Class	Order	Family	Genus	Species
WEEK 1						
Otu01702	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02454	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00024	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02306	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00524	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01529	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00076	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Tricladium	Tricladiumlendens
Otu01331	Ascomycota	Leotiomycetes	Helotiales	unclassified	unclassified	unclassified
Otu00647	Basidiomycota	Microbotryomycetes	Leucosporidiales	Leucosporidiaceae	Mastigobasidium	Mastigobasidium _intermedium
Otu00906	Basidiomycota	Tremellomycetes	Tremellales	Tremellales	Cryptococcus	Cryptococcus _dimennae
Otu01506	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Penicillium	Penicillium _brevicompactum
WEEK 2						
Otu00553	Chytridiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
WEEK 4						
Otu00214	Ascomycota	Dothideomycetes	Pleosporales	Massarinaceae	Saccharicola	Saccharicola
Otu00134	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
WEEK 8						
Otu00537	Glomeromycota	Glomeromycetes	Diversisporales	Acaulosporaceae	Acaulospora	unclassified

Otu00585	Glomeromycota	Glomeromycetes	Diversisporales	Acaulosporaceae	unclassified	unclassified
Otu02147	unclassified	unclassified	unclassified	unclassified	Fungi_unclassified	unclassified
Otu00812	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus_versiforme
Otu02122	Basidiomycota	Agaricomycetes	Agaricales	Hygrophoraceae	Hygrocybe	Hygrocybe
Otu01197	Ascomycota	Dothideomycetes	Pleosporales	Leptosphaeriaceae	Leptosphaeria	Leptosphaeria_MH_2001
Otu01663	Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporidiobolus	Sporidiobolus_aff_pararoseus_1_MCA_3691
WEEK 16						
Otu00393	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00987	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02304	Ascomycota	Dothideomycetes	Capnodiales	unclassified	unclassified	unclassified
Otu00879	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01211	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae	unclassified	unclassified
Otu02060	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales	Phoma	Phoma_paspali
Otu01970	Ascomycota	Dothideomycetes	Capnodiales	Schizothyriaceae	Zygophiala	Zygophiala_FS2
WEEK 38						
Otu00101	Ascomycota	Dothideomycetes	Jahnulales	Aliquandostipitaceae	Xylomyces	Xylomyces
Otu00361	Ascomycota	Sordariomycetes	Sordariomycetes	Annulatascaceae	Conlarium	Conlarium_duplumascospora
Otu00147	Ascomycota	Pezizomycetes	Pezizales	Ascobolaceae	unclassified	Ascobolaceae
Otu00188	Ascomycota	Ascomycota	Ascomycota	Ascomycota	Staphylotrichum	Staphylotrichum_Amy_4
Otu00031	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00072	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00103	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00189	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00245	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified

Otu00286	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00290	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00807	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00960	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01035	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00010	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	unclassified	Chaetomiaceae
Otu00124	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	Chaetomium _jatrophae
Otu00296	Ascomycota	Sordariomycetes	Sordariales	Chaetomiaceae	Chaetomium	unclassified
Otu00913	Ascomycota	Sordariomycetes	Chaetosphaeriales	Chaetosphaeriaceae	Chaetosphaeria	Chaetosphaeria
Otu00062	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	unclassified
Otu00066	Ascomycota	Eurotiomycetes	unclassified	unclassified	unclassified	unclassified
Otu00450	Ascomycota	Sordariomycetes	Sordariomycetes	Glomerellaceae	Colletotrichum	Colletotrichum _chlorophyti
Otu00036	Ascomycota	Leotiomycetes	Helotiales	Helotiales	Scytalidium	Scytalidium_2013
Otu00345	Ascomycota	Leotiomycetes	Helotiales	unclassified	unclassified	unclassified
Otu00008	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	unclassified
Otu02129	Ascomycota	Eurotiomycetes	Chaetothyriales	Herpotrichiellaceae	Cladophialophora	unclassified
Otu00152	Ascomycota	Sordariomycetes	Hypocreales	Hypocreales	Acremonium	Acremonium _dichromosporum
Otu00436	Ascomycota	Sordariomycetes	Hypocreales	unclassified	unclassified	unclassified
Otu00167	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Zopfiella	Zopfiella_marina
Otu00376	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	Podospora	Podospora _longicollis
Otu00825	Ascomycota	Lecanoromycetes	unclassified	unclassified	unclassified	unclassified
Otu00023	Ascomycota	Sordariomycetes	Sordariomycetes	Magnaporthaceae	unclassified	Magnaporthaceae
Otu00307	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Viridispora	Viridispora
Otu01112	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	unclassified	unclassified
Otu00968	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	unclassified	unclassified
Otu00607	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu00852	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified

Otu00976	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu01328	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu00122	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu01333	Ascomycota	Dothideomycetes	Pleosporales	unclassified	unclassified	unclassified
Otu02166	Ascomycota	Dothideomycetes	Dothideomycetes	Pseudeurotiaceae	Pseudeurotium	Pseudeurotium _hygrophilum
Otu00314	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu00787	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu00877	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu00947	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu01638	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu01285	Ascomycota	Sordariomycetes	unclassified	unclassified	unclassified	unclassified
Otu00107	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	Aspergillus _brasiliensis
Otu00726	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae	Talaromyces	unclassified
Otu00140	Ascomycota	Sordariomycetes	Trichosphaeriales	Trichosphaeriales	unclassified	Trichosphaeriales
Otu01820	Ascomycota	Dothideomycetes	Pleosporales	Tubeufiaceae	unclassified	Tubeufiaceae
Otu00032	Ascomycota	Eurotiomycetes	Chaetothyriales	unclassified	unclassified	Chaetothyriales
Otu00235	Ascomycota	Sordariomycetes	Xylariales	Xylariales	Microdochium	Microdochium _E9329c
Otu00616	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00298	Ascomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01932	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01537	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00626	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00635	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01270	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01673	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00390	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Arachnion	Arachnion_album
Otu02195	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Lycoperdon	unclassified

Otu00080	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00936	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu01996	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu01497	Basidiomycota	Agaricomycetes	unclassified	unclassified	unclassified	unclassified
Otu00320	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00555	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00027	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Thanatephorus	unclassified
Otu00153	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	unclassified	unclassified
Otu00731	Basidiomycota	Agaricomycetes	Polyporales	Ganodermataceae	Ganoderma	Ganoderma_lucidum
Otu02428	Basidiomycota	Agaricomycetes	Russulales	unclassified	unclassified	unclassified
Otu00681	Basidiomycota	Atractiellomycetes	Atractiellales	unclassified	unclassified	Atractiellales
Otu01720	Basidiomycota	Atractiellomycetes	Atractiellales	unclassified	unclassified	Atractiellales
Otu01477	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02321	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00767	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00416	Basidiomycota	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01266	Chytridiomycota	Chytridiomycetes	unclassified	unclassified	unclassified	unclassified
Otu00312	Chytridiomycota	Chytridiomycetes	Rhizophydiales	unclassified	unclassified	unclassified
Otu00343	Chytridiomycota	Chytridiomycetes	Rhizophydiales	unclassified	unclassified	unclassified
Otu01007	Glomeromycota	Glomeromycetes	Glomerales	unclassified	unclassified	unclassified
Otu00468	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00528	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae
Otu00556	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus
Otu00677	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae
Otu00735	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	Glomeraceae
Otu00800	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	Glomus	Glomus
Otu00908	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00957	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00966	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified
Otu00159	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae	unclassified	unclassified

Otu00243	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _brasilianum
Otu00247	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _brasilianum
Otu00709	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _occultum
Otu01257	Glomeromycota	Glomeromycetes	Paraglomerales	Paraglomeraceae	Paraglomus	Paraglomus _occultum
Otu00291	Glomeromycota	Glomeromycetes	Paraglomerales	unclassified	unclassified	unclassified
Otu00237	Glomeromycota	Glomeromycetes	Paraglomerales	unclassified	unclassified	unclassified
Otu00177	Glomeromycota	unclassified	unclassified	unclassified	unclassified	Glomeromycota
Otu00022	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00033	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00086	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00135	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00145	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00173	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00191	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00193	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00205	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00229	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00242	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00244	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00251	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00252	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00277	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00283	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00311	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00315	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00342	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00364	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Otu00368	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00400	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00411	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00446	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00478	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00514	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00545	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00582	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00598	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00618	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00640	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00649	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00655	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00705	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00718	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00748	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00850	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00854	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00878	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00899	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00970	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01031	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01096	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01099	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01153	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01208	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01209	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01263	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01300	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01308	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Otu01321	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01323	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01356	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01366	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01367	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01368	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01391	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01451	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01545	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01565	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01579	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01583	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01719	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01738	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01740	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01762	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01776	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01808	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01989	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02104	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02302	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02332	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02333	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02419	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00991	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00769	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01753	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00799	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01324	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00971	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified

Otu01703	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00847	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01514	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00344	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01448	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02081	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu02235	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00102	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00150	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00299	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00513	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01057	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01086	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01744	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00079	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00666	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00837	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01825	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00701	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu01953	unclassified	unclassified	unclassified	unclassified	unclassified	unclassified
Otu00009	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	Mortierella _rishikesha
Otu00275	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	unclassified
Otu00482	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	unclassified
Otu00911	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	Mortierella _horticola
Otu01085	Zygomycota	Zygomycota	Mortierellales	Mortierellaceae	Mortierella	Mortierella
Otu02025	Zygomycota	Zygomycota	Endogonales	unclassified	unclassified	Endogonales