DISSERTATION

IMPLEMENTING ORGANIC AMENDMENTS TO ENHANCE MAIZE YIELD, SOIL MOISTURE, AND MICROBIAL NUTRIENT CYCLING IN TEMPERATE AGRICULTURE

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ABSTRACT

IMPLEMENTING ORGANIC AMENDMENTS TO ENHANCE MAIZE YIELD, SOIL MOISTURE, AND MICROBIAL NUTRIENT CYCLING IN TEMPERATE AGRICULTURE

To sustain agricultural production into the future, management should enhance natural biogeochemical cycling within the soil. Strategies to increase yield while reducing chemical fertilizer inputs and irrigation require robust research and development before widespread implementation. Current innovations in crop production use amendments such as manure and biochar charcoal to increase soil organic matter and improve soil structure, water, and nutrient content. Organic amendments also provide substrate and habitat for soil microorganisms that can play a key role cycling nutrients, improving nutrient availability for crops. Additional plant growth promoting bacteria can be incorporated into the soil as inocula to enhance soil nutrient cycling through mechanisms like phosphorus solubilization. Since microbial inoculation is highly effective under drought conditions, this technique pairs well in agricultural systems using limited irrigation to save water, particularly in semi-arid regions where climate change and population growth exacerbate water scarcity.

The research in this dissertation examines synergistic techniques to reduce irrigation inputs, while building soil organic matter, and promoting natural microbial function to increase crop available nutrients. The research was conducted on conventional irrigated maize systems at the Agricultural Research Development and Education Center north of Fort Collins, CO. The first field experiment tested a temporally limited irrigation strategy with high application rates of

organic amendments (30 Mg ha^{-1}) to increase soil moisture, N and P retention, and enhance soil microbial activity. The experiment used biochar created from bio-energy production. The control plots contained 1.49% total soil carbon, and biochar addition increased total carbon to 2.67%. The biochar also had variable impacts on microbial extracellular enzyme activities, causing a 40% reduction in β-1,4-glucosidase and phosphatase activities, with repercussions for hydrolysis of soil P and cellulose. However, the biochar amendment did not enhance yield. This field experiment also found that the limited irrigation technique reduced water inputs by 30% while maintaining yield.

The second experiment of the dissertation determined the mechanism behind the decrease in extracellular enzymatic activities after biochar addition. Through a combination of a Bradford protein assay and a fluorometric assay of potential enzymatic activities, the pine wood biochar adsorbed and reduced both β-glucosidase and acid phosphatase activities by 75-100% relative to a control soil. Though highly variable, depending upon pH, the main factor influencing activity levels was the solid phase. The high temperature biochar had a large surface area within micropores. The substrate can diffuse into the micropores, where it is inaccessible to large enzymes; there is lower catalysis of those substrates, which indicates potentially lower nutrient release in the soil.

Finally, to examine the agronomic efficacy of biochar, a second maize field trial was developed also implementing full and limited irrigation. This experiment incorporated an engineered coconut hull biochar, characterized by a neutralized pH, removed toxins from the surface, and homogenized pores. The biochar was banded directly onto the seed row at a low application rate (0.8 Mg ha^{-1}). Additionally, a surface applied plant growth promoting P solubilizing bacterial inoculum was tested alone, and in combination with biochar. To determine

the efficacy of these amendments to improve soil nutrient availability and maize yields, the soil nutrient supply, crop nutrient concentration and accumulation, and soil bacterial community composition were measured. The bacterial community data was analyzed using a cutting-edge technique based on Exact Sequence Variants to analyze single nucleotide differences, enhancing comparability with future studies. In this experiment the biochar increased soil available K and S which correlated to crop uptake, shifted the early season microbial community, and increased by 20% over the control (+1.95 Mg ha^{-1}). The inoculum and combination treatments did not impact yield, but in these plots we observed the presence of bacterial families that were added in the original inoculum. Overall this work emphasized the efficacy of precision management strategies with biochar application to enhance yield.

This dissertation work underlines the importance of contentiously selecting specific amendment type, application rate and method to achieve either agronomic or environmental benefits. Continued research with synergistic approaches will help to develop best practices within the region to manage agroecosystems for improved resilience.

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Chapter 1: Introduction

The agricultural revolution 10,000 years ago developed a simple principle: increase food supply by managing soil for continued crop production (Larsen, 2006). The development of modern farming to effectively mine soil nutrients to produce higher yield and economic return results in the degradation of natural soil processes, increased erosion from tillage (Montgomery, 2007), and often environmental contamination from heavy use of chemical fertilizers and pesticides (Bünemann et al., 2006; Di and Cameron, 2002; Power and Schepers, 1989). Today agriculture faces many challenges including scarce resources such as limited P fertilizer (Neset and Cordell, 2012), and energy intensive N fertilizer production, and unprecedented climate conditions as seasonal average temperatures rise and drought increases in frequency and intensity (Reichstein et al., 2013). In the face of increasing drought and resource scarcity, agricultural management needs to efficiently produce yield and enhance the soil for the long-term provision of ecosystem services (Tilman et al., 2002).

Current conventional agricultural management can disrupt critical soil ecosystem processes, but innovative developments offer promising alternatives. These conventional practices can include the seasonal removal of crop biomass, use of monoculture, and implementation of long fallow periods, and all of these strategies reduce the quantity and diversity of natural plant inputs and disrupt soil nutrient cycling and organic matter formation (Marriot and Wander, 2006; Reganold et al., 1987). Alternative strategies may focus on crop breeding, such as improved drought tolerance (Agrama and Moussa, 1996; Ashraf, 2010), or novel soil management, such as mapping fields for precision irrigation (Khosla et al., 2008), addition of innovative organic amendments (Awad et al., 2013; Wu et al., 2017), manipulation of beneficial soil microbes (Chaparro et al., 2012), or combined strategies (Bakker et al., 2012). With this myriad of management options, prior to on-farm implementation, field and laboratory research can help elucidate the most effective techniques and the mechanisms behind the potential impacts.

To examine alternative management strategies in temperate agroecosystems, this dissertation research focuses on a case study in the semi-arid Western US, in northern Colorado, Fort Collins area. This area receives approximately 408mm of rainfall annually with an average temperature of 10ºC (US Climate Data, accessed June 2018) and serves as proxy for other semi-arid zones, including the Great Plains Region, where yields from rain fed agriculture are becoming less predictable and irrigation remains paramount to agricultural management. In this plains region, an increasing competition for scarce water resources will impact all irrigated agriculture. As maize comprises 40% of irrigated lands in the plains region, it is an important crop for studying water and overall agricultural efficiency (Payero et al., 2006). Maize (*Zea mays* L) crops also require high levels of nutrients, specifically N to support growth and development. The sustainable production of irrigated maize in semi-arid environments requires research experimentation to examine synergistic innovative management impact on yield, soil moisture, and microbial nutrient cycling.

This dissertation work assesses how organic amendments influence soil water and microbial nutrient cycling for sustaining crop yield with limited additional inputs in semi-arid temperate agriculture. The research combines the use of manure and biochar amendments and plant-growth promoting microbial inoculum to enhance both soil water content and plant available nutrients.

The following questions are addressed in three main chapters:

1. How do manure and biochar amendments impact soil moisture and microbial nutrient cycling for limited irrigation maize?

2. Do microbial extracellular enzymes adsorb to soil mineral and biochar surfaces and impact nutrient cycling activity?

3. Can precision biochar application and plant growth promoting bacterial inoculum improve crop available nutrients and yield under limited irrigation?

The subsequent research experiments were conducted at the Agricultural Research Development and Education Center and in the EcoCore laboratory facilities at Colorado State University.

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Chapter 2: Biochar and manure amendments impact soil nutrient contents and microbial enzymatic activity in a semi-arid irrigated maize cropping system[1]

Introduction

Increasing drought and competition for water resources among municipal, industrial, and agricultural sectors requires improved water conservation in semi-arid regions. Agricultural producers can reduce water use by adopting limited irrigation strategies (DeJonge et al., 2011; Fereres and Soriano, 2007), such as applying irrigation only at critical crop growth phases (Schneekloth et al., 2009). To enhance soil water retention under limited irrigation, traditionally, producers have treated soils with organic amendments, such as manure (Bulluck III et al., 2002). Alternatively, recent research indicates that a charcoal-like amendment, known as biochar, can have similar effects under limited irrigation, increasing soil volumetric moisture content even with reduced water inputs (Akhtar et al., 2014).

Biochar is created through the pyrolytic conversion of any organic feedstock in an oxygen limited environment, at temperatures >350°C (Lehmann and Joseph, 2015). The resulting product consists of highly stable condensed aromatic carbon (C) rings, with physiochemical characteristics that depend on pyrolysis conditions and feedstock type (Enders et al., 2012). This high variability in characteristics necessitates the investigation of different biochars in various soil types and climatic regions to determine which biochar can effectively achieve particular management goals (Novak et al., 2014). For example, use of biochar co-generated from bioenergy production from local feedstock in our study system in Colorado may

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[1] Foster EJ, Hansen N, Wallenstein M, Cotrufo MF (2016) Biochar and manure amendments impact soil nutrients and microbial enzymatic activities in a semi-arid irrigated maize cropping system. Agriculture, Ecosystems & Environment, 233, 404-414.

also have additional environmental and cost benefits (Field et al., 2013) compared to conventional amendments.

With high organic C content, both manure and biochar could have similar impacts on soil nutrients, structure, and microbial dynamics in agricultural systems. Soil fertility research has long established that manure amendments add nutrients to soils (*e.g.* organic N or ammonium (NH_4^+)) and also improve soil structure, therefore increasing nutrient retention and water holding capacity (Salter and Williams, 1968; Ware and Johnson, 1949). These changes can benefit crop production by improving nutrient cycling via stimulation of microbial growth and activity (Bulluck III et al., 2002; Elzobair et al., 2016; Peacock et al., 2001). Active soil microbes metabolize and turnover organic matter, secreting specific extracellular enzymes to break down large organic molecules into monomers, also available for plant uptake (Burns, 1982). Since specific enzymes are known to cycle C, N, and P substrates, shifts in extracellular enzymatic activities (EEAs) are often used as a proxy for changing metabolic pathways and thus microbial function in soils (Bell et al., 2013). The addition of organic material such as manure increases available C in the soil, which causes growth in microbial biomass (Witter et al., 1993), and can increase the production and activity of extracellular enzymes (Burns et al., 2013a). As a high C substance, with a large surface area and porosity, biochar also has the potential to similarly influence soil structure and nutrient retention, and thus microbial biomass and subsequent enzymatic activity.

In temperate agriculture, biochar addition influences microbial dynamics through physical changes to soil structure and through chemical changes to soil stoichiometry and pH (Ippolito et al., 2012; Lehmann and Joseph, 2015; Quilliam et al., 2013; X. Wang et al., 2015). By augmenting soil surface area and porosity, biochar can increase soil water holding capacity

(Brockhoff et al., 2010), and provide habitat and relief from predation for microbes (Jaafar et al., 2015). Aside from physical habitat, biochar's large surface area and reactivity attracts ions and low-molecular weight organic compounds; thus biochar can initially increase nutrient retention and potential sites for microbe-substrate interactions (Gul et al., 2015). Even with these known structural changes, the effect of pine-wood biochar on microbial biomass remains variable, ranging from no impact to 100% increases (Brantley et al., 2015; Domene et al., 2014; Gomez et al., 2014; Jin, 2010). Despite the wide variation in response of microbial biomass to biochar, few researchers have quantified how microbial function is altered by these induced soil physical changes in soil moisture and surface area, and chemical changes to nutrient retention and pH (Elzobair et al., 2016; Lehmann et al., 2011; Oleszczuk et al., 2014). Previous methods have quantified microbial functional shifts and changes to nutrient cycling by measuring EEAs (Bell et al., 2013; Burns et al., 2013b).

Enzyme activity is sensitive to pH and typically changes with nutrient dynamics, so quantification of these proteins can further our understanding of biochar's impact on microbial function and overall soil fertility. Current research on biochar-enzyme interactions assesses soil chemistry and stoichiometry. Since biochar can influence soil pH (alkaline pine biochar can lime soils by 1.0-1.4 units (Rogovska et al., 2014)), it can impact enzymatic activities that function within restricted pH ranges. The pH effect depends on the chemical composition of the biochar, which also can influence soil nutrients. Biochar addition alters soil stoichiometry due to the large organic C inputs. This increase of C in some temperate ecosystems can lead to an increase in microbial nitrogen (N) immobilization into biomass by up to three-fold (Güereña et al., 2012) and subsequent N stabilization on biochar surfaces (Brantley et al., 2015), although biochar addition does not always induce N immobilization (Cayuela et al., 2013). Biochar effects on N dynamics and N-cycling enzymes remains ambiguous (Bailey et al., 2002), as even soil N mineralization has been shown to decrease (Lentz et al., 2014), increase (Domene et al., 2014), and remain unchanged (Gaskin et al., 2010) after biochar addition. Recent biochar studies also show variable impacts on soil P: one greenhouse trial demonstrated no impact on soil P (Domene et. al 2014), a short incubation suggested biochar alters colloidal particles and P retention (Soinne et al., 2014), and another column study suggested that biochar lowered P bioavailability due to adsorption of orthophosphate and organic P compounds to its surface (Laird et al., 2010). Yet another consideration for nutrient stoichiometry and enzyme interactions is that biochar contains a small labile component that can provide readily available nutrients for soil microbes and stimulate activity (Anderson et al., 2011; Lehmann et al., 2011; Spokas et al., 2012; Warnock et al., 2007). These variable nutrient dynamics from laboratory and column studies prompt the examination of biochar and microbial nutrient dynamics within specific systems *in situ*.

We compared the effects of manure and bioenergy co-generated, fast-pyrolysis pine biochar amendments on maize yield under limited irrigation. We specifically analyzed soil moisture, microbial abundance, and enzymatic activities to assess changes to soil structure and microbial function. We hypothesized that the biochar would increase soil moisture and total soil C. Due to these increases, we predicted that biochar would enhance microbial biomass, increasing enzymatic nutrient cycling, and thus more effectively maintain yield even under limited irrigation. We predicted manure to have similar, but weaker effects in this semi-arid temperate agricultural system.

Methods

Field site and experimental design

This experiment was conducted at the Agricultural Research Development and Education Center, Colorado State University, Fort Collins (40.59°N, 105.14°W, 1560 m elevation). The climate is semi-arid, with an annual rainfall of 408 mm (average normal from 1981-2010) (usclimatedata.com, accessed 2016). After biochar application in October of 2013, the rainfall during the maize growing season (May 1-Oct 31, 2014) was 272 mm, and average air temperature 16.3°C, ranging between -3.44°C and 35.8°C (Colorado State University CoAgMet weather station, 40.65°N, 105°W). The soil is classified as a Fort Collins loam, with 51% sand, 20% silt and 29% clay (Abulobaida, 2014). The soil was further characterized by Abulobaida (2014) as having a 1.3g cm^{-3} bulk density, CEC of 24.65 $cmol_c$ kg^{-1}, 1.5% total C, 0.1% total N, 185.0 ppm K, 514.75 ppm Mg, 3904.458 ppm Ca, 81.458 ppm S, 0.583 ppm Zn, 2.242 ppm Mn, and 575.5 ppm Fe.

We implemented a split-split plot design with four replicate blocks. The main plots were “full” and “limited” irrigation treatments, further split into two maize hybrid subplots. We then applied three soil organic amendment treatments: biochar, manure, and a control, with no amendment, for a total of 48 sub-subplots. Soil samples were analyzed at the sub-subplot level (n=4). Each amended plot was 4.5m x 4.5m and planted with six rows of maize. A nine m alley separated the main irrigation plots on all sides.

The field was prepared in September of 2013 by tilling to 30 cm, followed by leveling in October. The pine-wood biochar and steer manure (Table 2.1), were surfaced applied at 30 Mg ha^{-1} (dry weight) and were disc-tilled in to 15cm on November 14, 2013. The biochar consisted of primarily virgin pine wood, that underwent fast-pyrolysis for energy generation at 400-700°C with five minutes of reaction time (Confluence Energy LLC, Kremmling, CO). Biochar and manure properties are reported in Table 2.1, including: total C and N, pH, bulk density, cation exchange capacity (CEC) (measured using an ammonium acetate protocol), Brunauer-Emmett-Teller surface area and pore volume (measured with N_2 gas) (see other laboratory methods below). The pine biochar had a particle size of 0.25-3.0mm and a moisture content of 49.2% at the time of application. Further analysis by Control Laboratories characterized the biochar as 10.8% ash, 4.5% O, 1.3% H, 0.38 % total P, 0.06 O:C ratio, and 0.21 H:C ratio (Watsonville, CA).

Irrigation occurred once per week for the well-watered "full" irrigation determined by the difference between accumulated evapotranspiration and precipitation during the week. For the "limited" irrigation treatment, all irrigation inputs were withheld from the appearance of the seventh collared leaf (V7) to maize tasseling (*i.e.* June 29 – July 28, 2014). This resulted in a 30% reduction in irrigation inputs.

Fertilizer was applied at 202N-45P-13S-1Z kg ha^{-1} on April 9, 2014, and tilled with a roller harrow to 10 cm. Herbicide and side-dressing were applied on June 17, 2014 at the following rates: Roundup® PowerMAX at 2.3L ha^{-1}, Status herbicide at 0.33L ha^{-1}, Ad-Wet 90 at 0.35 L ha^{-1}, and Ammonium Sulfate Sprayable at 0.49 kg ha^{-1}. On May 19, 2014 two Dupont® Pioneer maize hybrids (P8954AM and P9305AM) were seeded at approximately 79,000 seeds ha^{-1} with row spacing of 76 cm. Except for percent cob fill (see results), we did not observe significant differences between the two hybrids and results are averaged across them (n=8).

Soil sampling and characterization of soil moisture and nutrients

We sampled soils from 0-10 cm with a 2.5 cm-diameter hand corer on the following three dates in 2014: (A) June 29, 41 days after planting (before the start of the limited irrigation drought period), (B) July 27, 69 days after planting (at the end of the limited irrigation treatment), and (C) September 1, 105 days after planting (three weeks before the final harvest). Four random cores were taken to create one bulked sample per sub-subplot. Soils were sieved to 2 mm and stored in plastic bags and kept at ~4°C until final analyses, which occurred within a few days from sampling.

Lab analyses to characterize basic properties on all samples included gravimetric soil moisture, total soil C and total soil N content, pH, available P, and mineral N (ammonium (NH_4^+) and nitrate (NO_3^-)). Gravimetric soil moisture was determined on a 10 g subsample by drying in a 105°C oven for 24 h, and subsequently used for soil dry weight correction. The oven-dry soil samples were pulverized and used for the analyses of %C and %N on a LECO True-Spec CN analyzer (Leco Corp., St. Joseph, MI, USA) and for pH measurements in 1:5 deionized water using an Orion EA 9110 Meter (Thermo Scientific, Beverly, MA, USA). Available P was measured with the molybdenate blue method for alkaline soils (Dick and Tabatabai, 1977). Mineral N was extracted from field moist 15 g soil subsamples with 75 mL of 2M KCl for analysis on an Alpkem Flow Solution IV Automated wet chemistry system (O.I. Analytical, College Station TX, USA) (Miller and Keeney 1982). All analyses were completed at the EcoCore Analytical Facilities (Colorado State University, Fort Collins, CO). Additionally, using a subset of samples from November 2013 (n=3 per soil treatment), we measured plant available water with a pressure plate apparatus (Klute, 1986) as the difference between field capacity (-33 KPa) and wilting point (-1500KPa) (data not shown).

Microbial biomass and enzymatic activities

All soil samples were analyzed for microbial biomass and EEA within 10 days from collection. Microbial biomass was determined using two 8 g subsamples via the chloroform fumigation extraction method, modified to a 5 day incubation period (Brookes et al., 1985), with extractable total organic C and total N measured with a TOC-V-TN analyzer (Shimadzu Corp., Kyoto, Japan). As a proxy for microbial biomass, we used the chloroform fumigation-extracted C and N, referred to as microbial biomass C (MBC) and microbial biomass N (MBN). We tested for sorption of dissolved organic C and N onto the biochar surface (Jin, 2010) by adding biochar at the same rate of field application to five control soil samples directly before the fumigation. The calculated correction factors for sorption of dissolved organic C and N on the surface of the biochar had no significant impact on MBC and MBN results; thus uncorrected values are reported.

To assess potential EEA we used a high-throughput fluorometric assay for seven common extracellular enzymes (Table 2.2) that are known to breakdown C, N, and P substrates, as described by Bell et al. (2013) . Briefly, 91 mL of 50 mM Tris buffer (pH 8.3) was blended with 2.75 g of field moist soil for one minute. From this soil slurry, 800 µl was filtered and pipetted into a 96 deep-well plate, with seven rows filled with 200 µl of 200 µM substrate (Table 2.2). For each sample two standard plates were made with soil slurries (800 µl) mixed with the two fluorogenic moieties without substrate, at concentrations from 0 to 100 µM (Table 2.2, 4-Methylumbelliferone and 7-Amino-4methylcoumarine). From these two standard plates, we calculated curves to correct for quenching of fluorescence due to floating soil or organic particles. Each plate of soil-substrate mixture and corresponding two standard plates were incubated for 3h at 22°C. After incubation, the plates were centrifuged at 1500 RPM for 3 minutes and 200 µl of supernatant was transferred to a new 96-well black plate. The absorbance was measured at 365 nm excitation and 450 nm emission on an Infinite M200 Microplate Reader (Tecan Trading AG, Switzerland).

Maize biomass and yield

Plant aboveground biomass was measured on September 22, 2014 after the crop reached physiological maturity. All plants in a 2 m section of each sub-subplot were cut at the ground and biomass was weighed moist in the field. We then hand-harvested one plant per plot to calculate the moisture correction and grain biomass, by drying at 70°C and weighing each plant (Hay, 1995). Yield data are reported in Mg ha^{-1} dry grain and dry biomass (including grain, cob, stalks, and dropped leaves). Percent cob fill was measured as the length of the cob with kernels divided by the whole cob length. The harvest index was calculated as the grain mass over the total plant biomass.

Statistical Analysis

All statistical analyses were conducted using R version 3.2.2 (R Core Team, 2013). To examine the effects of irrigation, maize variety, and organic soil amendments over three sampling dates, we fit general linear mixed effect models with block as the random effect, and ran analysis of variance, followed by pairwise comparisons using lsmeans(). To ensure all data fit a normal distribution, transformation of log (x+1) were used for three response variables: NO_3^-, microbial biomass C, and total soil C. Due to multiple zeros, NH_4^+ data was analyzed for presence-absence using logistic regression. To analyze the activity of the seven enzymes, non-metric multidimensional scaling (NMDS) was used in the metaMDS package, using a Euclidean distance matrix, with random starting configurations. As three dimensions did not significantly further reduce stress, two dimensions are reported and goodness of fit was greater than 0.70 for all three ordinations. To test if differences in environmental soil data correlated to differences in EEA, an analysis of variance was conducted via a PerMANOVA using Adonis.

Results

Soil moisture and nutrients

Averaged over the three sampling dates, manure significantly increased gravimetric water content over the control by 15% (*p*=0.037) (Fig. 2.1). There was no significant interaction of soil amendment and irrigation level on soil moisture measurements. In July, at the height of the drought period, the limited irrigation treatment decreased soil gravimetric water content by 49% from the full irrigation (*p*=0.009, pairwise comparison). Soil amendments altered the percent of total soil C, the percent of total soil N, and the available P content, but not mineral N pools or soil pH (Table 2.3). Though manure had no impact on total soil C, biochar increased total soil C to 2.67%, an equivalent of an 80% increase over the control of 1.49% C (*p*<0.001) (Table 2.3). Manure significantly increased total soil N by 9.7% over the control (p<0.001) (Table 2.3). Over time, the percent total soil N accumulated in July (*p*<0.01) and then decreased again in September (*p*<0.001) (Table 2.3). Soil NH_4^+ and NO_3^- levels were unaffected by soil amendments. Levels of NH_4^+ changed only over time, with undetectable NH_4^+ levels in June, and higher values in July and September (*p*<0.001) (Table 2.3). Soil NO_3^- levels differed between irrigation treatments and over time. The primary difference between irrigation treatments occurred in July, when soil NO_3^- in the fully irrigated plots was significantly lower than in the other plots (*p*=0.018) (Table 2.3). For soil available P, biochar had no effect, but manure increased available P by 45% over the control, averaged over time (*p*<0.001) (Table 2.3). Available P also varied over time between the irrigation treatments: from June to July available soil P increased by 39% in the fully irrigated plots (*p*=0.055, pairwise comparison) and by 81% in the limited irrigation plots (*p*<0.001, pairwise comparison) (Table 2.3).

Microbial biomass

Soil amendments significantly impacted MBC (p=0.027) with major differences between biochar and manure (p=0.031, pairwise comparison) (Table 2.3). Manure significantly increased MBC by 15% over the control, while biochar decreased MBC slightly over the control (Table 2.3). Over time and irrigation treatments, between June and July MBC increased by 82% under full irrigation and by 33% under limited irrigation. In September, MBC decreased to similar levels under limited and full irrigation. MBN did not significantly differ by soil treatment (p=0.093), though manure maintained slightly higher MBN than the biochar treatment (Table 2.3). For MBN there was a significant interaction between irrigation and time, which occurred only in July. Averaged over soil amendment, in the fully irrigated plots MBN increased by 60.6% in July, while the limited irrigation decreased MBN by 46.2% in July (Table 2.3). In September, after the restart of irrigation, the MBN in the limited and fully irrigated plots increased by an average of 122% from July (p<0.001) (Table 2.3). These variable changes in MBC and MBN caused shifts in microbial C:N ratios with irrigation level, with the highest C:N ratios under limited irrigation in July (p<0.001) (Table 2.3). Soil amendments did impact microbial C:N ratios significantly, as averaged over other variables, microbial C tended to be higher in the manure plots (80.59 µg g^{-1} dry soil) than in the control (69.81 µg g^{-1} dry soil) or biochar plots (58.78 µg g^{-1} dry soil) (Table 2.3).

Potential extracellular enzymatic activities

Potential EEA (Table 2.2 for abbreviations) differed between soil amendments (p=0.001) and over time (p=0.001, PerMANOVA). EEA varied in response to biochar treatment, but was not significantly impacted by either manure nor limited irrigation treatments. Averaged over irrigation treatment and time, biochar increased AG, CB, and NAG activities by 186%, 70%, 571% over the controls, respectively (Fig. 2.2). Simultaneously, biochar decreased BG and PHOS overall activity by 41% and 43% from the controls, respectively (Fig. 2.2). There was no significant impact of biochar on LAP or XYL activity, but there was an impact of time and an amendment *x* time interaction. Averaged over amendment treatment, PHOS activity decreased by 50.2% and LAP increased by 20.3% in July (Fig. 2.2a and b). In September, XYL activity increased in biochar plots compared to the other amendment treatments (Fig. 2.2c). Further NMDS analyses revealed correlations between EEA and specific soil properties and microbial biomass (Fig. 2.3). Across all sampling dates in the biochar plots, the percent total soil C significantly correlated with increased AG, CB, and NAG activities, and lower slightly microbial biomass significantly correlated with the lower BG and PHOS activities (Fig. 2.3, PerMANOVA). Though amendments had no impact on LAP, increases in its activity correlated with high percent total soil N in July (Fig. 2.3b) and high NH_4^+ in September (Fig. 2.3c).

Maize yield and biomass

Maize grain yield, harvest index, total dry biomass, and percent cob fill were not significantly impacted by soil amendment (p=0.881) nor irrigation treatment (p=0.211) averaged over other treatments (Fig. 2.4). The limited irrigation showed slight trends toward decreasing yield by 1.16 Mg ha^{-1} (p=0.212) (Fig. 2.4), slightly decreasing harvest index by 0.06 (p=0.331), and slightly decreasing total dry biomass by 2.8% (0.29 Mg ha^{-1}) (p=0.299, pairwise comparisons). The lowest grain yield occurred in the biochar plots under limited irrigation (9.11 Mg ha^{-1}) and highest was the biochar plots under full irrigation (11.90 Mg ha^{-1}) (Fig. 2.4). The percent cob fill was significantly higher (10.75%) with the drought adapted maize hybrid (P8954AM) under limited irrigation (p=0.044). This was the only significant difference observed between the two maize hybrids; other measurements are averaged across the hybrids.

Discussion

Soil moisture and nutrients

Manure increased gravimetric moisture content, while biochar had no significant impact on moisture content, and overall effects on nutrients also proved highly variable between amendments. Despite the larger pore volume of the biochar, we observed greater moisture increases with manure amendments. Additionally, analysis of plant available water revealed no effect of amendment, as the treatment differences were less than 2% volumetric soil moisture (data not shown). This may be attributable to water held tightly in biochar micropores, reducing moisture availability (Downie et al., 2009). Biochar additions consistently increase water holding capacity in sandy soils (Basso et al., 2013) where increases in microporosity have larger impacts (Abel et al., 2013), but not necessarily in clayey soils. Alternatively, the null impact on soil moisture could be due to the hydrophobicity of the biochar, which can increase at pyrolysis temperatures over 300°C (Zornoza et al., 2016). Though the manure increased soil moisture, perhaps due to the sandy clay loam texture of our agricultural soil, the observed effect of amendment on soil moisture did not result in impact on yield. Researchers have previously attributed such results to the surface application of the amendment, which may not have impacted soil moisture in the deep maize rooting zone, as indicated with other crop species (Borchard et al., 2012). Our results warrant further research on the effects of biochar porosity and hydrophobicity on plant available water.

Biochar and manure had contrasting effects on soil nutrients. The high C content of the biochar (72.7%), applied at a 2.5% rate (w/w), added up to 19.6 Mg-C ha^{-1} to the soil C stock. This upholds previous laboratory studies of biochar recalcitrance and C sequestration (Stewart et al., 2013) and corroborates one primary benefit of biochar additions in temperate systems

(Jeffery et al., 2015; Spokas et al., 2012). Due to this high C addition, several previous temperate biochar field studies advise supplemental N additions to minimize biochar induced N limitations (Brantley et al., 2015; Jones et al., 2012; Lehmann et al., 2003; Tammeorg et al., 2014; Zheng et al., 2012). However, at the 30 Mg ha^{-1} addition rate, we observed no decrease in soil N pools, or increase in microbial N immobilization with the biochar plots. Though laboratory studies show biochar increased total soil N, when using a biochars with an initial N content of 0.61-1.22% (Ouyang et al., 2014; X. Wang et al., 2015), the negligible impacts on N dynamics in our field study matched the Jones et al. field trial (2012) with a pine biochar with an initial N content of 0.68%. These authors argue that the short term effects on soil nutrients observed in the laboratory were not observed in the longer-term, indicating that time since application may play a major role in biochar and N dynamics. As for other nutrients in our field trial, manure increased available P whereas biochar had no effect, despite containing a small amount of initial P (0.38%). In other field studies in temperate systems without P fertilization, biochar decreased extractable P (Nelson et al., 2011). This decline in available P has been attributed to soil alkalization (Jay et al., 2015) and sorption onto biochar surfaces (Laird et al., 2010). As we measured no change in pH levels with soil amendments, the unchanging available P pool may have resulted from the small initial input balanced with soil microbial immobilization of P or rapid plant uptake (Anderson et al., 2011; Karer et al., 2013).

Microbial biomass

Though previous studies using the chloroform-fumigation method measured significant sorption of extracted organic C and N onto pine-wood biochar (Jin, 2010), we did not measure any significant sorption due to biochar additions (data not shown); thus we present extraction values with no correction factor. As biochar did not enhance microbial biomass under limited irrigation, our results did not support our initial hypotheses. As observed with previous organic N field trials, manure increased MBC the most (Elzobair et al., 2016; Peacock et al., 2001; Witter et al., 1993). However, the observed slight decline in MBC with biochar addition contrasts with previous work in a maize agricultural field with a slow-pyrolysis maize stover biochar (30 Mg ha^{-1}) that demonstrated a doubling of microbial biomass (Domene et al., 2014). This 100% increase in microbial biomass with the maize stover biochar may have resulted from higher labile inputs from slow-pyrolysis production, but also includes a 1.77 correction factor used for biochar-sorbed dissolved organic C and N during the extraction, *versus* a 1.53 correction factor for the un-amended soils. In studies of other biochar types, observed increases in microbial biomass are often attributed to higher fungal and gram negative bacterial abundance (Gomez et al., 2014), related to changes in soil moisture and nutrient dynamics (Lehmann et al., 2011) that we did not observe in this study. Soil amendments did not impact microbial C:N ratios significantly, though microbial C:N tended to be higher in the biochar amended plots than in the other plots. Our findings of no impact on MBC:N ratios matches another field study with pine-wood biochar in a silt-loam soil cropped to maize (Brantley et al., 2015). Typically increases in microbial biomass are not observed as frequently with wood-derived biochars (Gul et al., 2015). Though we observed significant increases in MBC abundance with manure, and slight decreases with biochar, our analysis of soil enzymes revealed a more complex relationship between biochar and microbial function.

Potential extracellular enzymatic activities

The observed increases in soil moisture, total C and N and microbial biomass did not necessarily improve soil productivity under limited irrigation as hypothesized. Similarly with EEAs, we observed no significant amendment x irrigation interaction. The only significant impact on EEA occurred in the biochar plots. The surprising lack of effects on EEA from the manure N and P addition actually conforms to previous results from a similar temperate maize system (Elzobair et al., 2016). In a study of microbial response to fertilizer treatments, Bolton et al., (1985) also demonstrated a more pronounced increase in EEA and microbial biomass with organic C, rather than N treatments. This also may begin to explain the more pronounced impact on EEA with the high C input from biochar additions.

Throughout the season, relative to the control, biochar amendments increased AG, CB, and NAG activity, decreased BG and PHOS activity, and had little to no impact on LAP and XYL activity. The increases in NAG, AG, and CB correlated with the high total soil C content in the biochar plots. Therefore, we hypothesize that these increases relate directly to higher organic C substrate in the soil, or to co-location and stabilization of C substrate and enzymes on the biochar surface. Since biochar caused a slight decrease in MBC, we may rule out increased EEA due to higher microbial biomass and thus higher production of enzymes. The extremely high increase in NAG (571%) compares to changes observed by Bailey et al. (2011) with a fast-pyrolysis switchgrass biochar amended to three soils, including an irrigated alkaline cropland soil. It is also possible that the high C content of the biochar induced higher relative microbial N requirements due to increased access to C substrate (Atkinson et al., 2010; Cayuela et al., 2013), thus increasing production of NAG, a C and N cycling enzyme. Previous research of AG and CB activities has primarily observed no impacts with pine biochar (Elzobair et al., 2016), and decreases with maize stover biochar (Jin, 2010; R. Wang et al., 2015). We hypothesize our results are related to feedstock type and pyrolysis, though other important factors that could account for these discrepancies are the charge of the specific enzymes tested and their interaction with the biochar surface (Elzobair et al., 2016).

Several possible mechanisms exist to explain the observed decreases in BG and PHOS activities in our field site with biochar addition. The potential sorption of enzymes or substrate on biochar surfaces may decrease EEA if the enzyme is denatured. If the enzyme adsorbs to a surface, causing a change in the morphology of the active site, then the enzyme may no longer function (Burns, 1982). Alternatively, as the decreases correlated with slightly lower microbial biomass C, the decline in EEA may simply indicate lower microbial biomass and production of enzymes. The observed decrease in BG aligned with several previous studies: one in an alkaline irrigated crop soil amended with switchgrass biochar (Bailey et al., 2011), another in a maize field trail with maize stover biochar in a silt loam soil (Jin, 2010), and another laboratory study with sewage sludge biochar (Paz-Ferreiro et al., 2013). The decrease in PHOS, however, does not follow observed patterns with previous research in maize field trials with pine biochar (Brantley et al., 2015), or within a greenhouse maize biochar experiment (Masto et al., 2013), or in a majority of laboratory studies that demonstrate increases in PHOS with biochar additions, often associated with liming effects (Thies et al., 2015). Since our pine-wood biochar did not influence pH, as the calcareous soil already had a pH of 8.2, the observed decrease in PHOS did not relate to biochar liming the soil. However, since our biochar contained 0.38% P, this may have resulted in decreased production of PHOS initially if available P increased (Burns et al., 2013a). However, with no observed changes of available P in biochar plots, it is likely that this initial biochar-P was rapidly mineralized (Brantley et al., 2015). In another laboratory incubation with maize biochar in a fluvo aquic soil, Wang et al. (2015) explained that a decrease in PHOS activity may be due to sorption or blocking of the enzyme. This deactivation of enzymes may have also occurred in our biochar amended sandy clay loam soil. Further, we hypothesize that the pine biochar could also have interacted with signals for production of enzymes or for detection of substrate. This will require further research to elucidate direct mechanisms of decreased enzymatic activity.

The final two extracellular enzymes, LAP and XYL, showed no significant response to biochar additions, though other studies have found variable effects. In a 30 day lab incubation with an alkaline soils, Galvez et al. (2012) observed no impact of a 0.5% addition of green waste biochar on LAP. Similar to our study, the authors found the biochar amendment did not alter soil P, mineral N content, or microbial biomass. However, in a long term agricultural field trial, results differed from our study. Prommer et al (2012) observed a decrease in free amino acid production in similar a hard-wood biochar amended calcareous soil, possibly due to adsorption or occlusion of LAP in biochar. This mechanism requires further research of biochar-enzyme sorption reactions. In our study LAP activity mirrored N dynamics, correlating to total soil N in July (Fig. 2.3b) and NH_4^+ in September (Fig 2.3c). Despite this pattern and lack of impact from biochar, after a 90 day incubation researchers reported an increase in LAP activity with increasing biochar additions, suggesting that effect on N cycling enzymes depends upon biochar addition rate (Wang et al., 2015). Similarly, with measured XYL activities, results are variable. After a 36 day incubation with a loam soil, a 1.0% hardwood fast-pyrolysis biochar addition stabilized XYL against denaturation stress (Elzobair et al., 2015). Further, researchers observed a slight 16% increase in XYL activity with a 4% biochar addition in a silty arable soil with a pH of 6 (Bamminger et al., 2014). Since we observed no changes in LAP nor XYL, the variable results suggest that enzymatic response depends upon initial soil condition, including pH, biochar application rate, and feedstock type.

Maize yield and biomass

In terms of crop response, limited irrigation caused a very slight reduction in grain yield and biomass (Fig. 2.4), yet there was no interaction with soil amendments. This result matches the maize field trial of Brantley, et al. (2014) with pine-wood chip biochar addition. In contrast, a maize field trial conducted by Rogovska et al. (2014) revealed an 11-55% increase in yield with a hardwood biochar after addition of high maize residue, likely due to biochar sorption of allelochemicals released by maize residues. Often in temperate agricultural systems, biochar does not impact crop yield in the first year, but on average has either a net positive or null effect (Biederman and Harpole, 2013). Yield has been shown to increase over time (Crane-Droesch et al., 2013a), and thus we need longer-term results to reach a more definitive conclusion on the influence of biochar on maize yields.

Conclusion

As predicted, pine-wood biochar significantly increased total soil C, confirming its sequestration potential. Although only manure increased gravimetric soil moisture, this did not result in enhanced maize yield under full or limited irrigation. However, since maize yield did not significantly decrease under 30% reduced irrigation, this experiment did support temporal limitation as an effective method to save water inputs in semi-arid agriculture. In terms of soil fertility, the manure added N and P to the soil, and increased microbial biomass, but had no effect on enzymatic activities. Contrastingly, biochar amendments slightly reduced microbial biomass C and had wide ranging impacts on EEAs. The biochar substantially increased NAG (571%) and decreased BG (-41%) activities, which corresponds to previous studies. However, the increases in AG (186%) and CB (70%), and decrease in PHOS (-43%) contrasted previous work. Elucidation of direct mechanisms related to biochar surface characteristics due to feedstock and pyrolysis conditions, its potential to stabilize or denature specific enzymes, and impact on optimal soil conditions for enzymatic activities, all require further research. This future work may help to specify how the organic amendment impacts soil microbial function, plant available nutrients, and potentially crop yield in temperate agroecosystems.

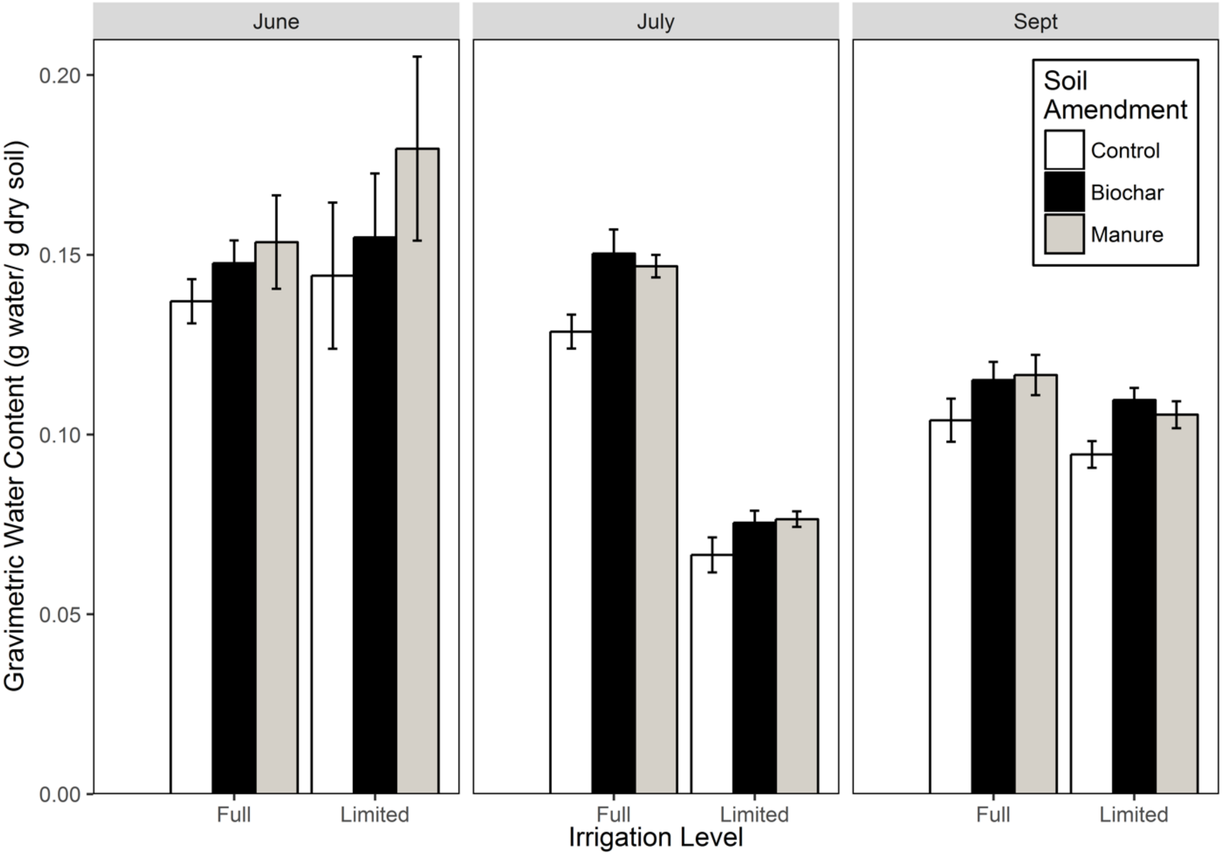

Figure 2.1. Gravimetric soil moisture response to biochar and manure amendments (applied to 15cm depth at 30 Mg ha^{-1}) are compared to the control soil without amendment. Panels represent the three sampling dates: (A) June 29 before irrigation treatments, (B) July 27 at the end of the drought period, and (C) September 01 before the final harvest. Limited irrigation treatment did not receive irrigation inputs for the month of July. Significant differences between full and limited irrigation occurred only in July. Data are the mean ± 1 SE are averaged over maize variety (n=8).

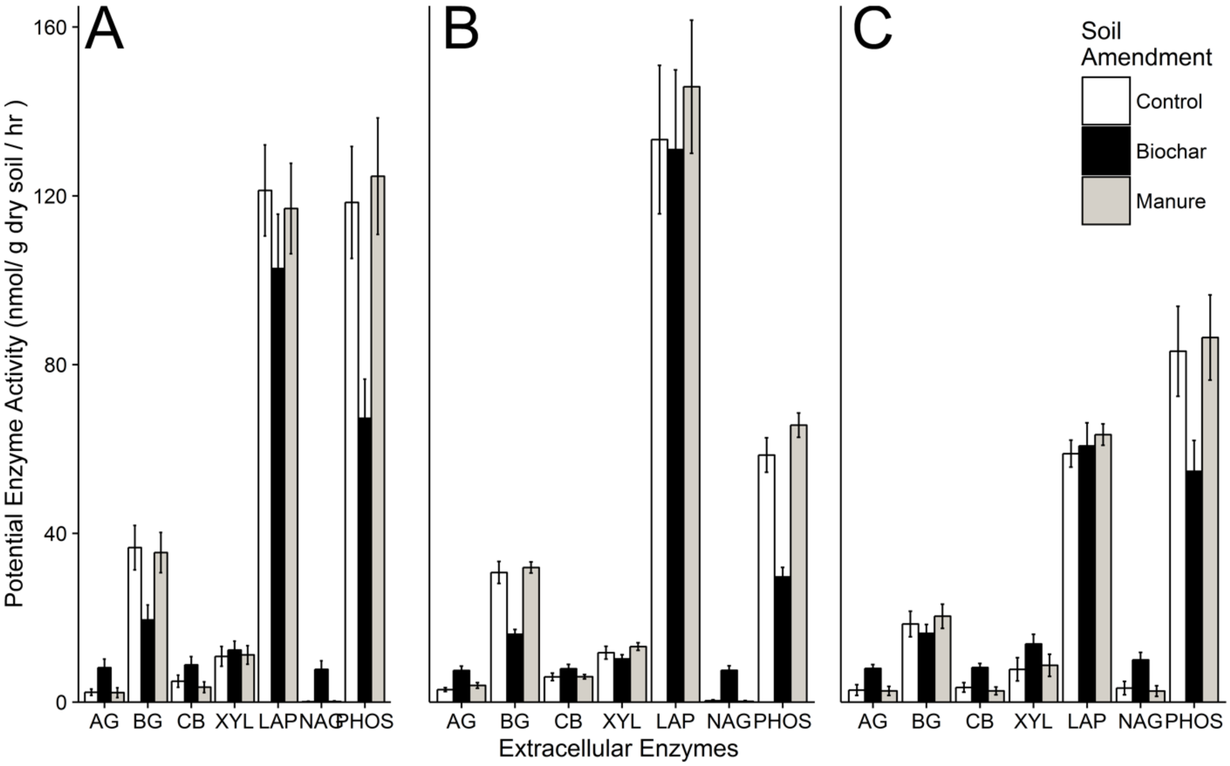

Figure 2.2. Response of seven extracellular enzymes (acronyms reported in Table 2.2) to biochar and manure amendments (applied to 15cm at 30 Mg ha^{-1}) compared to the control sandy-loam agricultural soil. Data are the mean ± 1 SE, and are averaged over maize variety and irrigation that showed no significant differences (n=16), over three sampling dates on (A) June 29 before irrigation treatments, (B) July 27 at the end of the drought period, and (C) September 01 before the final harvest.

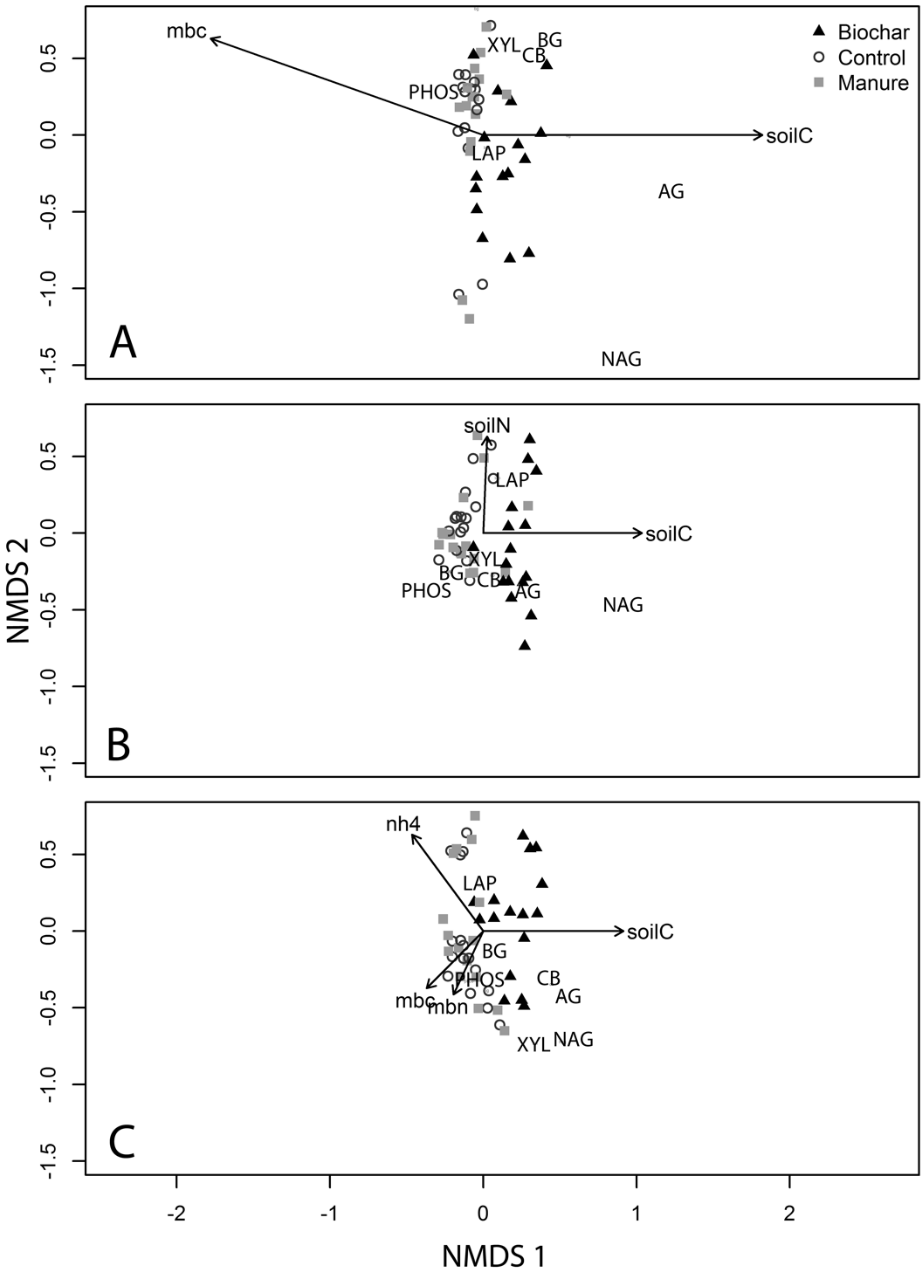

Figure 2.3. Non-metric multidimensional scaling ordinations indicate how soil amendments relatively impact enzymatic activities and correlate to soil environmental variable vectors (black arrows) ($p<0.05$). Overall mean EEAs for seven enzymes are indicated with abbreviated labels (see Table 2.2). The points represent mean EEAs for each soil amendment treatment averaged over irrigation and maize variety (n=16) (manure as squares, biochar as triangles, and the control soil as open circles). Panel A, B and C correspond to the three sampling dates: (A) June before limited irrigation treatment began, (B) July, at the end of the limited irrigation, and (C) September before final maize harvest. Significantly correlated soil properties included mbc (microbial biomass carbon), mbn (microbial biomass n), soil N (total % soil N), soil C (total % soil C) and nh4 (ammonium) (units in Table 2.3). Plots are rotated so that the total soil C vector runs along the primary axis. Goodness of fit was >0.70 for all ordinations.

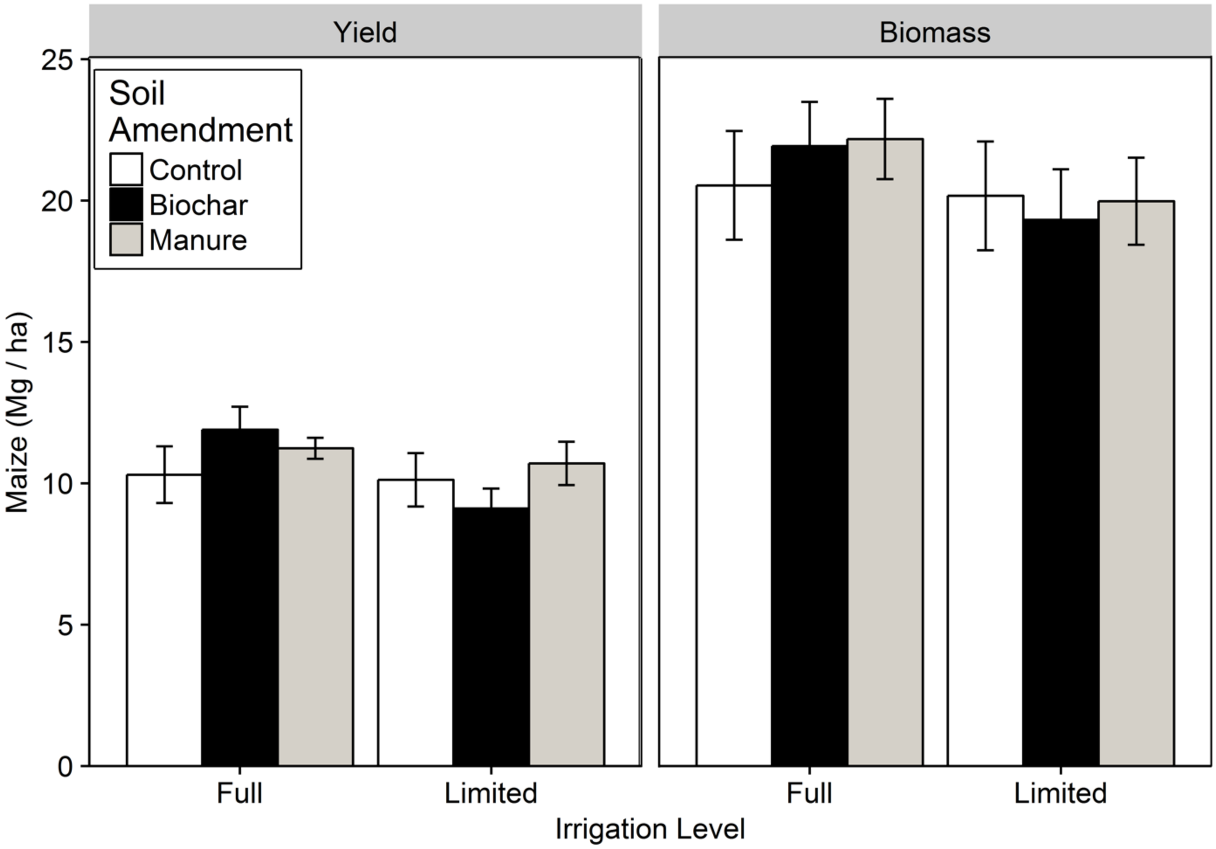

Figure 2.4. Response of maize harvest grain yield (left panel) and dried whole plant biomass (right panel) to organic soil amendments applied at 30 Mg ha^{-1}, data are presented as the mean ± 1 SE (n=8). No significant differences were found between the soil amendments or irrigation treatment at the *p*<0.05 level.

Table 2.1.
Characteristics of the agricultural control soil and the two amendments, applied at a rate of 30 Mg ha-1 and tilled to a depth of 15 cm in November of 2013. Surface area analysis was conducted using the Brunauer-Emmet-Teller method, using N2 desorption. Values are mean ± 1 SE. No SE available for BET analysis (n=1) or for biochar bulk density (analyzed by Control Laboratories, Watsonville, CA).

Treatment	Total C (%)	Total N (%)	pH	ρb (g cm^{-3})	CEC (cmol$_c$ kg^{-1})	Surface Area (m^2 g^{-1})	Pore surface area (m^2 g^{-1})	Pore volume (cm^3 g^{-1})
Biochar (B)	72.7 ± 2.30	0.5 ± 0.01	9.2	0.35	16.51 ± 0.53	232.72	60.40	0.16
Manure (M)	24.8 ± 0.64	1.5 ± 0.06	9.8	nd	46.91 ± 1.07	2.69	2.06	0.01
Control Soil (C)	1.49 ± 0.04	0.14 ± 0.002	8.7	1.35 ± 0.03	21.59 ± 1.21	27.50	18.76	0.03

Abbreviations: nd=no data

Table 2.1.

The seven extracellular enzymes measured fluorometrically in an agricultural soil amended with biochar and manure, and their abbreviations, general functions and substrates (adapted from Alster et al. 2013).

Enzyme	Abbreviation	Function	Substrate
α-1,4- glucosidase	AG	Complex carbohydrates, starch and glycogen	4-MUB-α-D-glucopyranoside
β-1,4-glucosidase	BG	Hydrolysis of cellulose (glucose)	4-MUB-β-D-glucopyranoside
β-D-cellobiohydrolase	CB	Hydrolysis of cellulose	4-MUB-β-D-cellobioside
L-leucine aminopeptidase	LAP	Hydrolysis of leucine residues at end of peptides/proteins	L-Leucine-7-amido-4-methylcoumarin hydrochloride
β-1,4-N-acetylglucosaminidase	NAG	Chitin degradation	4-MUB-N-acetyl-β-D-glucosaminide
Phosphatase	PHOS	Reduction of organic P to phosphate groups	4-MUB-phosphate
β-Xylosidase	XYL	Reduction of cellulose from xylan	4-MUB-β-D-xylopyranoside
Fluorogenic moiety:			
4-Methylumbelliferone	MUB	Fluoresces with enzyme catalyzed substrate degradation	
7-Amino-4-methylcoumarin	MUC	Fluoresces with enzyme catalyzed substrate degradation	

Abbreviations: irrig = irrigation treatment, amend = soil amendment, time=sampling date (June, July, Sept), variety = variety of maize hybrid, nd = no data, ns = not significant, df=degrees of freedom.

Table 2.3

Comparison of soil biogeochemical properties, between full and limited irrigation with biochar, manure or the no amendment control, for each sampling date over the growing season. Means ± 1 SE are averaged over the two maize varieties, which showed no significant differences, (n=8). P-values reported at $p<0.10$ with significant values bolded when $p<0.05$ from a mixed effects ANOVA of irrigation, maize variety, and amendment over time.

-			**Mineral N**				**Microbial Biomass**						**Elemental Content**						**Basic Properties**			
Experimental Treatments:		***Month:***	**NO_3^- (ug g^{-1})**		**NH_4^+ (ug g^{-1})**		**C (ug g^{-1})**		**N (ug g^{-1})**		**C:N Ratio**		**Total C (%)**		**Total N (%)**		**Available P (ppm)**		**%H_20 Content**		**pH**	
			mean	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**	**mean**	**SE**
Full	Biochar	June	48.38	9.99	0.00	0.00	38.17	4.50	5.35	0.87	9.12	2.14	2.86	0.30	0.15	0.00	12.77	2.07	14.77	0.63	8.55	0.09
		July	11.46	2.43	0.00	0.00	88.09	13.79	11.52	1.82	7.90	0.63	2.46	0.11	0.14	0.00	16.99	1.79	15.04	0.67	nd	nd
		Sept	4.45	1.00	2.80	0.61	60.13	6.50	14.88	0.81	3.96	0.25	2.62	0.14	0.13	0.00	nd	nd	11.51	0.51	8.69	0.10
	Control	June	48.61	7.77	0.00	0.00	58.34	4.97	10.77	2.20	6.48	0.96	1.50	0.16	0.14	0.00	9.37	2.09	13.71	0.62	8.66	0.04
		July	21.55	6.81	0.00	0.00	94.87	11.83	11.60	2.60	8.30	0.82	1.40	0.09	0.15	0.00	16.46	3.08	12.86	0.47	nd	nd
		Sept	5.12	0.86	2.65	0.61	73.16	13.09	17.60	2.66	4.05	0.23	1.40	0.16	0.13	0.00	nd	nd	10.40	0.60	8.68	0.07
	Manure	June	43.59	8.25	0.00	0.00	64.93	6.70	8.79	1.20	8.04	1.28	1.38	0.05	0.15	0.00	21.44	2.37	15.35	1.30	8.60	0.07
		July	10.60	2.25	0.00	0.00	110.9	15.77	16.88	2.02	6.32	0.63	1.59	0.12	0.15	0.00	26.71	2.16	14.68	0.31	nd	nd
		Sept	3.82	0.62	2.83	0.62	72.35	7.42	16.59	1.13	4.30	0.22	1.39	0.07	0.14	0.00	nd	nd	11.66	0.56	8.75	0.06
Limited	Biochar	June	46.89	9.67	0.00	0.00	44.36	3.69	7.47	0.79	6.29	0.64	2.52	0.14	0.14	0.01	15.38	3.27	15.48	1.78	8.51	0.05
		July	45.34	11.50	0.22	0.10	67.56	8.55	4.26	2.08	14.92	3.72	2.97	0.17	0.15	0.00	22.33	1.94	7.55	0.34	nd	nd
		Sept	14.35	3.05	2.84	0.62	54.37	4.63	13.47	0.61	4.03	0.28	2.61	0.17	0.13	0.01	nd	nd	10.96	0.33	8.61	0.06
	Control	June	39.96	8.46	0.00	0.00	59.82	7.02	8.60	0.69	6.93	0.62	1.46	0.05	0.13	0.01	14.57	1.45	14.42	2.03	8.64	0.06
		July	37.40	12.17	0.32	0.10	71.82	4.51	4.60	0.93	16.03	3.10	1.62	0.09	0.14	0.00	26.43	3.92	6.65	0.49	nd	nd
		Sept	17.83	6.42	2.85	0.63	60.88	7.19	12.74	1.68	5.26	0.94	1.53	0.07	0.13	0.00	nd	nd	9.45	0.37	8.65	0.07
	Manure	June	41.04	5.90	0.00	0.00	66.43	8.58	9.34	1.72	7.74	0.80	2.04	0.25	0.16	0.01	14.73	2.15	17.95	2.56	8.70	0.06
		July	44.63	9.44	0.14	0.07	89.33	9.68	4.82	1.39	15.47	1.85	1.67	0.06	0.16	0.00	33.96	2.02	7.65	0.22	nd	nd
		Sept	10.35	2.52	2.95	0.54	79.61	4.70	17.33	0.66	4.59	0.18	1.55	0.10	0.14	0.01	nd	nd	10.55	0.38	8.67	0.07
		df									**P-values**											
	irrig	1	**0.043**		ns		ns		**0.039**		**0.011**		ns		ns		ns		ns		ns	
	amend	2	ns		ns		**0.027**		0.093		ns		**<0.001**		**<0.001**		**<0.001**		**0.037**		ns	
	variety	1	ns		ns		ns		ns		ns		ns		ns		ns		ns		ns	
	time	2	**<0.001**		**<0.001**		**<0.001**		**<0.001**		**<0.001**		ns		**<0.001**		**<0.001**		**<0.001**		0.077	
	irrig x amend	2	ns		ns		ns		ns		ns		ns		ns		0.086		ns		ns	

irrig x variety	1	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
amend x variety	2	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
irrig x time	2	**<0.001**	ns	ns	**<0.001**	**<0.001**	ns	ns	**0.013**	**<0.001**	ns
amend x time	4	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
variety x time	2	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
irrig x amend x variety	2	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
irrig x amend x time	4	ns	ns	ns	ns	ns	**0.003**	**0.037**	ns	ns	ns
irrig x variety x time	2	0.054	ns	ns	ns	ns	ns	ns	ns	ns	ns
amend x variety x time	4	ns	ns	ns	ns	ns	ns	0.052	ns	ns	ns
irrig x amend x variety x time	4	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns

Abbreviations: irrig = irrigation treatment, amend = soil amendment, time=sampling date (June, July, Sept), variety = variety of maize hybrid, nd = no data, ns = not significant, df=degrees of freedom.

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Chapter 3: Sorption to wood biochar impedes soil enzyme activity[2]

Introduction

Amending soils with biochar, the solid co-product of bioenergy production, can have variable impacts on soil health (Atkinson et al., 2010; Biederman and Harpole, 2013; Jeffery et al., 2011; Lehmann, 2007). Differences in pyrolysis times and temperatures create a wide variability in biochar surface area and charge, pore size distribution, pH, and chemical composition (Enders et al., 2012; Lehmann, 2007; Lehmann and Joseph, 2009). Due to these physiochemical differences, the impact of biochar on soil structure and biogeochemistry also varies widely. To assess the effect of biochar on soil function, researchers can analyze the activity of microbial extracellular enzymes (Alkorta et al., 2003; Allison, 2005; Bell et al., 2013). The extracellular proteins are excreted by microbes to catalyze the rate-limiting step of biochemical reactions by breaking down macromolecules for uptake (Burns et al., 2013b; Caldwell, 2005; Makoi and Ndakidemi, 2008). The specific structure, or the enzyme conformation, maintains the active site, an area shaped precisely to break down a specific substrate. Each enzyme acts most efficiently within a narrow optimal range of pH, temperature, and moisture levels. When the soil environment changes, the enzyme catalytic efficiency changes (Alster et al., 2016; Sinsabaugh et al., 2008). Due to this sensitivity, enzymes provide rapid indication of soil quality, microbial activity, and nutrient cycling (Caldwell, 2005; Paz-Ferreiro et al., 2012).

Biochar surfaces have a high potential to sorb organic molecules, including enzymes and substrate, thus altering enzyme activities (Bailey et al., 2011; Elzobair et al., 2015). Due to the

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[2] In preparation for Agriculture with E.J. Fogle and M.F. Cotrufo

varied nature of enzyme-solid phase interactions, impacts of biochar on enzyme activities remain nebulous. For example, in a single agricultural field trial, a 2.5% (w/w) addition of pine wood biochar increased activities of α-1,4- glucosidase, β-D-cellobiohydrolase, and β-1,4-N-acetylglucosaminidase and significantly decreased β-1,4-glucosidase and phosphatase activities (Foster et al. 2016). Of particular concern are the observed decreases in enzyme activities, which may reduce soil carbon and nutrient cycling. Specifically, this agricultural field trial found a 41% decrease in a glucose cycling hydrolytic enzyme, β-glucosidase (BG), and a 43% decrease in an organic phosphorus cycling enzyme, phosphatase (PHOS). Decreased enzyme activity in soil may relate to changes in soil structure and nutrient diffusion rates, to sorption of substrate, or to the direct sorption of the enzymes. These interactions require in-depth laboratory analysis before further interpretation of field results, especially if the enzymes sorb to biochar directly, resulting in loss of activity and biogeochemical cycling.

Managers need to understand the impact of biochar on extracellular enzymes before designing amendments that maximize, rather than impede, nutrient release. Numerous studies on enzyme-soil mineral interactions reveal that sorption frequently occurs and can alter activity rates (Burns, 1982; Nannipieri et al., 2002). The sorption of enzymes, either adsorption to the solid phase surface or absorption into pore spaces, involves potential electrostatic, pH-controlled, hydrophobic, and physical interactions (Quiquampoix and Servagent-Noinville 2002; Sandhya et al. 2005). Depending on the mechanism, sorption to solid phases can either maintain the protein structure and functional active site (Elzobair et al., 2015; Sarkar et al., 1989), or alter the shape of the active site, reducing activity levels (Datta et al., 2017; Quiquampoix and Burns, 2007; Quiquampoix and Servagent-noinville, 2002). Certain biochars can stabilize (Elzobair et al., 2015) and increase activity for select enzymes (Foster et al. 2016; Wu et al. 2013). However, more frequently, biochar exposure reduces enzyme activity, due to sorption of substrate (Bailey et al., 2011; Lammirato et al., 2011; Swaine et al., 2013), or direct interaction of the enzyme with biochar hydrophobicity and surface area (Keiblinger et al., 2015; Lammirato et al., 2010; Swaine et al., 2013). Despite this growing research field, to our knowledge, no experiment directly quantifies the sorption and activity of biochar-immobilized enzymes in response to biochar surface properties.

This laboratory experiment tested the mechanisms behind previously reported field results: Does direct sorption of enzymes account for the observed ~40% reduction in BG and PHOS enzyme activities? The assay explicitly measured enzyme sorption and subsequent activity after immobilization onto three solid phases, two contrasting biochars, the pine and a grass char, and a control sandy clay loam soil at three pH levels. We quantified sorption via Bradford protein assay, followed by a fluorescence-based analysis of immobilized enzyme activities. The sorption of substrate was also tested with a similar activity assay. Based on previous *in situ* results from Foster et al., 2016, we predicted that extracellular BG and PHOS would sorb onto pine biochar at similar rates, resulting in reduced activities. When compared to a control soil and low surface area grass biochar, we predicted that the high surface area pine biochar would adsorb more enzyme and reduce activities the most. If physical surface area alone correlated with sorption, then we predicted a higher percentage of PHOS sorption due to its smaller size, leading to lower PHOS activity than BG. Finally, we predicted higher sorption and lower activity would occur at the lowest assay pH, as the solid phases and enzymes approach their isoelectric points of zero charge.

Materials and Methods

Two commercially available enzymes were selected to match the previous field study: β-glucosidase (BG) (from *Aspergillus niger*, Sigma-Aldrich 49291) and acid phosphatase (PHOS) (from sweet potato, Sigma-Aldrich P1435) (Table 3.1). The acid PHOS was selected rather than alkaline PHOS, to provide a comparison between enzymes with similar optimal pHs and maintain assay consistency (Table 3.1). The enzymes were dissolved into 50 mM Tris at a concentration of 2 mg mL^{-1} for BG and 4 mg mL^{-1} for PHOS. These different concentrations were specifically chosen to meet detection limits of the Bradford protein assay (ThermoFisher Scientific; Waltham, MA, USA) and to help equalize the units of activity (U) present in each well per mg of enzyme (Table 3.2). The enzyme solutions were buffered to a pH of 6, 7, and 8. The highest pH matched the initial pH of the alkaline field soil, and the lower pH levels were slightly closer to the optimum conditions for the two enzymes.

Solid phases

Enzyme activity was quantified after sorption onto three air-dried and ground solid phases (Table 3.2). The pine biochar from the previous field experiment had a high surface area (Foster et al., 2016); for contrast we tested both the original sandy clay loam and a low surface area grass biochar. The grass biochar (BC Grass) was produced at a lower pyrolysis temperature and has higher hydrophobicity than the pine biochar (BC Pine) (Table 3.2). Hydrophobicity was measured on triplicate samples using water drop penetration time (Vogelmann et al., 2015) and each sample given a rating based on infiltration time of either low (< 15s), medium (15-30s), or high (>30s). The solid phases were characterized by measuring their isoelectric points, the pH at which the surface charge, or zeta potential, equals zero. Briefly, the protocol of Asadi et al. (2009) was followed, modified by first grinding the solid phases. The solid phase was suspended in a 0.01 M KNO_3 solution with pH levels from 1 to 6 with dilute KOH or HNO_3, bringing samples to a final concentration of 1.5 mg solid phase mL^{-1}. Samples were analyzed on a NanoBrook Omni Zeta Potential Analyzer (Brookhaven Instruments Corp, NY, USA) to calculate a final average from 10 runs. The soil possessed a negative zeta potential at pH 1, the lowest limit of the assay.

Enzyme sorption assay

To prepare the sorption assay, the three solid phases were air-dried and ground on a roller table into a powder. Five replicate 5 mg samples were weighed into microcentrifuge tubes, into which 100 μL of BG or PHOS enzyme solution was added. After vortexing, the mixed solution was incubated for one hour at ambient temperature (~25ºC). Incubation times longer than one hour resulted in measurements higher than the protein amount initially added, likely due to interference with the Bradford assay from other organic molecules coming from the solid phases. This background interference was measured for each solid phase and later subtracted from the final value. After centrifugation at 282 *x g* for 3 minutes, 5 μL of supernatant was pipetted into a microplate with 250 μL of Coomassie Reagent to conduct a colorimetric Bradford Protein Assay (ThermoFisher Scientific; Waltham, MA, USA). After ten minutes of reaction time, the plates were read at 595 nm with an Infinite M200 Microplate Reader (Tecan Trading AG, Switzerland). Each enzyme plate had a standard curve of six points prepared from the enzyme stock solution and the Coomassie Reagent. The supernatant protein concentration measured by the Bradford Assay was subtracted from the total protein added to calculate the quantity of enzyme immobilized according to the following equation:

Eqn. 1:

$$Enzyme\ sorbed\ (\%) = \frac{Total\ protein\ added\ (mg) - [Supernatent\ protein\ (mg) - Background\ protein\ in\ the\ solid\ phase\ (mg)]}{Total\ protein\ added\ (mg)} * 100\%$$

Enzyme activity assay

After completing the sorption experiment, we conducted a high-throughput fluorometric activity assay on the immobilized enzymes. Fluorometric assays are more accurate than colorimetric methods for enzyme activity to account for quenching with biochar (Bailey et al. 2011). Negative controls of the solid phases alone were run without added enzyme to determine the background activity. We also ran three positive controls, with enzyme only, to quantify the maximum activity of the free enzyme at pH 6, 7, and 8. This allowed analysis of activity at the initial pH of the field soil, as well as pH levels slightly closer to the enzyme optimum activities (Table 3.1). Standard curves specific to each solid phase, enzyme, and pH were created to account for differences in fluorescence due to the assay conditions, including adsorption of reaction product to the solid phase. Due to space constraints on the plate and time sensitive changes to buffer pH, to assay all samples simultaneously under precisely the same conditions, the grass biochar was run only at pH 7.

To measure the immobilized enzyme activity, we first used 405 μL of buffer to dilute the remaining 95 μL enzyme and solid phase. This suspension was vortexed and pipetted into a deep-well plate. We added an additional 500 μL to the microcentrifuge tube to ensure all of the solid phase was transferred, confirmed visually. This rinse solution was also pipetted into the deep well plate, bringing each well to a 1000 μL final volume. The deep-well plate was then centrifuged for three minutes at 2,900 *x g* and the supernatant was aspirated, leaving the solid phase and immobilized enzyme. Additional tests of number and volume of rinses demonstrated that the initial dilution effectively removed unbound enzyme and further rinses started to remove the solid phase. Before the activity assay, another 800 μL of buffer was added to suspend the solid phase.

The assay measured maximum potential activity via release of fluorescent moieties from enzyme-specific substrate. Following the procedure of Bell et al. 2013, 200 μL of a 200 μM fluorescent substrate was added to each well (4-Methylumbelliferyl β-D-glucopyranoside for BG and 4-Methylumbelliferyl phosphate for PHOS). For each pH, enzyme, and solid phase combination on the sample plate, there was a corresponding standard curve. The standard plates contained the sample suspension and the fluorogenic moiety 4-Methylumbelliferone only, without the attached substrate. The standard curves were made at concentrations ranging from 0 to 200 mM and corrected for quenching due to the solid phase.

Both the sample and standard plates were allowed to react at ambient temperature (~25 ºC) for 24 hours. The longer assay time more closely simulated field conditions, accounting for any desorption or stabilization of the enzyme as might occur naturally. Controls showed that no uncatalyzed hydrolysis of the reactant or degradation of the product occurred over this time period. Fluorescence was read at 365 nm excitation and 450 nm emission on an Infinite M200 Microplate Reader (Tecan Trading AG, Switzerland). The gain was optimized and adjusted for each solid phase and standard curve, as the pine biochar quenched the standard curves more than the soil samples. The initial results are presented as substrate degraded in nmols (Table 3.3).
To further analyze the activity data, we calculated catalytic efficiency using the following equation:

Eqn. 2:

$$\textit{Enzyme Activity } (\mu mols\ \ mg^{-1}\ enzyme\ hr^{-1}) = \frac{Substrate\ Degraded\ (\mu\text{mols})}{Added\ enzyme\ (mg) * \%\ Sorbed\ Enzyme/100\ \ * 24hrs}$$

This equation incorporates the amount of immobilized enzyme present in the well by multiplying the amount of enzyme added by the percent of sorbed enzyme.

Assay of substrate stability and sorption

We ran an additional assay to test if the substrate sorption to the solid phases impacted activity levels. We allowed the substrate to interact with each solid phase for 24 hours and then conducted a modified activity assay. Separately, we vortexed 5 mg of the three solid phases with 300 μL of the 200 μM BG and PHOS substrate and MUB fluorescent standard in 50 mM Tris buffer at pH 6, 7, and 8, in the same mixtures and conditions as the previous assays. There also were controls with substrate only and no solid phase. The slurries incubated for 24 hours, as in the previous assay, to test the stability of the compounds through the incubation period. Then the slurries were centrifuged for three minutes at 2,900 *x g* and 100 μL of each supernatant was moved to a deep plate well with an additional 400 μL of buffer and 50 μL of enzyme (2 mg mL^{-1} BG and 4 mg mL^{-1} PHOS). This volume of enzyme matched the ratio of substrate to enzyme in previous activity assays. The standard curves and fluorescence microplate readings were carried out exactly as the initial assays (Section 2.3) with a standard curve for each solid phase, pH, and enzyme. The solid phase specific standard curves account for the adsorption of reaction products in the assay.

Statistics

An analysis of variance (ANOVA) tested the effect of solid phase, pH, and enzyme on the percent sorption, substrate degraded (nmols), and rate of activity. Tukey post-hoc adjustments were used to make pairwise comparisons for significant variable interactions at the $\alpha = 0.05$ level, unless otherwise noted. The enzyme and substrate sorption activity data were transformed by log (x+1) to achieve normality. To improve normality rates lower than -1.0 μmols mg^{-1} enzyme hr^{-1} were set to zero, which then produced an additional significant three-way interaction between enzyme, solid phase, and pH. The final activity values are presented without subtraction of the background activity, because this added unnecessary variability and did not change interpretation of results. All analyses were conducted using R statistical software version 3.3.3 (R Core Team, 2017).

Results

Enzyme Sorption

The Bradford protein assay revealed higher variability of PHOS sorption (from 2.5-47.0%) relative to BG (from 17.0-50.2%) averaged across the solid phases and pH levels. As hypothesized, the pine biochar sorbed significantly more enzyme than the soil (+13.3%, P = 0.0431) and not significantly more than the grass biochar (+11.9%, P = 0.3524). Contrary to our hypothesis, on average at pH 6 there was lower amount of sorption than pH 7 (-22.0%) (P = 0.0018). The differences between sorption at different pH levels was driven by the 43.7% lower sorption of PHOS onto soil at pH 6 verses pH 7 (P = 0.0361).

Enzyme Activity

In the activity assay, we detected a small amount of background activity (<0.002 μmols) from the biochars, and a larger amount in the soil (PHOS = 0.0067 μmols and BG = 0.0028 μmols) at the native soil pH 8. However, subtraction of this background did not alter the interpretation of results; thus initial values are presented in Table 3.3 and Fig 3.2. The amount of substrate degraded depended upon the interaction of the enzyme, solid phase, and pH of the assay. On average, the amount of substrate degraded by PHOS activity was higher than that of BG during the 24-hour assay. This pattern emerged clearly with grass biochar, as PHOS degraded 30 nmols more than BG (Table 3.3). When sorbed to soil, PHOS also degraded more substrate than BG at pH 7 (+12.1 nmols) and pH 8 (+24.2 nmols), but no significant differences existed at pH 6. Overall the most notable difference between solid phases was the low activity levels of enzymes sorbed to the pine biochar. Pine biochar significantly decreased the substrate degraded by PHOS relative to the grass biochar at pH 7 ($P<0.0001$) and to the soil at all pH levels ($P<0.0001$). The BG immobilized on pine biochar degraded less substrate than BG on the soil at pH 6 and 7 ($P< 0.0001$), but not at pH 8.

The amount of substrate degraded demonstrated differences between the solid phase, enzymes, and pH levels (Table 3.3). However, this measurement did not take into account the amount of enzyme in each well. To differentiate the wells without sorbed enzymes from those in which sorption potentially deactivated the enzymes, we calculated activity rates per mg of immobilized enzyme (Eqn. 3.2, Fig. 3.2). The interaction of solid phase *x* enzyme *x* pH significantly impacted enzyme activities ($P = 0.0498$). Overall, pine biochar immobilization of BG and PHOS decreased activities relative to the grass biochar and soil at pH 7 ($P = 0.05$). At pH 8, the activity of PHOS immobilized on pine biochar was slightly higher than pH 7. Enzymes immobilized on both biochars caused reduced activities relative to the soil. Considering both enzymes averaged together, pine biochar reduced enzyme activity by 1.37 μmols mg^{-1} enzyme hr^{-1} relative to the soil ($P = <0.0001$) and by 0.71 μmols mg^{-1} enzyme hr^{-1} relative to the grass biochar ($P < 0.05$). The grass biochar slightly reduced enzyme activity by 0.65 μmols mg^{-1} enzyme hr^{-1} relative to the soil ($P = 0.078$).

To further examine these patterns and illustrate the variability between the two enzymes, we plotted the initial data on percent sorption *versus* the percent of substrate degraded out of the potential activity of a free enzyme (Fig. 3.3A, Fig. 3.3B). These figures show the higher efficiency of PHOS, with more points along or above the dotted 1:1 line, when sorbed to the soil and grass biochar. This demonstrates the low activity of BG at pH 8 (black diamonds and squares (Fig. 3.3A) and low activity of both enzymes immobilized on the pine biochar (squares, Fig. 3.3A, Fig. 3.3B).

Assay of substrate stability and sorption

The substrate sorption assay with specific standard curves and plate runs showed only slight differences due to the solid phases in interaction with pH ($P = 0.0965$) (data not shown). Pairwise comparisons revealed no significant differences between the controls without solid phase versus the soil, pine or grass biochar. The enzyme activity rates with the solid phase-exposed substrate did change in response to pH and enzyme. The activity at pH 6 was lower than pH 7 or 8 ($P < 0.015$) and PHOS activity was lower than BG activity rates ($P = 0.0319$).

Discussion

Enzyme Sorption

The enzyme, solid phase, and pH all affected the amount of sorption. Both enzymes sorbed to the biochars. PHOS sorption was more variable than the BG sorption, possibly, as hypothesized, due to its slightly smaller size (110-112 kDa) (Watanabe et al., 1992), allowing more enzyme to cover the same surface area than the larger BG (220 kDa) (Durmus et al., 1999) (Table 3.2). Surprisingly, the high surface area pine biochar sorbed the enzymes only 10% (BG) to 15% (PHOS) more than the soil (Fig. 3.1), and this interaction depended upon pH level. This was likely due to the fact that one third of the pine biochar surface area occurs within pore spaces with an average width of 4.51 nm (Table 3.1), far smaller than the enzymes tested in this study (Quiquampoix and Burns 2007). This result indicates that enzyme adsorption and stability depends on biochar pore size and does not merely correlate with surface area alone, in agreement with previous work (Elzobair et al., 2015).

The similarity in observed enzyme sorption onto the three solid phases is attributed to similar surface charges both on the solid phases and on the enzymes. Since the assay was run at pH 6-8, higher than the isoelectric point of the solid phases (Table 3.2), each surface had a similar negative charge, resulting in similar sorption capacities. This explains the relatively similar sorption onto pine biochar, despite its much larger surface area. Additionally, the initial cation exchange capacity of this agricultural soil was 21.58 $\text{cmol}_c\ \text{kg}^{-1}$, merely 5.07 $\text{cmol}_c\ \text{kg}^{-1}$ higher than the pine biochar (16.51 $\text{cmol}_c\ \text{kg}^{-1}$) (Foster et al. 2016), reiterating their similar surface charges. Furthermore, the surface charge of the enzymes was also relatively similar. High sorption onto negatively charged mineral surfaces occurs at the isoelectric point of an enzyme, when it possesses no charge (Baron et al., 1999; Datta et al., 2017). This was observed previously with a wood biochar and BG at a pH of 5, close to its isoelectric point (Lammirato et al., 2011). The pH levels in our experiment were above the isoelectric points of the enzymes, as the pH was set to match the pH 8 of the original soil. Above the isoelectric points for BG (4) and PHOS (5.2), both enzymes possessed negative charges (Lammirato et al., 2010) and thus similar sorption rates occurred. Surprisingly, the decrease in negative surface charge at low pH was not observed across our range of pH from 6 to 8. Another consideration is that the measured pH of the bulk solution may be higher than the pH precisely at the solid phase surface. This may explain why the lab incubation resulted in a more variable pattern, with the lowest sorption at pH 6, a finding that contradicted our prediction based on enzyme surface charge.

Though the grass biochar possessed a negative charge, the low surface area and high hydrophobicity likely caused lower sorption rates than the pine biochar. Lower temperature biochars are more hydrophobic (Keiblinger et al., 2015); the grass biochar used in this study would repel hydrated amino-acid sidechains (especially for BG), as previously observed with clay minerals (Baron et al., 1999). So due to low surface area, in addition to hydrophobicity, the measureable sorption to grass biochar was lower than the pine biochar. To tease apart the exact mechanism involved in sorption, future research must consider the exact hydrogen ion concentration at the surface, and both electrostatic and hydrophobic interactions of enzymes and biochar. From this assay we can conclude that as hypothesized pine biochar immobilized both BG and PHOS more than the grass biochar and soil.

Enzyme Activity

Exposure to pine biochar caused a loss of 75-100% of observed BG and PHOS activity at pH levels of 6, 7, and 8, relative to activity rates in soil. This result corroborates the decrease of BG and PHOS activities measured in our previous pine biochar field experiment (Foster et al. 2016). In this assay, the decline in enzyme activities resulted primarily from direct sorption and possible deactivation of the enzymes. Simultaneously, a small amount of substrate sorption also occurred, particularly onto the pine biochar. Averaged over pH, sorption of substrate to pine biochar reduced BG activity by 41% relative to the control. Therefore, we do not exclude the possibility of BG substrate adsorption to the pine biochar as a mechanism for reduced activity rates, as the polar glucose substrate may readily adsorb to negatively charged solid phases. The phosphate substrate in contrast contains both the hydrophobic fluorescent moiety and the negative phosphate group, so the reduced phosphatase activity is likely due to direct sorption of the enzyme rather than substrate. Previous laboratory incubations reveal that switchgrass biochar can sorb the substrate (Bailey et al., 2011) and the reaction products of colorimetric enzyme assays (Swaine et al., 2013). Since we used a fluorometric assay, with solid phase-matched standard curves, this provided a more accurate quantification of enzyme activity with biochar. Although the standard curves for pine biochar were lower than the others, producing slightly negative values (Table 3.3), each curve fit the data with an R^2 between 0.94 - 0.99. Since we detected fluorescence of MUB for the standard curve, the reduced activity on pine biochar in the final assay was not merely due to quenching of the fluorescent product. As previously hypothesized, we also cannot rule out the solid phase interaction with enzyme cofactors or allosteric regulators (Bailey et al., 2011) or inhibiting compounds such as phenols and polyphenols (Lammirato et al., 2011) which could also impact enzyme activities.

As the primary mechanism for reduced activity loss, direct sorption of enzymes could cause either a conformational change in the enzyme active site or rotation of the active site toward the biochar surfaces (Leprince and Quiquampoix, 1996). Specifically, the lower BG activity on pine biochar may relate to protein sorption with the active site facing inwards or to weaker internal bonds of BG causing it to unfold easily (Datta et al. 2017). This reasoning leads to the conclusion that on the soil and grass biochar the immobilized BG maintained its active site morphology. Further, the activity levels over 100% (Fig. 3.3A, Fig. 3.3B) also indicate a possible stabilization effect, particularly for PHOS. This immobilization could serve as protection for enzymes against stress, as observed on low-surface area biochar (Elzobair et al., 2015), and in soil, where 60-70% BG activity is associated with macroaggregates (Miller and Dick, 1995). Further physical properties of the pine biochar, such as pore size distribution, could have caused reduced enzyme activities due to the substrate diffusing into micropores too small for enzymes to access (4.51nm, Table 3.1) (Quiquampoix and Burns 2007). In contrast, the grass biochar had larger mean pore size diameter (19.12 nm) that would allow more enzyme access.

The patterns of enzyme efficiency at different pH levels did not follow our predictions of higher sorption and thus low activity at lower pH levels. The pattern of lower BG efficiency at higher pH may relate to increasing distance from the enzyme optimal pH (Fig. 3.2, Table 3.2), as observed with BG in soil (Makoi and Ndakidemi, 2008), or relate to changes in soil surface functional group electronegativity and sorption altering the active site morphology (Quiquampoix and Servagent-noinville, 2002). Alternatively, the impact of pH on the charge of the enzyme and the soil surface may have changed the orientation of the enzyme and active site accessibility (Baron et al., 1999). For example, at pH 8, the BG may have sorbed to the soil with the active site inaccessible to substrate, as found with protein on montmorillonite clays (Quiquampoix and Servagent-noinville, 2002). With PHOS the slight, but not significant, increase of activity rate from pH 7 to 8 matches the increase in substrate degraded by the free enzyme (Table 3.3), which we attribute to assay variability. The complexity of these biochar-enzyme interactions require further study to develop a complete mechanistic understanding. This study underlines the importance of testing specific enzymes and biochar types before widespread implementation.

This lab assay explicitly tested if the high surface area pine biochar sorbed enzymes more readily than the other solid phases, and found that this biochar did impact substrate degradation. The observed decreases in activity corroborate patterns observed with biochar priming native soil organic matter: less priming occurs with additions of high temperature wood biochars, and higher C mineralization of native soil organic matter occurs with low temperature grass biochar (Zimmerman et al., 2011). With the complexity of these enzyme-solid phase interactions, the exact conditions of the laboratory assay require careful consideration when predicting field responses. Prior research shows that depending on setting, biochar-enzyme interactions can increase (Du et al., 2014; Oleszczuk et al., 2014), decrease (Lammirato et al. 2010; Paz-Ferreiro et al. 2012; Foster et al. 2016) or have no effect on catalytic capacity (Paz-Ferreiro et al., 2012). The effect of the interaction can depend on the specific enzyme (Bailey et al. 2011; Elzobair et al. 2015; Foster et al. 2016), biochar application rate (Oleszczuk et al., 2014; X. Wang et al., 2015), soil type (Bailey et al., 2011), and indirect effects on soil physio-chemical properties. The latter properties include the pH of the solid phase and bulk soil solution (Baron et al., 1999), sorption of inorganic and organic chemicals (Shindo et al., 2002), water retention, and pore structure (Sopeña and Bending, 2013). This lab assay highlights how biochar surface area, pore size distribution, and surface charge interact with specific enzymes to alter activity rates.

Conclusion

This lab experiment found that exposure to high pyrolysis temperature pine biochar reduced the detectable activity of BG and PHOS enzymes by 75-100%. To our knowledge, the activity level of enzymes directly immobilized on biochar surfaces has never before been tested. The decreased activity of pine biochar immobilized enzymes explains previous *in situ* findings of reduced BG and PHOS activities in an amended agricultural soil. The enzyme interaction with the pine biochar differed from the low-temperature grass biochar, indicating that biochar type, as well as specific enzyme, affects the amount of sorption and activity level. A distinct interaction of the solid phase, enzyme, and pH underlined the importance of measuring zeta potentials and hydrogen ion concentration within the system to assess distance from the enzyme optimal pH, isoelectric points, and electronegativity of both the enzymes and solid phase surfaces. These results further highlight pyrolysis temperature, surface area, and pore size distribution as key indicators of potential biochar-enzyme interactions due to the influence on overall charge and hydrophobicity. This experiment explicitly tested the enzyme activity levels after immobilization, rather than enzymes exposed to biochar; thus, it provides one explanation for the negative priming of native organic matter observed after wood biochar addition. We recommend that managers consider biochar surface characteristics prior to use as an agricultural amendment to ensure the organic addition will help, rather than hinder, soil carbon and nutrient cycling.

Table 3.1: Characteristics of the two commercial enzymes.

Enzyme	Abbrev.	Source	Expected Activity (U/mg)[c]	Optimal pH	Isoelectric Point (pH)	Atomic Weight (kDa)
β-Glucosidase	BG	*Aspergillus niger*	≥ 0.75	4.0	4 [a]	240 [a]
Acid Phosphatase	PHOS	Sweet potato	0.5-3.0	4.8	5.2 [b]	110-112 [b]

[a] Watanabe et al. (1992) examined an isoform of BG from Aspergillus niger. [b] Durmus et al. (1999) examined an isoform of acid PHOS from sweet potato. The commercial enzymes used in this experiment may have contained multiple isoforms of the enzyme.
[c] Each unit (U) of enzyme degrades 1.0 μmol of P-Nitrophenyl substrate (either Phophate or *β*-D glucopyranoside) per minute at the optimal pH and 37°C.

Table 3.2: Physical properties of three solid phases, with the pH and hydrophobicity measured in triplicate, and BET surface area and isoelectric point measured on a single sample.

Solid Phase	Description	pH	BET Surface Area (m^2 g^{-1})	BET Average Pore Width (nm)	Isoelectric Point (pH)	Hydrophobicity (seconds)
Soil	Irrigated sandy clay loam	8.7	27.5	6.16	< 1	Low (7.7)
Pinewood Biochar	Max pyrolysis temperature: 400-700ºC[a]	9.2	232.7	4.51	1-2	Medium (22)
Grass Biochar	Max pyrolysis temperature: 300ºC	9.9	6.3	19.12	1	High (>300)

[a] This range is reported due to variability in the commercial bioenergy and biochar production processed used for this product.

Table 3.3: *The amount of substrate degraded (nmols) by two enzymes (ß-Glucosidase (BG) and Acid Phosphatase (PHOS)) sorbed to the three solid phases (Soil, Pine Biochar (BC Pine), and Grass Biochar (BC Grass)) compared to the free enzyme in solution. Results are presented as means and 1 SE (n=5).*

		Substrate degraded (nmols)							
		Soil		BC Pine		BC Grass		Free Enzyme	
Enzyme	pH	Mean	SE	Mean	SE	Mean	SE	Mean	SE
BG	6	8.59	0.06	-1.17[a]	0.22	nd	nd	40.59	1.10
BG	7	8.62	0.91	-0.56[a]	0.40	-0.60[a]	4.11	40.20	0.34
BG	8	2.29	0.25	0.79	0.08	nd	nd	37.10	0.41
PHOS	6	13.40	1.62	-0.71[a]	1.07	nd	nd	33.05	2.24
PHOS	7	20.75	0.71	-2.78[a]	0.88	29.42	5.32	33.87	2.73
PHOS	8	26.46	2.73	1.18	0.38	nd	nd	40.03	1.10

[a] Negative values occurred when the standard curve overestimated the slope or intercept; thus, activity was below detection limits. No data (nd) was collected for pH 6 and 8 for the grass biochar.

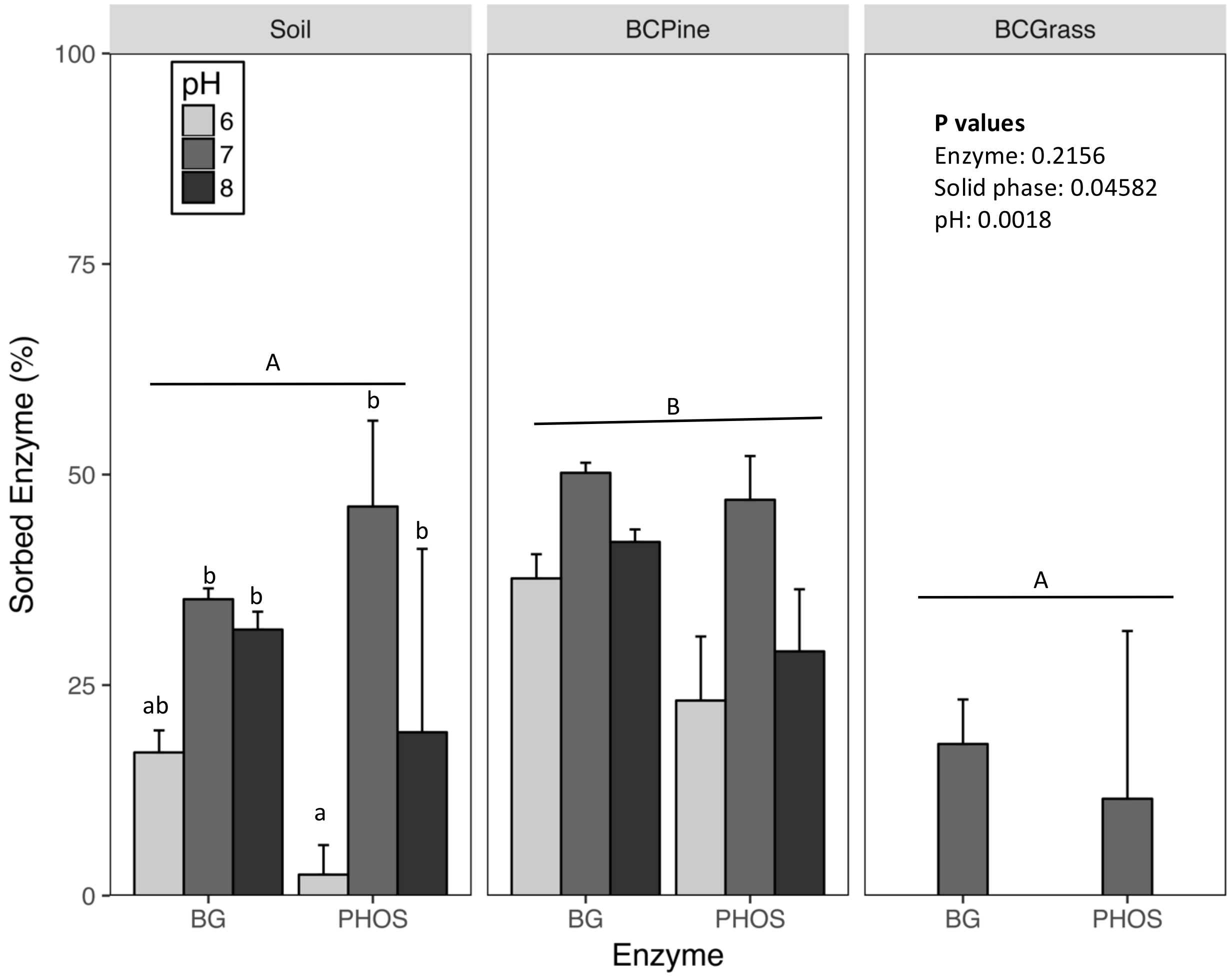

Figure 3.1. *The percent of enzyme (ß-Glucosidase (BG) or Acid Phosphatase (PHOS)) sorbed to the three solid phases (Soil, Pine Biochar (BC Pine), and Grass Biochar (BC Grass)) at three pH levels was calculated as the difference between the total enzyme added and the amount in the supernatant divided by the total enzyme added (Eqn 1). Results are as means +1 standard error (n=5). Significant differences (P <0.05) are labeled as capital letters for the contrasts between solid phases averaged over other factors and as lower case letters for contrasts of pH levels for each immobilized enzyme.*

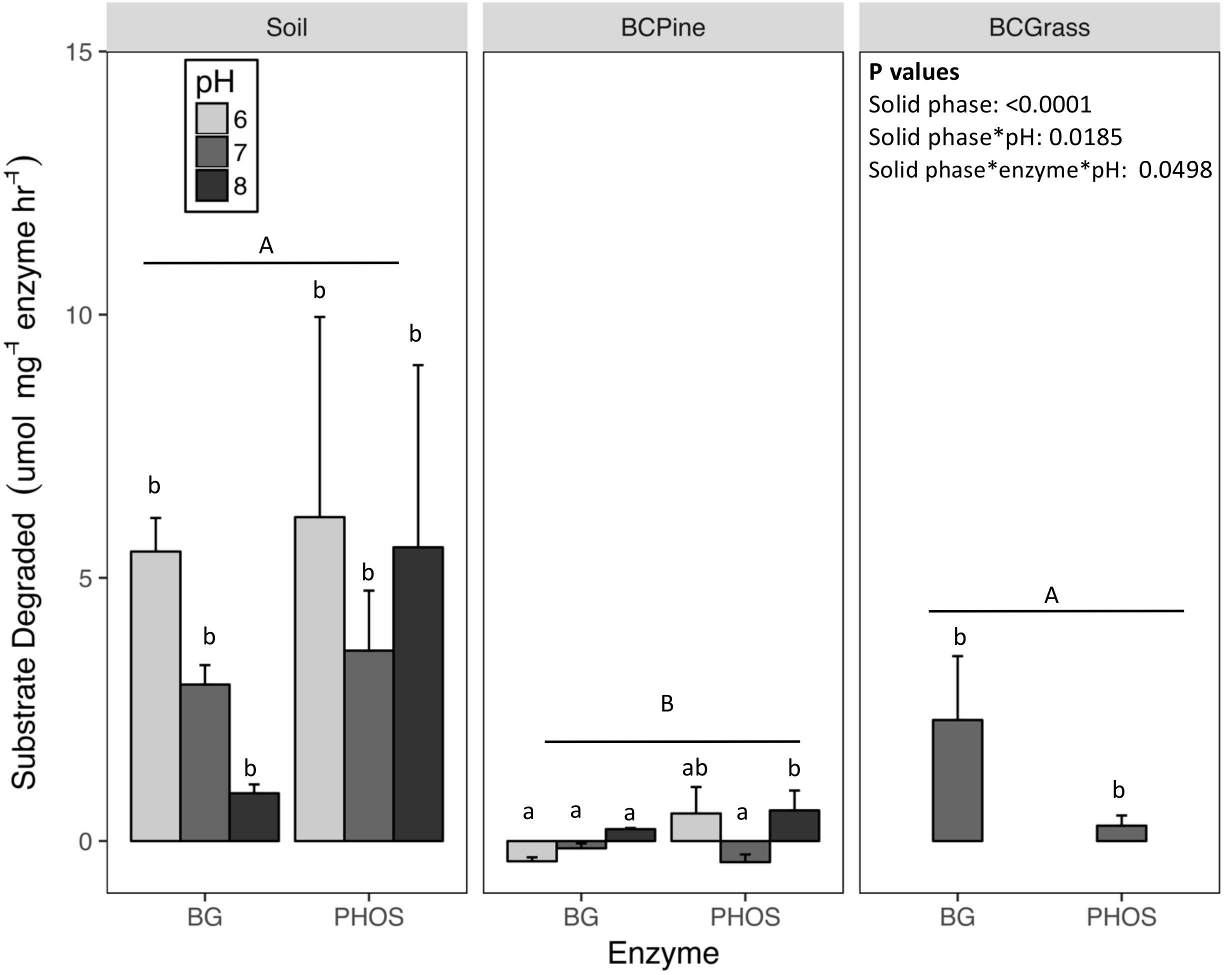

Figure 3.2. *The calculated activity rates for two enzymes,* ß-*Glucosidase (BG) and Acid Phosphatase (PHOS) sorbed to the three solid phases (Soil, Pine Biochar (BC Pine), and Grass Biochar (BCGrass)) (Eqn. 2), at three pH levels. Results are means + 1 SE. Significant differences (P <0.05) are labeled as capital letters for the contrasts between solid phases averaged over other factors and as lower case letters for contrasts of pH levels for each immobilized enzyme. Negative values were due to standard curve calculation and method detection limits.*

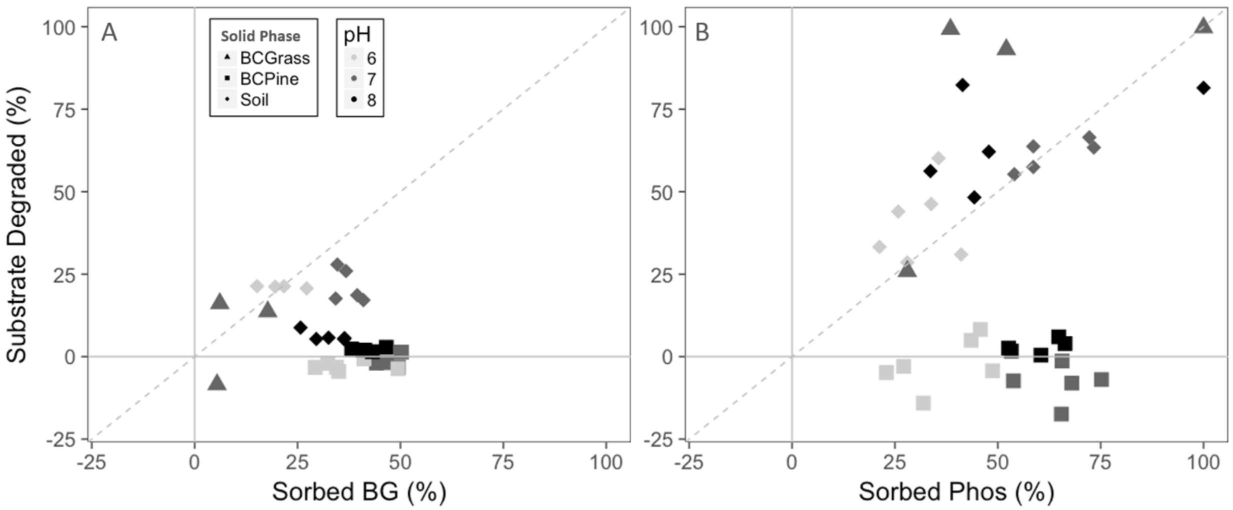

Figure 3.3A and 3.3B. *Percent of sorbed enzymes, (ß-Glucosidase (BG) and Acid Phosphatase (PHOS), plotted versus their uncorrected percent activities (umols degraded by the sorbed enzyme multiplied by the ug of enzymes present) when adsorbed to three soil phases (Soil (diamonds), Pine Biochar (BC Pine, squares), and Grass Biochar (BCGrass, triangles)). The assay was conducted at three pH (6=light gray, 7=dark gray, 8=black). Each data point represents a single well with added BG (Fig. 3.3A) or PHOS enzyme (Fig. 3.3B). The dotted line represents a one to one relationship between sorption and activity. The solid gray lines represent zero sorption or activity level. Negative values were due to standard curve calculation and method detection limits.*

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Chapter 4: Precision biochar and inoculum applications alter soil nutrient dynamics, maize yield, and bacterial community composition [3]

Introduction

Crop productivity depends upon climatic and edaphic conditions, including soil physical, chemical, and biologic properties. Managing for all three of these edaphic factors can increase crop available nutrients and agricultural input use efficiency, reducing the need for chemical fertilizers (Bennett et al., 2014). Managers can enhance crop nutrient uptake via direct addition of fertilizer and/or organic amendments, or by soil inoculation of plant-growth promoting rhizobacteria (PGPR) (Bonanomi et al., 2018). High organic matter content and active microbial communities increase nutrient availability and alter energy flow patterns in the soil. Recent research has focused on innovative nutrient management approaches such as organic biochar amendments and PGPR inoculum to increasing plant available nutrients and crop yield (Biederman and Harpole, 2013; Burrell et al., 2016; Crane-Droesch et al., 2013b; Jeffery et al., 2011).

Biochar amendments are formed from any organic feedstock that undergoes thermochemical conversion at temperatures >350°C with minimal oxygen (Lehmann and Joseph, 2015). During the pyrolysis conversion, aside from a small amount of labile compounds, most of the organic material is transformed into highly recalcitrant carbon (C) rings. As microbial metabolism of aromatic rings is highly inefficient, the biochar will not decompose and remain in soil for hundreds of years (Zimmerman et al., 2011). Biochar amendment to soils can increase soil porosity, water holding capacity, reactive soil surface area and nutrient retention, and

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[3] In preparation for submission to *Applied Soil Ecology* with P. Baas, M.D. Wallenstein, and M.F. Cotrufo

provide a protective habitat for soil microbes (Gul et al., 2015). Depending on feedstock type, pyrolysis temperature (Enders et al., 2012; Zimmerman, 2010), and initial soil properties, biochar can have wide ranging effects on soil fertility (Anderson et al., 2011), microbiology (Budai et al., 2016; Lehmann et al., 2011), and crop yields (Biederman and Harpole, 2013; Jeffery et al., 2011), but often with short-term effects in temperate agriculture (Quilliam et al., 2013). The physical and chemical differences between biochar types will affect soil chemical properties, such as reactive surface area, soil nutrient status (Anders et al., 2013) and pH (Laghari et al., 2016; Sheng and Zhu, 2018). These soil physiochemical changes also can impact microbial activity, abundance, and diversity. With this high variability, manufacturers now engineer ‘designer’ biochars, with post processing to neutralize pH and remove toxins to cater to specific soil environments (Novak et al., 2014). Innovative research has also expanded in the area of biochar and soil microbiology, including use of biochar to carry microbial inocula, particularly with phosphorus solubilizing bacteria (Mercl et al., 2018; Postma et al., 2013).

Biochar and other organic amendments have been purported as carriers for PGPR to inoculate agricultural soils. The microbes are added to soils to fix N, solubilize P, sequester Fe, suppress ethylene production by roots, produce plant growth hormones, antibiotics and antifungal compounds, and enhance competitive exclusion of plant pathogens (Bonanomi et al., 2018). One critical function of inoculation is to enhance nutrient conversion and cycling within the rhizosphere, expanding crop access to nutrients. The challenges to PGPR inoculation include survival patterns of microbes post application related to poor adaptation to local soil and environmental conditions like pH, moisture, temperature and redox status (Okon; and Labandera-Gonzalez, 1994), and low colonization rates due to initial low survival in storage, low cell counts, or poor vertical distribution of the inoculum (Hale et al., 2014). The use of biochar as a carrier rather than direct application of PGPR has been shown to improve cell survival, even distribution of bacteria into the soil, yet had no impact on bacterial abundance (Hale et al., 2014). Increased P concentration was also measured in soil solution after application of P solubilizing bacteria with wood ash (Mercl et al., 2018). With the enhanced survivability up to four weeks (Hale et al, 2015), a combination of biochar and P solubilizing inoculum may increase soil nutrient availability and yields in agricultural systems. More research is needed to elucidate direct changes to crop nutrient uptake and maximize efficacy.

This field experiment examines three soil management treatments to enhance crop yield and available nutrients in a temperate irrigated maize field (*Zea mays* L.). The overall experimental objective was to increase crop nutrient uptake and yield by managing soil bacteria via biochar and bacterial inoculation, and to test the responses to these amendments under full and reduced irrigation, with no irrigation between maize phenology stage V4-V14 (27 days). We predicted that all three amendments would enhance crop yields. Biochar would directly add nutrients to the soil and improve microbial habitat, increase bacterial diversity, nutrient cycling and availability for crop uptake. The addition of PGPR would increase relative abundance of bacteria that increase P solubilization. The combined treatment would have additive effects of both biochar and inoculum resulting in the highest yields, especially relative to the control under limited irrigation. To understand how the management treatment changed crop-nutrient dynamics, soil nutrient availability and crop nutrient content were measured at both an early and a late maize phenology stage. The response of the bacterial community to management treatments was analyzed via 16S genomic analysis of Exact Sequence Variants.

Materials and methods

Soil amendments and field experiment design and management

To manage soil nutrient supply in the maize field, three main soil conditioning techniques were evaluated: targeted biochar amendment, plant growth promoting bacterial inoculum and their combination. The biochar was derived from coconut hulls subjected to slow pyrolysis with a maximum temperature of approximately 600ºC (Cool Planet, Greenwood Village, CO, USA). The resulting biochar had a small particle size <2 cm, a neutral pH, total C content of 76%, and surface area of 230 m^2 g^{-1} (Table 4.1 for additional properties).

This bacterial inoculum consisted of four strains, reported at the following densities: *Pseudomonas putida* (20 x 10^6 CFU/mL), *Comamonas testosterone* (40 x 10^6 CFU/mL), *Citrobacter freundii* (60 x 10^6 CFU/mL), and *Enterobacter cloacae* (80 x 10^6 CFU/mL) (MAMMOTH P®, Growcentia, Fort Collins, CO, USA). The inoculum contained 1% bacteria culture, 2% alfalfa extract, and water. Prior to application, 1 mL of inoculum was diluted in 3.8 L of water (approximately 1:4). The diluted inoculum was sprayed precisely along each corn row at a rate of 2.1 L ha^{-1}. The inoculum was applied per manufacturer's recommendation three times throughout the growing season to coincide with specific crop phenology (Table 4.2).

The 'combined' treatment consisted of a single co-application of the biochar and inoculum. Two weeks prior to field application, we incubated the inoculum in the lab, shaking at 25°C for 24 h. After this growth period, we hand mixed 50 mL of inoculum per kg of biochar. This treatment design allowed the comparison between the suggested three-time surface applications of inoculum *versus* a single application with biochar to examine survivability over time.

The three soil treatments were applied at a field site located at the Agriculture Research Development and Education Center, Fort Collins, CO (40.59ºN, 104.14ºW). The climate at the is semi-arid and averages 408 mm of rainfall and the soil is a Fort Collins Loam (USDA – NRCS Web Soil Survey, accessed Dec. 2017; Foster et al., 2016)). The strip-strip plot design incorporated two irrigation treatments (full and limited by 20%), and four amendment levels: control without amendment, biochar (0.8 Mg ha^{-1}), bacterial inoculum, and a combined treatment. Each treatment was replicated across four blocks for a total of 32 plots, each 350 m^2 covering 1.05 ha total. In March of 2016 the field was tilled to 10 cm and ripped to 30 cm, and on May 13 the soil was fertilized with 88N-31P-1.5Zn applied at 285 L ha^{-1} (271 kg N ha^{-1}, 77 kg P ha^{-1}, 3.7 kg Zn ha^{-1}). Half of the biochar was inoculated in the lab on April 27 and stored at room temperature (~23 °C) in woven polypropylene bags. The untreated and inoculated biochar was applied on May 13 using Gandy boxes to target application directly into the maize row. We planted Northern King N29T-3111, Syngetna® maize on May 14 at 85,000 seeds ha^{-1} to a 10 cm depth. Roundup herbicide was applied on May 31 (2.3 L ha^{-1}) in congruence with best practices for the region.

Remaining field management practices corresponded to maize phenology stages as listed in Table 4.2. The maize emerged on May 25, 12 days after planting and the first application of plant growth promoting bacterial inoculum (diluted approximately 1:4 water) was sprayed on the surface at a rate of 17.8 mL dilute solution ha^{-1}. Linear irrigation was applied within two days of inoculation. Throughout the growing season a linear irrigation system applied water to meet crop need for the full irrigation treatment. When the maize had five collared leaves (phenology stage V5), a second round of inoculum was applied and the limited irrigation treatment began. When the maize had fourteen collared leaves (V14) the irrigation was restarted and subsequently the inoculum was applied a third time. Over a three-week period the limited treatment reduced water input by 8 cm; total limited irrigation amounted to 36 cm versus the full irrigation of 45 cm. During the course of the growing season the field received 13 cm of rainfall. The maize reached the first reproductive phase (R1) the last week of July and final physiological maturity (R6) in the first week of September.

Soil and crop nutrient analysis

Soil nutrient supply was measured during two distinct crop growth periods using plant root simulator (PRS) probes analyzed by Western Agricultural Innovation (Saskatoon, Canada) (Johnson et al., 2005; Sharifi et al., 2009). The first sampling period captured soil nutrient supply during the early growth phase (V1-V4) before the limited irrigation began. The PRS probes were inserted into the soil at an approximately 45° angle on May 27 (V1) and removed 18 days later (V4). For the second time point, the probes were inserted on July 14 (V15) and removed 14 days later (R1), to capture the post-drought period for the limited irrigation plots. At the end of the early (V4) and late (R1) sampling phase, soil samples were collected from the maize root zone. In each plot two maize plants were pulled and soil shaken from the roots into polyethylene bags. The root zone samples were immediately moved to the lab and stored at -80ºC until further processing. Additional bulk soil samples were collected in between the maize rows (0-10 cm) for measurement of soil pH. A 1:5 slurry (soil: deionized water) was mixed for ten minutes, allowed to rest five minutes, and then analyzed with an Orion EA 9110 m (Thermo Scientific, Beverly, MA, USA).

To analyze treatment impact on the maize crop, we measured leaf nutrients at V4, and at harvest we measured grain nutrients, total plant biomass, and total grain yield. For the crop nutrient analysis, we collected leaves from two plants per plot and grain from three plants per plot, bulked the respective plant tissues by plot, and then ground the samples. Then 0.5 g of plant tissue was digested in 3.0 mL of nitric acid and 2 mL of perchloric acid for analysis via inductively coupled plasma mass spectrometry (Optima 7300 DV Optical Emission Spectrometer, Perkin Elmer, Wlatham, MA, USA) (Zasoski and Burau, 1977). The measured grain nutrients concentrations (mg kg^{-1}) were multiplied by grain biomass to calculate grain nutrients accumulation (kg ha^{-1}) per plot. Final dry maize biomass and grain yield were measured on three plants per plot on September 27 after dry down, and field moist biomass along a 2 m transect for each plot was used to extrapolate yield and dry biomass to Mg ha^{-1} (Earl and Davis, 2003).

Soil sampling and DNA extraction for 16S sequencing

A total of 64 samples collected from the root zone were used for genomic analysis via Illumina MiSeq. Nucleic acids were extracted from approximately 30 mg of soil using the PowerSoil® DNA isolation kit (MoBio Laboratories, Carlsbad CA, USA). Isolated DNA was quantified with Pico-Green and amplified via polymerase chain reaction using a MyiQ Thermal Cycler (Bio-Rad Laboratories Inc., Hercules, CA, USA). The following universal primers were used to target the V4 variable region of the 16s rRNA gene: 515F (5’-GTGCCAGCMGCCGCGGTAA-3’) and 806R (5-GGACTACHVGGGTWTCTAAT-3’). The cycle conditions for PCR included denaturation at 95ºC for 10 min, then a subsequent 25 cycles of a denaturation at 95ºC for 10 min, annealing at 50ºC for 10 min, and an extension at 72ºC for 1 min. All successful amplifications were confirmed with gel electrophoresis. Amplicons were cleaned using the MoBio Qiagen UltraClean PCR Cleanup kit and quantified again with Pico-Green. Amplicons were pooled equimolar and the final 64 samples, one from each plot at two sampling dates, were paired-end sequenced (2x250) using the Illumina Miseq platform (2x250 bp) (Colorado State University Next Generation Sequencing Core Facility, Fort Collins, CO, USA).

The raw sequence data were processed using the QIIME2 pipeline (qiime2-2018.4, http://qiime2.org/) (Caporaso et al., 2010). Sequences were trimmed to ensure an average base quality score >20. In addition forward sequence reads were trimmed at 230 bp and reverse reads trimmed at 135 bp. The DADA2 sample inference pipeline was used to filter and dereplicate sequence reads, remove chimeras, mitochondrial and chloroplast DNA, and merge paired-end reads to infer Exact Sequence Variants (ESVs) (https://github.com/benjjneb/dada2). Using ESVs improves resolution to the level of single-nucleotide differences, equivalent to clustering data into Operational Taxonomic Units of 100% similarity to create “zero-OTUs” (Callahan et al., 2017, 2016). Taxonomy was assigned to ESVs using the SILVA 132 reference database (Pruesse et al., 2007) and naïve Bayes trained classifier in QIIME2, generating 2,390 total unique ESV features. Phylogenetic trees were generated via FastTree 2 within QIIME2, using maximum-likelihood alignments. The feature table, rooted phylogenetic trees, and taxonomy table were imported into R for statistical analysis. A full taxonomy list is presented in the Appendix Table 1.

Statistical Analysis

To test the effect of management on crop and soil nutrients and yield measurements, we used a two-way ANOVA with soil treatment and irrigation as the fixed effects and block as a random effect. Nutrient data were scaled by subtracting the mean (from n=4 per treatment) and dividing by the standard deviation, and then normalized using log transformations. Kruskal-Wallis post hoc adjustments were used in pairwise comparisons, with significance set at $\alpha<0.10$ level to highlight nuanced ecological patterns, rather than mere statistical significance (Sullivan and Feinn, 2012). The relationships between crop and soil nutrients to yield were measured with individual Pearson correlations and with ANCOVA with yield as the response variable, and soil or plant nutrients as the independent variables with block as the strata. Finally, non-metric multidimensional scaling (NMDS) was used to visualize the direction and magnitude of relationships between soil nutrient supply and crop nutrient levels at the two sampling dates, using block as the strata. The nutrient NMDS ordinations were run on Euclidean distance matrices calculated from unscaled data with random starting configurations, and two axis were selected to reduce stress to <0.07. All data analytics were performed using the R statistical program (Version 3.5.5, R Core Team, 2013).

Multivariate analysis of community structure and diversity

The bacterial community was analyzed using ESVs identified with lowest available taxonomic rank. Bacterial community composition and ESV diversity were assessed via steps detailed by Anderson and Willis (2003) and implemented by Hartman et al. (2012): (1) unconstrained ordination, (2) constrained analysis to assess specific hypotheses, (3) hypothesis testing via analysis of similarities (ANOSIM), and (4) indicator species analysis. All analyses were conducted using a Bray-Curtis similarity matrix of the community relative abundance (Bray and Curtis, 1957). Due to results from the initial unconstrained ordination principle coordinate analysis (PCoA), subsequent analyses were separated by date. Differences in the bacterial community structure due to management treatments and soil and crop environmental data were visualized via Canonical Analysis of Principle Coordinates (CAP) using capscale() in vegan using a cumulative sum square normalized Hellinger distance matrix. A PerMANOVA explicitly tested the effect of treatments and environmental variables on the community at $\alpha<0.1$ significance level, with block as strata. After rarefying to a depth of 1,848 sequences, community diversity was calculated as Chao1 richness, Inverse Simpson's index for evenness, and

Shannon's diversity index (Chao and Shen, 2003; Shannon and Weaver, 1963; Simpson, 1949). Finally the indicator 'species' analysis was run using multipatt() in the indicspecies package in R (De Caceres and Legendre, 2009). The function calculates the overall indicator statistic as a combination of the 'specificity' statistic A, the probability that a sample belongs to the treatment group where it has been found, and the 'fidelity' statistic B, the probability of finding that species in that treatment group. A specificity of 1 indicates that the bacteria is only found in that treatment group, while a fidelity of 1 indicates that the bacteria was detected in every single sample within that treatment group. The indicator bacteria were examined for each soil treatment and sampling period and results are reported at $\alpha<0.1$ significance level.

Results

Treatment effect on yield, soil, and crop nutrients

Overall maize grain yield in control plots was 9.65 Mg ha^{-1} (Fig. 4.1). Relative to the control, averaged across irrigation treatment, biochar increased yield by 20% (+1.95 Mg ha^{-1}) (P = 0.05). The inoculum and combined treatment had no effect on yield (Fig. 4.1). The limited irrigation decreased yield by 0.88 Mg ha^{-1} relative to the control fully irrigated treatment (P = 0.09). Under limited irrigation the inoculum had a 2.0 Mg ha^{-1} more grain yield than the control, but due to variability this was not statistically different. Maize biomass was not significantly impacted by treatment (Fig. 4.2).

Soil treatments impacted measured soil nutrient availability. At the early sampling period (V1-V4) the biochar treatment increased soil K availability (P=0.10, Fig. 4.3A, Table 4.3) and during the second sampling period (V15-R1) the biochar increased soil S availability (P=0.07, Fig. 4.3B). Also during the first sampling period the combined treatment decreased Zn availability relative to the inoculated plots (*P*=0.08) and the control (*P*=0.01). Soil pH remained unchanged, irrespective of irrigation and soil treatment.

Soil treatments and irrigation had little and varying effect on crop nutrient accumulation. Leaf nutrient concentration did not vary with irrigation treatment. Leaf nutrient accumulation of Mg, Mo, and S were significantly impacted by the biochar soil treatment (Table 4.3). Grain nutrient accumulation of Cu was higher in full irrigation plots (P = 0.07) and grain accumulation of N was affected by soil treatment (P=0.07), however the biochar treatment only slightly increased accumulation (data not shown).

Correlations between yield and nutrients

Available soil nutrients did not correlate with crop yield directly, but did correlate with certain crop nutrients (Table 4.4, Fig. 4.4). The early soil S availability negatively correlated with grain S (r=-0.37, *P*=0.04), grain Mg (r=-0.32, *P*=0.08), grain N (r=-0.42, *P*=0.02), grain P (r=-0.38, *P*=0.05), and leaf Cd (r=-0.46, *P*=0.009) but tended to positively correlate at the later sampling date (data not shown). Although soil K increased initially under the biochar treatment (Fig. 4.3A), it did not correlate with grain K or other crop nutrient uptake.

Specific leaf nutrient concentration (mg g^{-1}) and grain accumulation (kg ha^{-1}) were highly correlated with yield (Table 4.4). Leaf nutrient uptake that positively correlated with yield included P, S, Cu, N, Mg, Ca, K, Mn, Zn, Mo, Fe, and Ni. When analyzed with all other nutrients, leaf nutrient uptake of Mg (*P*=0.03) and P (*P*=0.07) positively influenced grain yield, but no treatments had a significant effect these nutrient-yield relationship (*P*=0.16). At the early sampling date, soil NH_4^+, P, and Pb significantly correlated with leaf nutrient uptake overall, with NH_4^+ positively correlated to leaf N content (NMDS, p<0.10, Fig. 4.5A).

Grain nutrient accumulation that positively correlated with yield from greatest to least were S, K, Mg, Zn, P, N, Cu, Mo, and Ni (*P* <0.05, Pearson correlation) (Fig. 4.4). When analyzed with all other nutrients and across treatments, grain P uptake positively impacted grain yield (*P*=0.08, ANCOVA). At the later sampling date higher soil NO_3^-, Mg, and Zn positively correlated with their respective grain nutrients (NMDS, p<0.10, Fig. 4.5B). All grain nutrients positively correlated with corresponding leaf nutrient uptake (data not shown).

Bacterial community structure and diversity

The sequencing efforts resulted in 2,390 unique features found in 61 filtered, high quality samples with a total of approximately 0.5M reads. Three samples were excluded due to low read counts. Taxonomic assignment identified 29 phyla, 72 classes, 130 orders, 171 families, 219 genera and 18 species (Appendix Table 1). Relative to the overall total, the most abundant phyla at the first and second sampling date included: Acidobacteria (early abundance of 7.8%, and a later abundance of 8.9%), Proteobacteria (6.8% and 6.7%), Actinobacteria (5.7% and 5.0%), Bacteroidetes (1.0% and 4.3%), and Planctomycetes (1.6% and 1.9%) (Fig. 4.6). Overall only 5.4% of the reads remained unclassified at the phylum level.

The influence of management treatment on bacterial community structure was measured separately for the early (V1-V4) and late (V15-R1) sampling periods. This separation was chosen based on results from the unconstrained principle coordinate analysis (PCoA) of ESV relative abundance, where sampling date explained the most variance (Fig. 4.7, ANOSIM R=0.15, P=0.001). Larger variance existed between samples at the later R1 sampling. Soil treatment slightly influenced overall bacterial community structure at the first sampling period (ANOSIM R= 0.05, P=0.07; PerMANOVA P=0.1).

The CAP ordination of normalized Hellinger transformed ESV abundance data and subsequent fit of management treatments and nutrient data revealed differences in community structure between soil treatments (Fig. 4.8A, B, and C). At the early sampling period, soil treatment had a slight effect on the overall community structure (PerMANOVA $P=0.09$, Fig. 4.8B). Community structure under all of the treatments significantly differed from the control ($P<0.01$) and additionally, the inoculum treatment differed from the biochar and combination treatments ($P<0.01$). The later sampling date showed an effect of irrigation on the bacterial community composition (PerMANOVA $P = 0.001$, Fig. 4.8C), and significant pairwise interactions with soil treatments. Based on pairwise comparisons of the environmental factors in the CAP ordination, irrigation level impacted the bacterial community structure within every soil treatment except the control ($P<0.1$). Under full irrigation the inoculum and combined treatment altered the bacterial community relative to the control ($P<0.07$), but the bacterial community in the biochar plots did not differ from other treatments at the later sampling date. Under limited irrigation the control community structure was different than all other treatments ($P<0.1$), but the biochar and inoculum treatment community structures remained similar.

Significant correlations of the bacterial community with specific soil and crop variables existed, as shown with environmental vectors on Fig. 4.8A, C, and C (CAP, PerMANOVA). When overlaid as environmental vectors, crop yield oriented towards the communities in the biochar treatments. Furthermore, crop dry biomass improved the model of the bacterial community structure more than yield (AIC, backward model selection, $P<0.01$). Yield and total biomass were not significant in subsequent models and therefore removed from models including soil nutrient supply to prevent over-fitting. When specific soil nutrients were fit to the CAP ordination and overlaid as vectors at the early V4 stage, soil Zn, P, and NO_3^- supply correlated the most with the bacterial community data, and of these variables soil NO_3^- was the most significant (AIC, backwards model selection, P=0.06). At the later R1 stage, the bacterial community composition correlated with soil supply of Zn, Fe, S, Mn, Cu and NH_4^+ (P<0.10). Soil supply of both Mn and Zn significantly influenced bacterial community structure (AIC, backward model selection, P<0.03).

The normalized alpha diversity of ESVs within each sample was significantly higher at the early sampling date than the later sampling date for all indices (P<0.05, Fig. 4.9). Irrigation had no effect on bacterial diversity. Soil treatments had no significant impact on bacterial community diversity.

Indicator bacteria analysis

The top ten indicator ESVs, those with high specificity and high fidelity, classified at the family level for the early sampling period were: Burkholderiaceae, Pirellulaceae, Streptosporangiaceae, Sphingomonadacea, Gemmataceae, bacteriap25, Ilumatobacteraceae, Hymenobacteraceae, (uncultured Gemmatimonadetes), and Opitutaceae, excluding three uncultivated ESVs of the Class Gammaproteobacteria, MB-A2108, BD2-11 terrestrial group, and OM190) (Table 4.7). The top ten indicator ESVs, classified at the Family level for the late sampling period were: Pedosphaeraceae, Enterobacteriaceae, Hyphomicrobiaceae, Opitutaceae, JG30-KF-CM45, Micromonosporaceae, Burkholderiaceae, Sphingobacteriaceae, Glycomycetaceae, and Azospirillaceae, excluding four additional uncultured ESVs of the classes, OM190, Acidimicrobiia, and Subgroup 6. The top ten results classified to genus are listed in Table 4.5 and full indicator species tables by soil amendment are in Appendix Table 2.

Indicator bacteria differed between the full and limited irrigation at the later sampling date (Table 4.6). The top ten indicator ESVs were all associated with the limited irrigation treatment except for the Nitrospira and Skermanella *sp*. found primarily in the fully irrigated plots.

The biochar communities all contained the following indicator families: Gemmataceae, Micromonosporaceae, Xanthobacteraceae, WD2101 soil group, Steroidobacteraceae, Chthoniobacteraceae, and Fibrobacteraceae. Families found primarily in the inoculated plots included: Xanthomonadaceae, Pirellulaceae, Gemmataceae, Pedosphaeraceae, Longimicrobiaceae, Rhizobiaceae, and Haliangiaceae. The top indicator families from the combined treatment included: Dongiaceae, Micromonosporaceae, WD2101 soil group, Gemmataceae, Haliangiaceae, JG30-KF-CM45, Enterobacteriaceae, Burkholderiaceae, Glycomycetaceae, and Chthoniobacteraceae (Table 4.7). The families Chthoniobacteraceae and WD2101 soil group was found in the combined and biochar plots, but no overlapped occurred between the combined and inoculated plots at the family level.

The analysis of specific ESVs revealed several variants that match the added inoculum at the family level (Table 4.7). At the first sampling date a sequence variant in the Bukholderiaceae family had a specificity with a positive predictive value of 0.61 for the combined treatment plots and 0.23 for the inoculated plots. This ESV matched the taxonomy of the Burkholderiacaea Comamonas *spp* added in the inoculum. Furthermore the fidelity, or sensitivity, of Burkholderiacaea indicator was 0.86 for the combined treatment and 0.38 for the inoculated plots, but only 0.14 for the other treatments. At the second sampling date, a similar Burkholderiaceae sequence variant and another Enterobacteriaceae sequence variant matched the added inoculum at the family level. The Burkholderiaceae variant had a 0.80 specificity to the combination treatment and 0.80 for the inoculated plots. The fidelity of the Burkholderiaceae variant was 0.5 in the combined plots, 0.13 in the inoculated plots, but was not found in the other treatments. Further, the Enterobacteriaceae sequence variant had a 0.93 specificity for the combined treatment, and a 0.5 fidelity to the combination treatment and was also found in the control plots at a sensitivity and fidelity <0.1.

Discussion

Soil-crop nutrient dynamics and yield

To improve soil nutrient availability and crop production, we need to understand the effects of specific management strategies on bacterial cycling of plant nutrients within agricultural fields. Our study shows that precision biochar amendment increased maize yield by approximately 20% through changes in soil K and S supply and crop uptake, and indirectly through changes to the bacterial community.

In our field trial, a low application of conditioned coconut biochar increased soil K supply at the early growth phase (V4) and S supply later in the season (R1). The increase in nutrient supply correlated to grain accumulation of K and S and ultimately yield. Increases in soil nutrients have been previously attributed to direct addition in natural Amazonian Dark Earth soils (O'Neill et al., 2009), in column studies showing increases in Ca, K, Mn, and organic C (Novak et al., 2014) and in greenhouse and field experiments with biochar induced increases in K, Ca, N, P, S and Mg (Mercl et al., 2018). Despite the fact that these cations, particularly Ca, K, and Mg, directly compete for reaction sites in soil, the enhanced nutrient supply can increase crop nutrient uptake (Mercl et al., 2018; Song et al., 2018).

In this field experiment, soil amendments only had slight effects on soil nutrient supply and crop uptake. First, soil treatments had no direct impact on available soil P or crop uptake, though grain P accumulation accounted for the largest differences in yield (ANCOVA, P=0.08), suggesting that this was a limiting nutrient. The negative correlation between grain P, early soil S and Zn supply, and late Mg supply indicates a more nuanced interaction between the biochar and these critical crop nutrients. A second unexpected result was that the combined treatment did not have the same impact on soil nutrient supply as the biochar. This could be due to interactions during the two weeks of storage prior to application, including the following mechanisms: the metabolism of the biochar labile fraction, an altered bacterial community due to interaction and competition between the added inoculum strains and bacteria initially on the biochar, or microbial biomass, products and residues covering of the cation or anion exchange sites on the biochar surface. The null effect of the combination treatment suggests that the biochar increased yields through direct addition of nutrients to the soil.

Previously, biochar impact on crop nutrient uptake and yield also has been attributed to changes in soil physiochemical properties (Chen et al., 2018; Cheng et al., 2018; Jin, 2010). The high surface area of biochar can attract cations (X. Wang et al., 2015), increase soil water and nutrient retention (Chen et al., 2018), and even lime soils, resulting in increased nutrient availability. However, in our field experiment the biochar had no impact on the pH of the calcareous soil (data not shown), and the low application rate makes it less likely that any significant shifts in nutrient retention occurred directly due to structural changes. One possibility is that the biochar improved early root growth and development of the seedling. An extended root zone may have reduced nutrient limitations over the course of the growing season. Another possible mechanism is that the slight alteration of soil physiochemical properties shifted soil habitat niches and therefore microbial community structure and function (Lehmann et al., 2011).

Bacterial community structure

The overall distribution of the bacterial phyla and the variation in community composition over the course of the cropping season aligns with certain previous biochar field experiments (Anderson et al., 2014; Jin, 2010). Maize biomass correlated to bacterial community structure, which could indicate more inputs into the soil via root exudation and thus a community shift and wider variability in composition later in the season. In addition to community shifts over time, the fertilizer input before planting and the specific crop and hybrid chosen likely impacted bacterial community structure, potentially overshadowing the influence of the biochar treatment at the later sampling date (Anderson et al., 2014; Rousk and Bååth, 2011). Furthermore, at the later sampling date the community structure responded to additional interactions between soil treatment and irrigation. Although soil moisture can control bacterial growth rates and biomass (Rousk and Bååth, 2011), the short drought period of the limited irrigation resulted in few distinct shifts in relative abundance. The bacteria might have been simply dormant during the three week limited irrigation and reactivated when irrigation resumed. Under limited irrigation, the data show a trend toward yield increasing with the added inoculum. This matches previous results showing larger effects of plant growth promoting bacteria under drought conditions (Rubin et al., 2017).

At the early sampling date, all of the soil treatments caused shifts in bacterial community structure relative to the control. At this early stage, soil bacterial community structure correlated with soil available NO_3^-, P, and Zn and crop uptake correlated with NH_4+, P, and Pb. Soil treatments did not impact soil available N and P directly, but impact on nutrient rich biofilms may have been undetected, as these bacterial residues coat soil surfaces and do not move through soil solution. Trends indicate that the biochar increased soil NO_3^- (+32% relative to the control plots), but this was not statistically significant. However, biochar enhanced grain N accumulation; we hypothesize that biochar increased cycling of crop available N. Again these critical changes to N and additional soil nutrients could have occurred primarily in biofilms undetected by the PRS probe method (Mercl et al., 2018).

Later in the season through the beginning of the maize reproductive phase (R1), the soil nutrient supply of NO_3^- , Mg, and Zn directly correlated to grain nutrient accumulation which correlated slightly with grain yield. Final grain nutrient accumulation of K, S, and N was influenced by the biochar treatment via increased soil nutrient availability (especially of early K and later S). At this R1 stage the soil supply of NH_4^+, S, and Zn also correlated with the bacterial community structure, suggesting that dynamics between biochar and the soil bacterial community influenced crop accumulation of N and S especially during the late maize reproductive phase. Interestingly, the influence soil Zn supply on the bacterial community remained consistent over both sampling periods and the inoculated plots maintained higher Zn supply, particularly late in the season, possibly tied to increased solubilization by excretion of organic acids (Goteti et al., 2013). Since the bacterial community with the inoculum remained different than the control under limited irrigation later in the season, the slightly higher yields could relate to these inoculum increases in soil Zn, but this was not measured in crop uptake.

Although in the combined treatment bacterial community structures differed later in the season from all other treatments, this did not significantly impact soil nutrient availability or crop uptake. We hypothesize the lack of effect of the combined treatment on both soil nutrient supply and yield are due to interactions during the two week storage period in the lab prior to field application. The combined treatment also did not have the same bacterial community composition as the inoculum alone; the biochar did not enhance effect of inoculation. The short lab incubation time, along with the two weeks in-between inoculation of the biochar and field application, due to inclement weather, likely reduced effectivity of the combined treatment. An expanded lab analysis of inoculation methods and survival rates would help to answer this question and add to a growing body of research on biochar as an inoculum carrier (Hale et al., 2015, 2014b).

Bacterial diversity and indicator analysis

Despite no detectable shifts in diversity indices or consistent indicator bacteria over time, there were several key indicator bacteria unique to specific soil management treatments. In this field study the biochar significantly changed the community early in the season. Biochar amendments have been shown to have no short-term impact diversity unless combined with fertilizer (Jaiswal et al., 2018). Long-term experiments have shown that biochar additions may increase diversity (You et al., 2018, O'Neill et al., 2009). Furthermore, recent 16S genomic analyses found important changes in community structure can occur with biochar application (Ahmad et al., 2016; Chen et al., 2018; Xu et al., 2016) which have been attributed to labile C addition (Smith et al., 2010) and changes in soil physiochemical properties that change soil habitat (Jin, 2010) and raise the pH (Cheng et al., 2018). Particularly in temperate systems, biochar has been shown to stabilize the bacterial community over time (Anderson et al., 2014), with only minor impacts on community structure (Anders et al., 2013), which matches our finding of slight shifts in bacterial community composition with biochar addition, but no changes to diversity indices.

In our field experiment, the biochar amendment induced early season changes in bacterial community structure, which was manifested in four important indicator families: Gemmataceae, Micromonosporaceae, Xanthobacteraceae, and WD2101. The Micromonosporaceae family is part of the Actinobacteria phylum that degrades C-rich recalcitrant compounds and exists in high abundance in natural dark earth and soils high in pyrogenic organic matter (Khodadad et al., 2011). However, a greenhouse study found a 7% decrease in this Micromonosporaceae family with a high pine biochar addition, which contrasts with our results (Anderson et al., 2011). A second family, Xanthobacteraceae, also occurred primarily in the biochar plots, has at the order level (Rhizobiales increased with a 5% biochar addition (Cheng et al., 2018), as well as the gram negative phyla Alphaproteobacteria (Nielsen et al., 2014). This general pattern of increased gram negative copiotrophic bacteria with fast growth rates has been observed frequently with biochar amendment (Cheng et al., 2018; Gomez et al., 2014; Jiang et al., 2016; Sheng and Zhu, 2018).

On the phylum-level, the biochar plots contained indicator taxa that included Actinobacteria, Planctomycetes, Proteobacteria, and Gemmatimonadetes. Actinobacteria and Proteobacteria, both gram positive, k-selected slow growing bacteria, are found in soils with high pyrogenic organic matter (O'Neill et al., 2009), as well as with maize straw biochar (Xu et al., 2016), soybean and pine biochar addition (Ahmad et al., 2016). However, decreases after biochar addition have also been observed in Proteobacteria (Cheng et al., 2018) and Actinobacteria and Gemmatimonadetes due to changes in C substrate availability with biochar addition (Chen et al., 2018). The contrasting effects found after biochar amendment and in pyrogenic organic matter rich soils underlines the importance of exact taxonomic resolution. Our mixed results highlight the critical role of initial soil properties and biochar type when discussing specific biochar-soil bacteria dynamics.

In this study we expected important changes in bacterial function to emerge in response to the soil management treatments. However, relative to the control, the biochar and inoculum increase P, or abundance of soil P solubilizing bacteria, as observed previously (Warnock et al., 2007). The combination plots did contain higher abundance of the soil S and Fe oxidizing bacteria Sphingomonadaceae (You et al., 2018), but this had no detectable influence on soil nutrients or crop uptake. Without better taxonomic assignment to the genus level, the relationship between the bacterial community composition and nutrient dynamics remains tenuous and even unlikely (Mercl et al., 2018). However, it is possible that the biochar enhanced bacteria that improved yield due to factors we did not measure, such as increased competition with plant pathogens, production of organic acids or siderophores for macronutrient transport (Khan et al., 2014), or changed microbial signaling in the soil (Masiello et al., 2013).

The inoculum and combined treatment did not impact soil P but did contain two families that encompass the specific strains from the inoculum. The Bukholderiaceae family to which the added *Comamonas testeroni* belongs, maintained a high specificity to the combined treatment (0.61) and significant specificity to the inoculated plots (0.23) for both sampling dates. During the maize reproductive phase the family Enterobacteriaceae, to which the added *Enterobacter cloacae* belongs, also served as an indicator species for the combined treatment (0.93 specificity, 0.05 fidelity). This matches previous work with *Enterobacter cloacae* and pine biochar as an inoculum carrier in a sandy loam soil (Hale et al., 2014b).

With numerous potential factors at play, including direct addition of biochar labile substrate, changes to soil reactive surface area and porosity, and creation of protective habitat for bacteria, the mechanism behind biochar increased crop nutrient accumulation and yield increase remain nebulous, but likely involve increases in soil available N, S and K. A field study with increased replication and number of seasons would substantially improve our understanding of biochar and soil bacterial nutrient cycling dynamics. Particularly expanding the genomic sampling to include fungal taxa would enhance our knowledge of the full microbial community interactions and particularly phytopathogens (Jin, 2010; Warnock et al., 2007). Extended field research and continued utilization of ESV analyses will enhance comparability between biochar studies and improve our understanding of management impacts on critical microbial function in cropping systems.

Conclusion

The results from this maize field experiment indicate that an engineered coconut hull high pyrolysis biochar banded directly next to the maize seed at a rate of 0.8Mg ha^{-1} can increase maize yield by 20% (1.95 Mg ha^{-1}). The biochar increased availability of soil K and S, enhancing early crop (V4) leaf nutrient concentration of S and grain accumulation of S, K, and N, potentially avoiding nutrient limitation. The plant growth promoting P solubilizing bacterial inoculum and combined application of inoculum with biochar had no impact on plant nutrient uptake, but indicator ESVs demonstrated that two of the four inoculum strains potentially persisted in the soil until the first maize reproductive stage (R1). The biochar-induced changes in crop nutrient uptake may relate to the early season changes (prior to maize phase V4) in the soil bacterial community. With no observed changes in diversity and divergence from previous 16S genomic studies of bacterial communities, further lab and field experiments are needed to elucidate precise interactions between amendments, soil bacteria, and crop nutrient uptake. This field experiment suggests that innovative agricultural management requires rigorous testing prior to on farm application, particularly when implementing combined strategies.

Table 4.1
Characteristics of the biochar used in our study to amend irrigated maize fields. Values provided by CoolPlanet (Greenwood Village, CO, USA) and conducted at Wallace Labs El (Segundo, CA, USA).

Biochar Basic Properties	Value	Units
Feedstock	Coconut hulls	
Duration of max pyrolysis temp	Slow pyrolysis,	max temp ~600°C
Moisture	30	% of total mass, dry basis
Organic Carbon	75	% of total mass, dry basis
Total Ash	4	% of total mass, dry basis
Total N	0.67	% of total mass, dry basis
pH	7.1	
Electrical Conductivity	2.08	dS m^{-1}
Particle size distribution	80	(% > 0.5mm)
Surface Area	230	m^2 g^{-1}
Ca	135.5	mg kg^{-1}
Fe	18.5	mg kg^{-1}
K	3274	mg kg^{-1}
Mg	76	mg kg^{-1}
Mn	2.2	mg kg^{-1}
P	124	mg kg^{-1}
S	60	mg kg^{-1}
Zn	1.4	mg kg^{-1}

Table 4.2

Field management timeline corresponding to maize phenology stages.

Date	Days after Planting	Crop Phenology	Management Treatments	Soil sampling
5/14/16	0	Planted seeds	Apply biochar and fertilizer	
5/27/16	14	V1	Inoculation #1	Install PRS Probes
6/14/16	30	V4	Start Limited irrigation treatment	Remove PRS probes, sample soil bacteria
6/16/16	34	V5	Inoculation #2	
7/10/16	57	V14	End Limited irrigation treatment	
7/14/16	63	V15	Inoculation #3	Install PRS Probes
7/28/16	75	R1		Remove PRS probes, sample soil bacteria
9/1/16	110	R6	No irrigation, dry down begins	
9/23/16	132	132	Harvest	

Table 4.3
ANOVA F-statistics and p-values for management effects on soil nutrient supply early (V1-V4) and late (V15-R1), leaf nutrient concentration, and grain nutrient accumulation. Significant p-values are in underlined in bold.

	Treatments	**df**	**Ca**	**Cu**	**Fe**	**K**	**Mg**	**Mn**	**Mo**	**NO3.N**	**NH4.N**	**P**	**Pb**	**S**	**Zn**
Soil nutrient	Irrigation	1	2.23	10.68	0.33	1.86	0.25	0.88	nd	0.38	2.23	2.57	3.90	0.04	0.10
	p-values:		*0.23*	***0.05***	*0.61*	*0.27*	*0.65*	*0.42*		*0.58*	*0.23*	*0.21*	*0.14*	*0.86*	*0.78*
	Amendment	3	0.67	1.07	2.14	2.56	0.76	0.42	nd	1.08	1.31	0.22	0.59	0.87	2.92
	p-values:		*0.58*	*0.39*	*0.13*	***0.09***	*0.53*	*0.74*		*0.39*	*0.30*	*0.88*	*0.63*	*0.47*	***0.06***
	Irrigation:Amendment	3	1.99	2.11	0.79	0.42	1.60	0.73	nd	1.25	1.80	0.16	1.29	0.85	0.30
	p-values:		*0.15*	*0.13*	*0.52*	*0.74*	*0.22*	*0.55*		*0.32*	*0.18*	*0.92*	*0.31*	*0.49*	*0.83*
Soil nutrient	Irrigation	1	1.98	0.34	0.52	0.01	3.11	0.47	nd	0.57	0.03	0.78	5.09	0.92	3.82
	p-values:		*0.25*	*0.60*	*0.52*	*0.92*	*0.18*	*0.54*		*0.51*	*0.87*	*0.45*	*0.11*	*0.41*	*0.15*
	Amendment	3	0.07	1.02	0.33	0.70	0.11	0.11	nd	1.21	0.17	0.42	0.05	3.04	0.11
	p-values:		*0.97*	*0.41*	*0.80*	*0.56*	*0.95*	*0.95*		*0.34*	*0.92*	*0.74*	*0.98*	***0.06***	*0.95*
	Irrigation:Amendment	3	2.37	1.26	0.13	0.46	1.81	1.28	nd	0.45	0.64	0.80	0.69	1.76	0.28
	p-values:		***0.10***	*0.32*	*0.94*	*0.71*	*0.18*	*0.31*		*0.72*	*0.60*	*0.51*	*0.57*	*0.19*	*0.84*
	Amendments	**df**	**Ca**	**Cu**	**Fe**	**K**	**Mg**	**Mn**	**Mo**	**N**	**Ni**	**P**	**Pb**	**S**	**Zn**
Leaf nutrients	Irrigation	1	2.63	3.44	4.17	0.00	3.10	2.93	0.51	2.85	2.69	2.86	0.06	2.58	3.15
	p-values:		*0.20*	*0.16*	*0.13*	*0.98*	*0.18*	*0.19*	*0.53*	*0.19*	*0.20*	*0.19*	*0.83*	*0.21*	*0.17*
	Amendment	3	1.68	3.12	1.77	1.38	2.55	1.61	2.84	0.99	0.44	2.12	4.72	3.09	1.92
	p-values:		*0.21*	***0.05***	*0.19*	*0.28*	***0.09***	*0.22*	***0.07***	*0.42*	*0.72*	*0.13*	***0.01***	***0.05***	*0.16*
	Irrigation:Amendment	3	1.21	1.25	0.38	0.95	0.87	0.61	0.20	0.73	0.38	0.50	2.28	1.12	0.61
	p-values:		*0.33*	*0.32*	*0.77*	*0.44*	*0.47*	*0.62*	*0.89*	*0.55*	*0.77*	*0.69*	*0.11*	*0.37*	*0.62*
Grain nutrients	Irrigation	1	1.01	7.70	0.02	0.08	0.53	0.98	0.47	1.67	0.05	0.33	nd	2.44	0.46
	p-values:		*0.39*	***0.07***	*0.89*	*0.79*	*0.52*	*0.39*	*0.54*	*0.29*	*0.84*	*0.61*		*0.22*	*0.55*
	Amendment	3	0.58	2.14	1.55	1.30	0.94	0.75	1.60	2.77	1.11	0.80	nd	2.23	1.42
	p-values:		*0.63*	*0.13*	*0.25*	*0.31*	*0.44*	*0.54*	*0.22*	***0.07***	*0.37*	*0.51*		*0.12*	*0.27*
	Irrigation:Amendment	3	1.25	0.55	2.28	1.58	0.19	0.95	1.25	0.05	0.39	0.15	nd	0.15	1.76
	p-values:		*0.32*	*0.66*	*0.13*	*0.23*	*0.90*	*0.44*	*0.32*	*0.98*	*0.76*	*0.93*		*0.93*	*0.19*

Abbreviations: nd = not detected, df=degrees of freedom. Soil Mo supply was not measured.

Table 4.4 Total nutrient accumulation kg/ha

Correlations between maize yield and crop nutrients. F-values and significance of the ANOVA to analyze effect of soil management on significant nutrients.

Grain Nutrient		Ca	**Cu**	Fe	**K**	**Mg**	Mn	**Mo**	**N**	**Ni**	**P**	Pb	**S**	**Zn**
	Pearson r:	0.219	**0.798**	0.015	**0.92**	**0.886**	-0.078	**0.6**	**0.832**	**0.35**	**0.873**	nd	**0.925**	**0.875**
	P-value:	0.228	**<0.001**	0.944	**<0.001**	**<0.001**	0.673	**<0.001**	**<0.001**	**0.05**	**<0.001**	nd	**<0.001**	**<0.001**
ANOVA, F-values	df													
Irrigation	1	1.01	7.70	0.02	0.08	0.53	0.98	0.47	1.67	0.05	0.33		2.44	0.46
		0.39	**0.07**	0.89	0.79	0.52	0.39	0.54	0.29	0.84	0.61		0.22	0.55
Treatment	3	0.58	2.14	1.55	1.30	0.94	0.75	1.60	2.77	1.11	0.80		2.23	1.42
		0.63	0.13	0.25	0.31	0.44	0.54	0.22	**0.07**	0.37	0.51		0.12	0.27
Irrig:Trt	3	1.25	0.55	2.28	1.58	0.19	0.95	1.25	0.05	0.39	0.15		0.15	1.76
		0.32	0.66	0.13	0.23	0.90	0.44	0.32	0.98	0.76	0.93		0.93	0.19

Leaf nutrients		**Ca**	**Cu**	**Fe**	**K**	**Mg**	**Mn**	**Mo**	**N**	**Ni**	**P**	Pb	**S**	**Zn**
	Pearson r:	**0.765**	**0.859**	**0.7**	**0.778**	**0.811**	**0.748**	**0.726**	**0.844**	**0.38**	**0.925**	-0.17	**0.87**	**0.734**
	P-value:	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**<0.001**	**0.03**	**<0.001**	0.35	**<0.001**	**<0.001**
ANOVA, F-values	df													
Irrigation	1	2.63	3.44	4.17	0.00	3.10	2.93	0.51	2.8516	2.69	2.86	0.06	2.58	3.15
		0.20	0.16	0.13	0.98	0.18	0.19	0.53	0.1899	0.20	0.19	0.83	0.21	0.17
Treatment	3	1.68	3.12	1.77	1.38	2.55	1.61	2.84	0.9933	0.44	2.12	4.72	3.09	1.92
		0.21	0.05	0.19	0.28	0.09	0.22	0.07	0.4184	0.72	0.13	0.01	0.05	0.16
Irrig:Trt	3	1.21	1.25	0.38	0.95	0.87	0.61	0.20	0.7256	0.38	0.50	2.28	1.12	0.61
		0.33	0.32	0.77	0.44	0.47	0.62	0.89	0.5498	0.77	0.69	0.11	0.37	0.62

Abbreviations: nd = not detected, ns = not significant, df=degrees of freedom.

Table 4.5

Top 10 indicator ESVs classified to Family level for soil amendments. Indicator species analysis produces an overall statistic as a combination of sensitivity and fidelity to the group. Data can vary between 0 and 1. If the sensitivity = 1 then that ESV is only found within that group. If fidelity =1 then every sample within that treatment contains that ESV. All indicator statistics 0.70 or higher are in bold to show which treatments are best predicted.

Full irrigation		Overall Indicator Statistic	Sensitivity				Fidelity			
Family	*Genus*		Control	Biochar	Inoculum	Combined	Control	Biochar	Inoculum	Combined
Burkholderiaceae	Ramlibacter	0.7	0.1	0.1	0.2	0.6	0.1	0.1	0.4	**0.9**
Pirellulaceae	Pirellula	0.7	0.2	0.0	**0.8**	0.0	0.1	0.0	0.6	0.0
Streptosporangiaceae	Nonomuraea	0.7	0.2	0.0	0.6	0.2	0.6	0.1	**0.8**	0.6
Sphingomonadaceae	Sphingomonas	0.7	0.3	0.1	0.5	0.1	**0.7**	0.3	**0.9**	0.3
bacteriap25	(uncultured)	0.7	**1.0**	0.0	0.0	0.0	0.4	0.0	0.0	0.0
Gemmataceae	(uncultured)	0.7	0.0	**1.0**	0.0	0.0	0.0	0.4	0.0	0.0
(uncultured)	(uncultured)	0.7	0.0	0.0	0.0	**1.0**	0.0	0.0	0.0	0.4
(uncultured)	(uncultured)	0.7	0.4	0.1	0.3	0.2	**1.0**	**0.7**	**0.9**	**0.7**
Ilumatobacteraceae	Ilumatobacter	0.6	0.1	0.3	0.5	0.1	0.3	0.6	**0.9**	0.1
Hymenobacteraceae	Adhaeribacter	0.6	**0.7**	0.0	0.1	0.1	0.6	0.0	0.1	0.1
(uncultured Gemmatimonadetes)	(uncultured)	0.6	0.2	0.5	0.3	0.1	0.4	**0.9**	0.5	0.1
Opitutaceae	Opitutus	0.6	0.2	0.5	0.2	0.1	0.3	**0.9**	0.4	0.3
(uncultured)	(uncultured)	0.6	0.0	0.6	0.2	0.3	0.0	**0.7**	0.1	0.3
Dongiaceae	Dongia	0.6	0.1	0.0	0.0	**0.9**	0.1	0.0	0.0	0.4

Limited irrigation		Overall Indicator Statistic	Sensitivity				Fidelity			
Family	*Genus*		Control	Biochar	Inoculum	Combined	Control	Biochar	Inoculum	Combined
Pedosphaeraceae	(uncultured)	0.7	0.0	0.0	**1.0**	0.0	0.0	0.0	0.5	0.0
(uncultured)	(uncultured)	0.7	0.3	0.0	0.0	**0.7**	0.1	0.0	0.0	0.6
Enterobacteriaceae	(uncultured)	0.7	0.1	0.0	0.0	**0.9**	0.1	0.0	0.0	0.5

Hyphomicrobiaceae	Pedomicrobium	0.7	0.1	0.2	0.1	0.6	0.1	0.4	0.1	**0.8**
(uncultured)	(uncultured)	0.7	0.0	0.0	**0.9**	0.1	0.0	0.0	0.5	0.1
Acidimicrobidae	(uncultured)	0.7	0.1	0.2	0.2	0.5	0.4	0.6	0.6	**0.9**
Opitutaceae	Opitutus	0.6	0.1	0.3	0.5	0.1	0.1	0.4	**0.9**	0.4
JG30-KF-CM45	(uncultured)	0.6	0.0	0.1	0.2	**0.7**	0.3	0.3	0.5	0.6
Micromonosporaceae	Actinoplanes	0.6	0.1	0.1	0.2	0.5	0.3	0.4	0.4	**0.8**
(uncultured)	(uncultured)	0.6	0.1	0.2	0.4	0.3	0.5	0.5	**1.0**	**0.8**
Burkholderiaceae	Rhizobacter	0.6	0.0	0.0	0.2	**0.8**	0.0	0.0	0.1	0.5
Sphingobacteriaceae	Pedobacter	0.6	0.4	0.1	0.3	0.3	**1.0**	0.4	0.6	**0.8**
Glycomycetaceae	Glycomyces	0.6	0.2	0.0	0.0	**0.8**	0.1	0.0	0.0	0.5
Azospirillaceae	Skermanella	0.6	0.2	0.1	0.2	0.5	0.4	0.1	0.3	**0.8**

All values are significant indicators at the P <0.10 level after adjusted for false discovery rate.

Table 4.6

Top 10 indicator ESVs classified to Family level for irrigation treatments. Indicator species analysis produces an overall statistic as a combination of sensitivity and fidelity to the group. If the sensitivity = 1 then that ESV is only found within that group. If fidelity =1 then every sample within that treatment contains that ESV. All indicator statistics 0.65 or higher are in bold to show which treatments are best predicted.

Late(R1)		Overall Indicator Statistic[a]	Sensitivity		Fidelity	
Order	*Family*[b]		Full	Limited	Full	Limited
Tepidisphaerales	WD2101 soil group	**0.8**	0.3	**0.7**	0.5	**1.0**
Tepidisphaerales	WD2101 soil group	**0.8**	0.3	**0.7**	**0.8**	**1.0**
SBR1031	(unclassified)	0.8	0.7	0.3	0.9	0.8
(unclassified)	(unclassified)	0.8	0.2	0.8	0.2	0.8
(unclassified)	(unclassified)	0.8	0.6	0.4	1.0	0.8
Blastocatellales	Blastocatellaceae	**0.8**	0.4	0.6	**1.0**	**1.0**
Xanthomonadales	Xanthomonadaceae	**0.8**	0.4	0.6	**0.9**	**1.0**
Cytophagales	Hymenobacteraceae	**0.8**	0.4	0.6	**0.7**	**1.0**
Chthoniobacterales	Chthoniobacteraceae	**0.8**	0.4	0.6	**0.9**	**1.0**
uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	**0.8**	0.4	0.6	**0.9**	**1.0**
(unclassified)	(unclassified)	**0.8**	0.4	0.6	**0.9**	**1.0**
(unclassified)	(unclassified)	**0.8**	0.4	0.6	**1.0**	**1.0**
(unclassified)	(unclassified)	**0.8**	0.4	0.6	**0.9**	**1.0**
uncultured bacterium	uncultured bacterium	**0.8**	0.6	0.4	1.0	**0.8**
Steroidobacterales	Woeseiaceae	**0.8**	0.4	0.6	0.4	**0.9**
(unclassified)	(unclassified)	**0.8**	0.4	0.6	**0.9**	**1.0**
Pirellulales	Pirellulaceae	**0.8**	0.4	0.6	0.6	**0.9**
Nitrospirales	Nitrospiraceae	**0.8**	0.6	0.4	**0.9**	**0.9**

[a] All values are significant indicators at the P <0.10 level after adjusted for false discovery rate.

[b] Taxonomic resolution was insufficient to present data at the Genus level or below.

Table 4.7

Indicator bacteria for soil treatment. Indicator species analysis produces an overall statistic as a combination of sensitivity and fidelity to the group. If the sensitivity = 1 then that ESV is only found within that group. If fidelity =1 then every sample within that treatment contains that ESV. All indicator statistics 0.65 or higher are in bold to show which treatments are best predicted. A dash indicates where taxonomic assignment was not provided.

	Sample Date	Family	Genus	Sensitivity	Fidelity
Control	Early(V4)	bacteriap25	metagenome	**1.0**	0.4
	Early(V4)	Hymenobacteraceae	Adhaeribacter	**0.7**	0.6
	Late(R1)	Hyphomicrobiaceae	Pedomicrobium	**1.0**	0.4
	Late(R1)	Microscillaceae	Ohtaekwangia	**1.0**	0.4
	Late(R1)	Pirellulaceae	Pirellula	**0.9**	0.4
	Late(R1)	Opitutaceae	Opitutus	**0.7**	0.5
Biochar	Early(V4)	Gemmataceae	uncultured	**1.0**	0.4
	Early(V4)	Micromonosporaceae	uncultured	**0.8**	0.3
	Early(V4)	Xanthobacteraceae	Pseudolabrys	**0.8**	0.3
	Early(V4)	WD2101 soil group	uncultured planctomycete	**0.7**	0.3
	Early(V4)	WD2101 soil group	uncultured bacterium	**0.7**	0.6
	Late(R1)	Steroidobacteraceae	Steroidobacter	**0.8**	0.4
	Late(R1)	Chthoniobacteraceae	Chthoniobacter	**0.7**	0.4
	Late(R1)	Fibrobacteraceae	possible genus 04	**0.7**	0.4
Inoculum	Early(V4)	Xanthomonadaceae	Stenotrophomonas	**0.8**	0.4
	Early(V4)	Pirellulaceae	Pirellula	**0.8**	0.6
	Early(V4)	Gemmataceae	Gemmata	**0.7**	0.5
	Late(R1)	Pedosphaeraceae	uncultured soil bacterium	**1.0**	0.5
	Late(R1)	uncultured bacterium	uncultured bacterium	**0.9**	0.5
	Late(R1)	Longimicrobiaceae	uncultured bacterium	**0.8**	0.4
	Late(R1)	Rhizobiaceae	Mesorhizobium	**0.8**	0.4
	Late(R1)	-	-	**0.8**	0.4
	Late(R1)	Haliangiaceae	Haliangium	**0.7**	0.5
	Late(R1)	uncultured	uncultured bacterium	**0.7**	0.4
Combined	Early(V4)	uncultured bacterium	uncultured bacterium	**1.0**	0.4
	Early(V4)	Dongiaceae	Dongia	**0.9**	0.4
	Early(V4)	Micromonosporaceae	Actinoplanes	**0.8**	0.4
	Early(V4)	WD2101 soil group	uncultured planctomycete	**0.8**	0.4
	Early(V4)	Gemmataceae	uncultured	**0.8**	0.4

Early(V4)	-	-	**0.8**	0.3
Early(V4)	Haliangiaceae	Haliangium	**0.7**	0.4
Early(V4)	-	-	**0.7**	0.4
Early(V4)	Micromonosporaceae	Actinoplanes	**0.7**	0.4
Late(R1)	JG30-KF-CM45	uncultured bacterium	**1.0**	0.4
Late(R1)	Enterobacteriaceae	-	**0.9**	0.5
Late(R1)	Burkholderiaceae	Rhizobacter	**0.8**	0.5
Late(R1)	Unknown Family	Acidibacter	**0.8**	0.4
Late(R1)	Glycomycetaceae	Glycomyces	**0.8**	0.5
Late(R1)	uncultured bacterium	uncultured bacterium	**0.7**	0.6
Late(R1)	Chthoniobacteraceae	Chthoniobacter	**0.7**	0.5
Late(R1)	JG30-KF-CM45	-	**0.7**	0.6

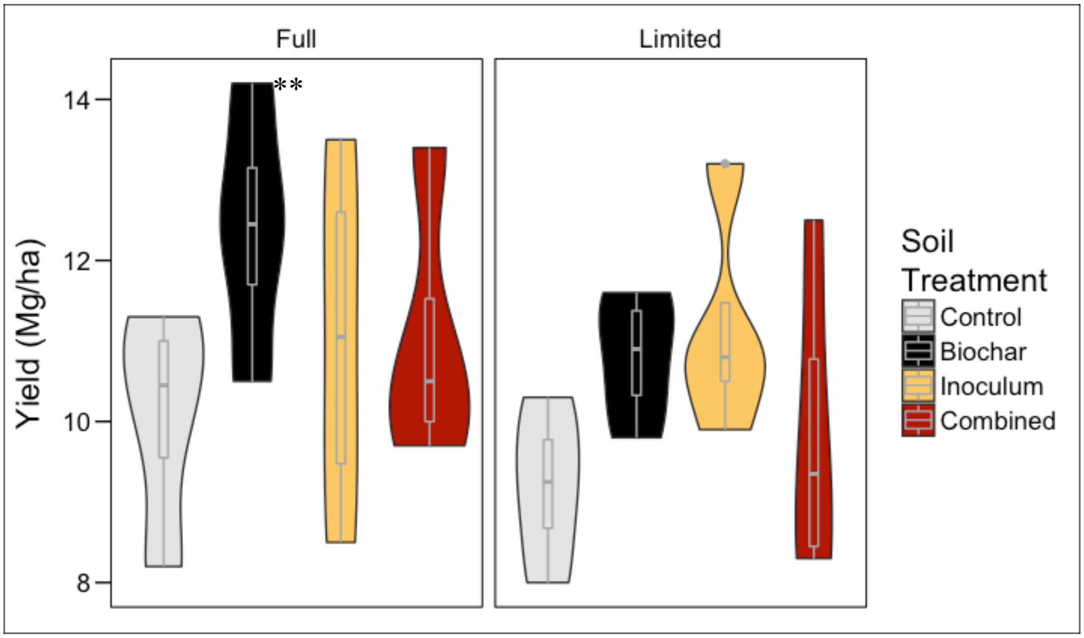

Figure 4.1. Violin distribution plots with boxplots of the 25, 50 and 75th quartile to represent maize yield (Mg ha^{-1}) with the control, amended with biochar, plant growth promoting inoculum, and a combination treatment, under full (left panel) and limited (right panel) irrigation. Data are means ± 1SE, each with 4 replicates and the double asterisks represent significant differences at $P<0.05$.

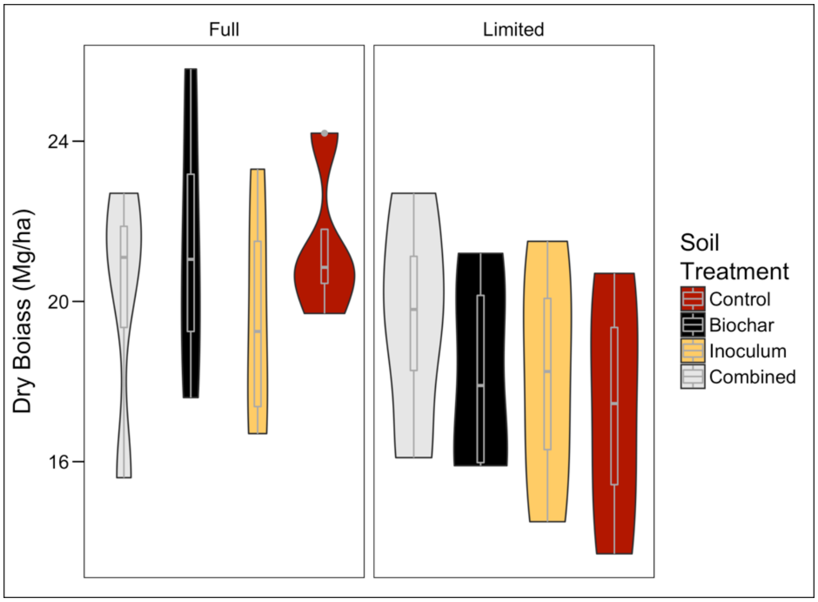

Figure 4.2. Maize dry biomass (Mg ha^{-1}) response in control plots without amendment, biochar, plant growth promoting inoculum, and a combination of the two treatments, under full (left panel) and limited (right panel) irrigation. Data are means ± 1SE.

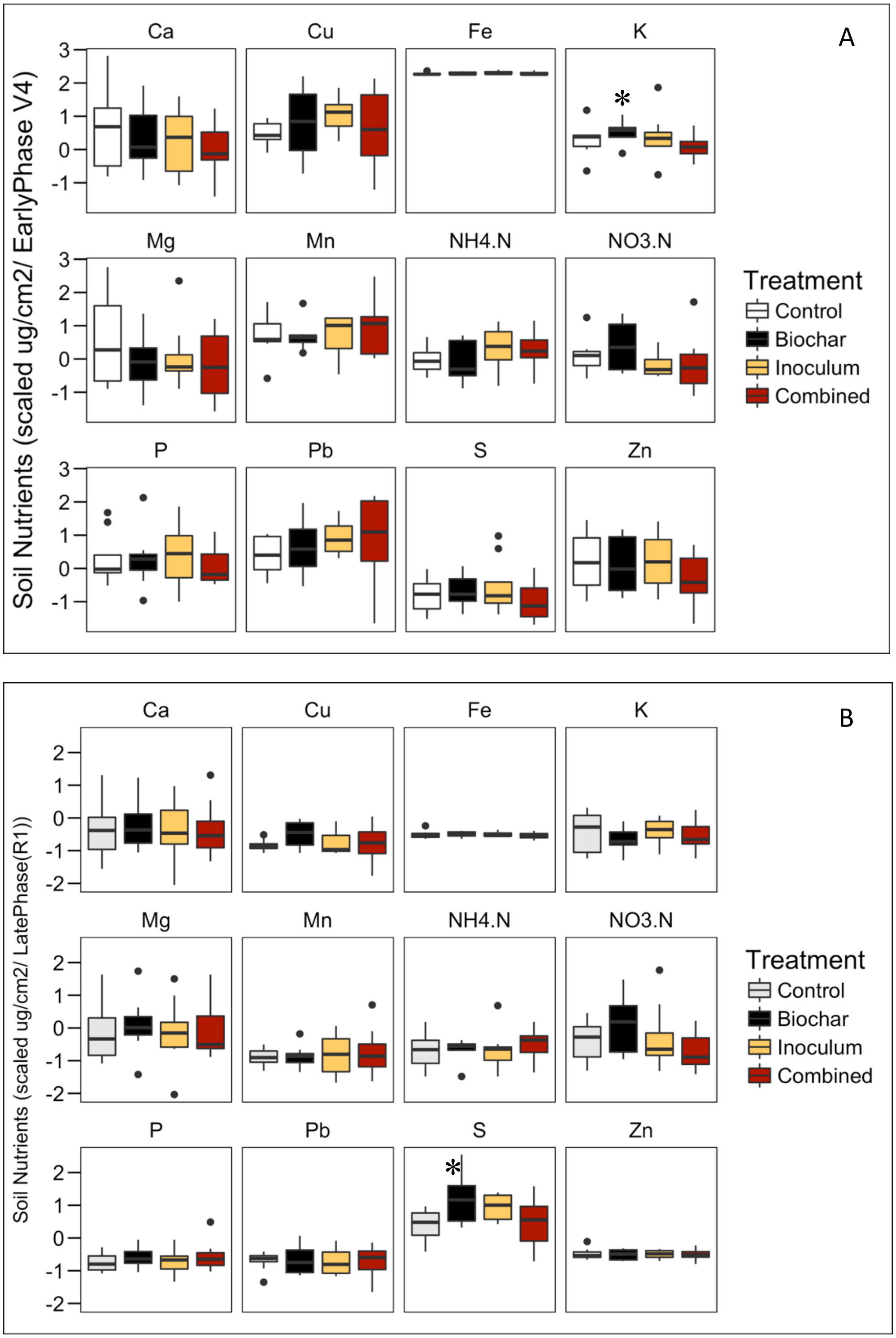

Figure 4.3A and B. Response of soil nutrient supply to soil amendment (control, biochar, inoculum, and a combination) during the early maize growth phase (V1-V4) (A) and during the late maize growth phase (V15-R1, B). Asterisks indicate statistical significance at P<0.10. Each set of nutrient data are scaled around their own mean and data are presented as means averaged across irrigation level (n=8).

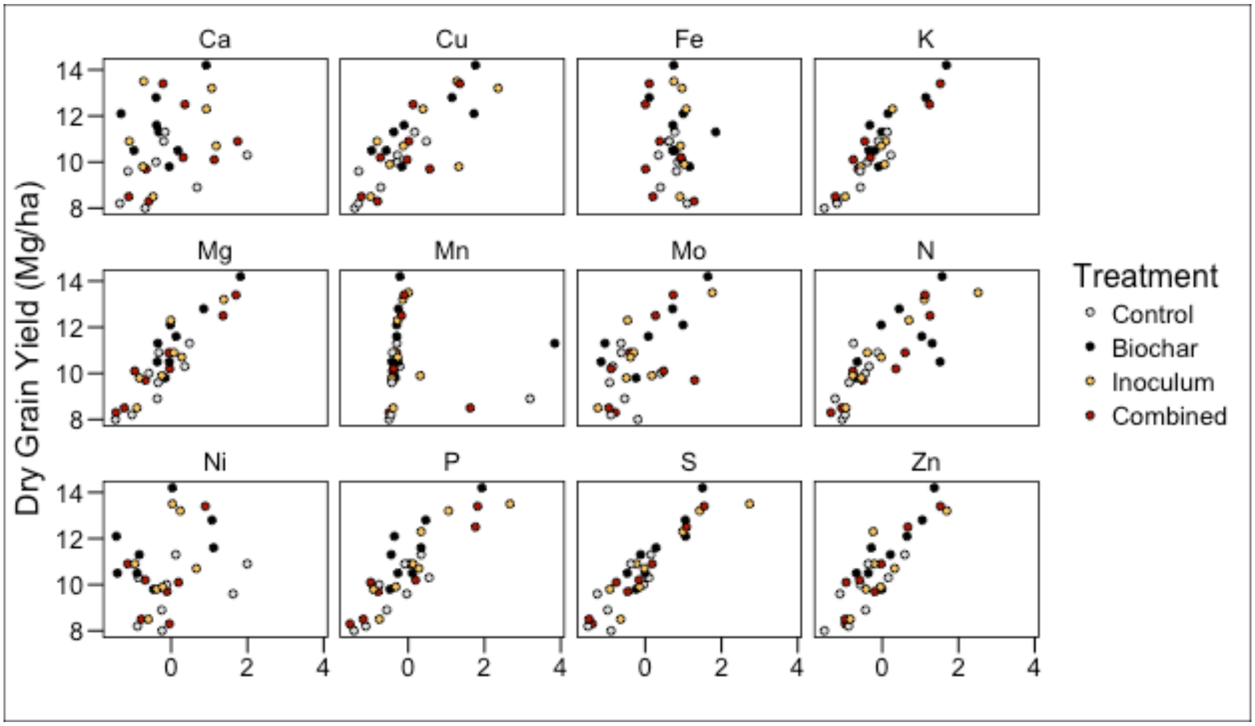

Figure 4.4. Maize dry grain yield (Mg ha^{-1}) correlated to specific grain nutrient content collected at harvest under each of the four soil treatments (control, biochar, inoculum, and a combined treatment). Each set of nutrient data are scaled around their own mean and data are presented as means averaged over irrigation treatment (n=8).

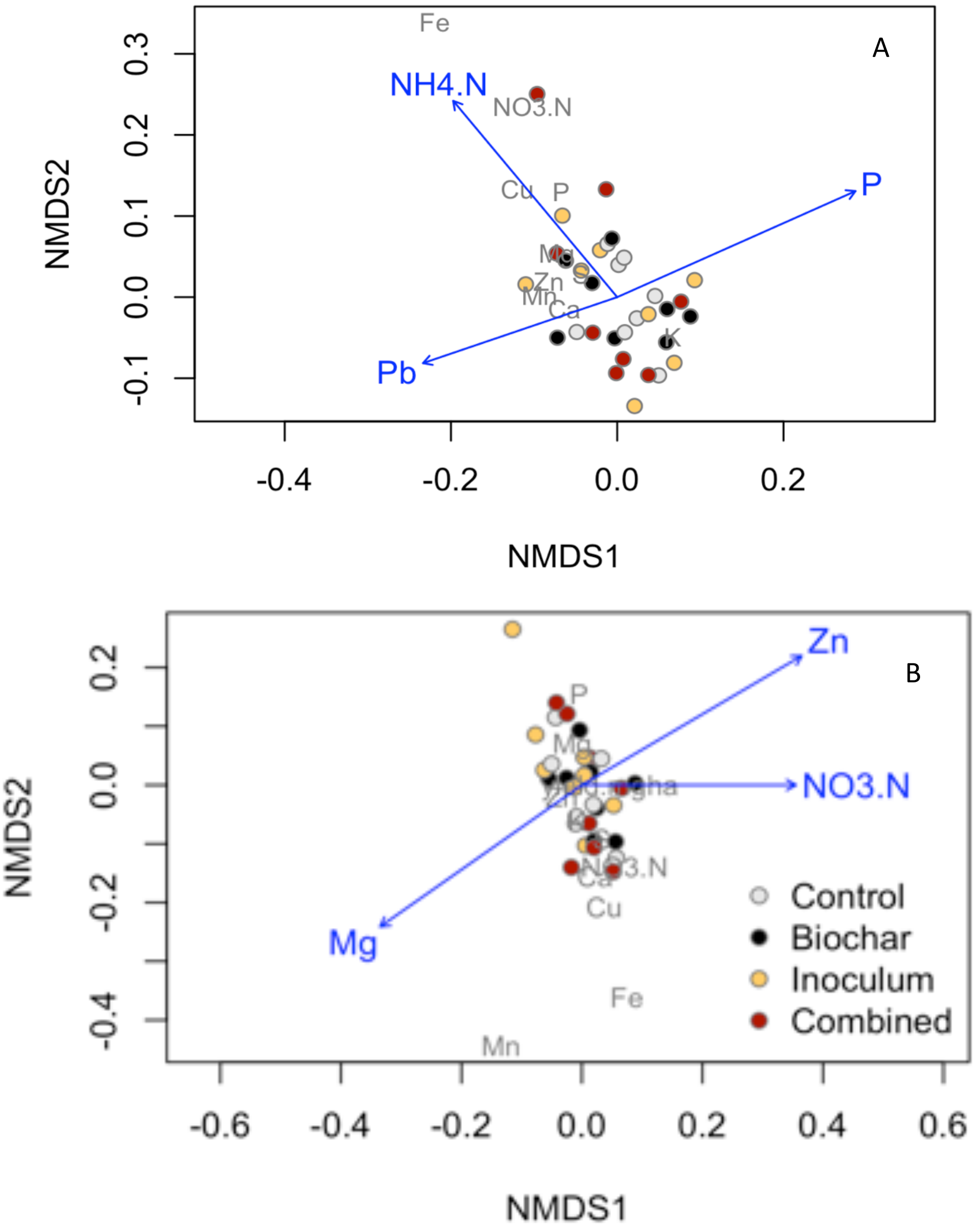

Figure 4.5A and B. The non-metric multidimensional scaling ordinations represent the crop nutrient concentration at the two sampling periods. The colored circles represent the crop nutrient concentration, the gray text represents mean crop nutrient content, and the blue vectors represent the significantly correlated soil nutrients ($p<0.10$). Plotted leaf nutrient content (mg g^{-1}) and correlated soil nutrient supply during the early sampling period, maize growth stage (V1-V4) (A) and plotted grain nutrient concentration (kg ha^{-1}) and correlated soil nutrient supply during the late sampling period, maize growth stage (V15-R1) (B). Stress for both NMDS plots was reduced by using two axis to <0.10.

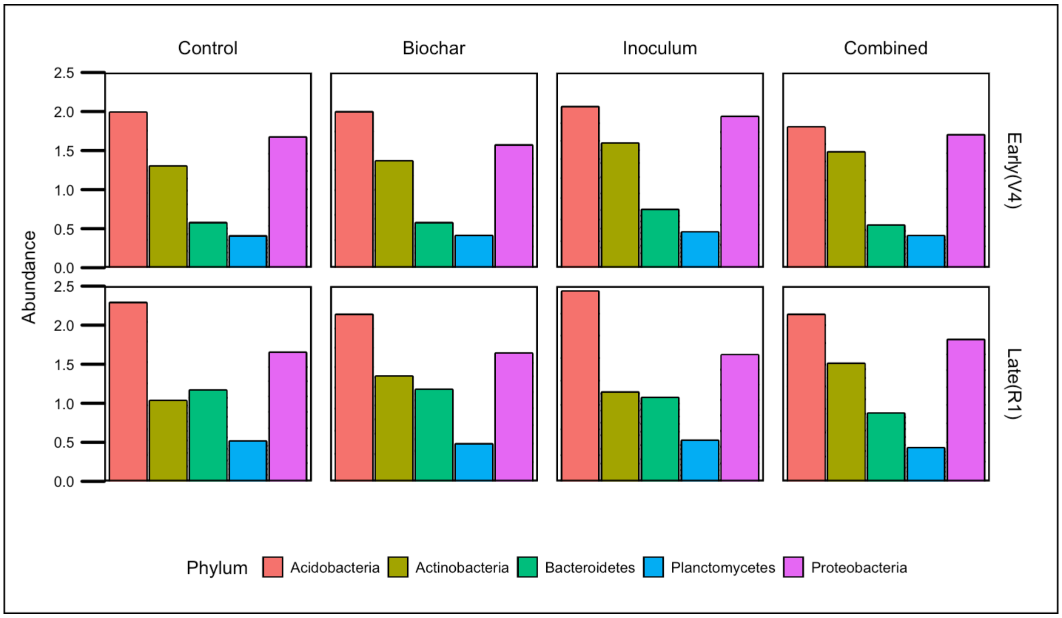

Figure 4.6. Relative abundances of the five most abundant phyla between the early (V4) and late (R1) sampling period for each soil amendments: control, biochar, inoculum, and combination treatment.

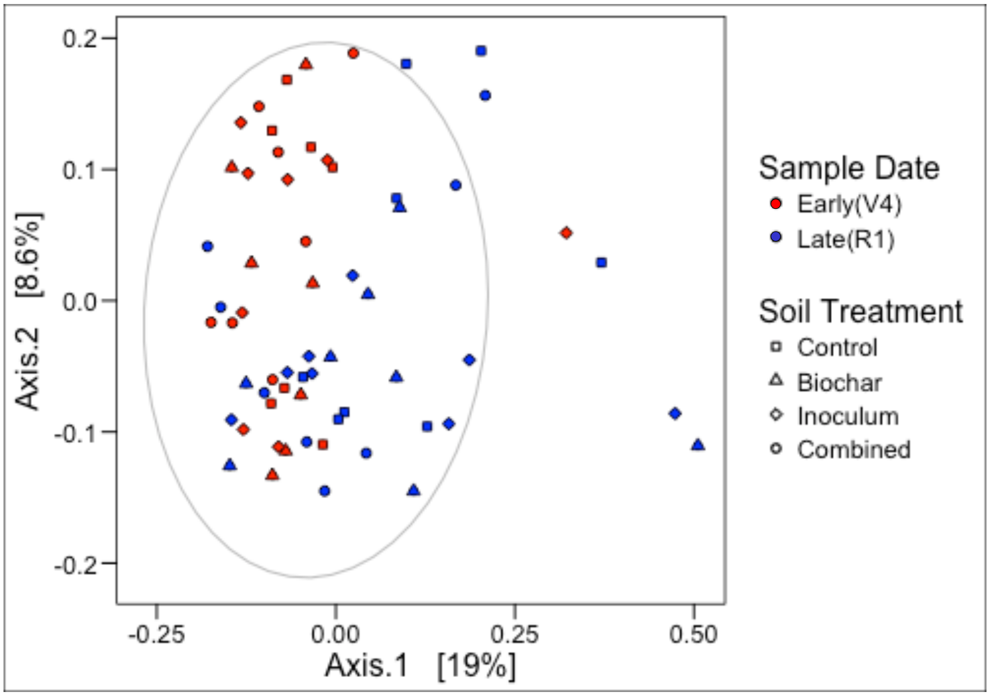

Figure 4.7. The unconstrained principle coordinate analysis of bacterial community composition based on Bray-Curtis distance of ESV relative abundance with soil treatment as shape and Sample Date early(V4) filled in red and Late(R1) in blue. The gray ellipse encircles communities at 90% confidence level of the mean. The first axis explained 19% of the variance between samples.

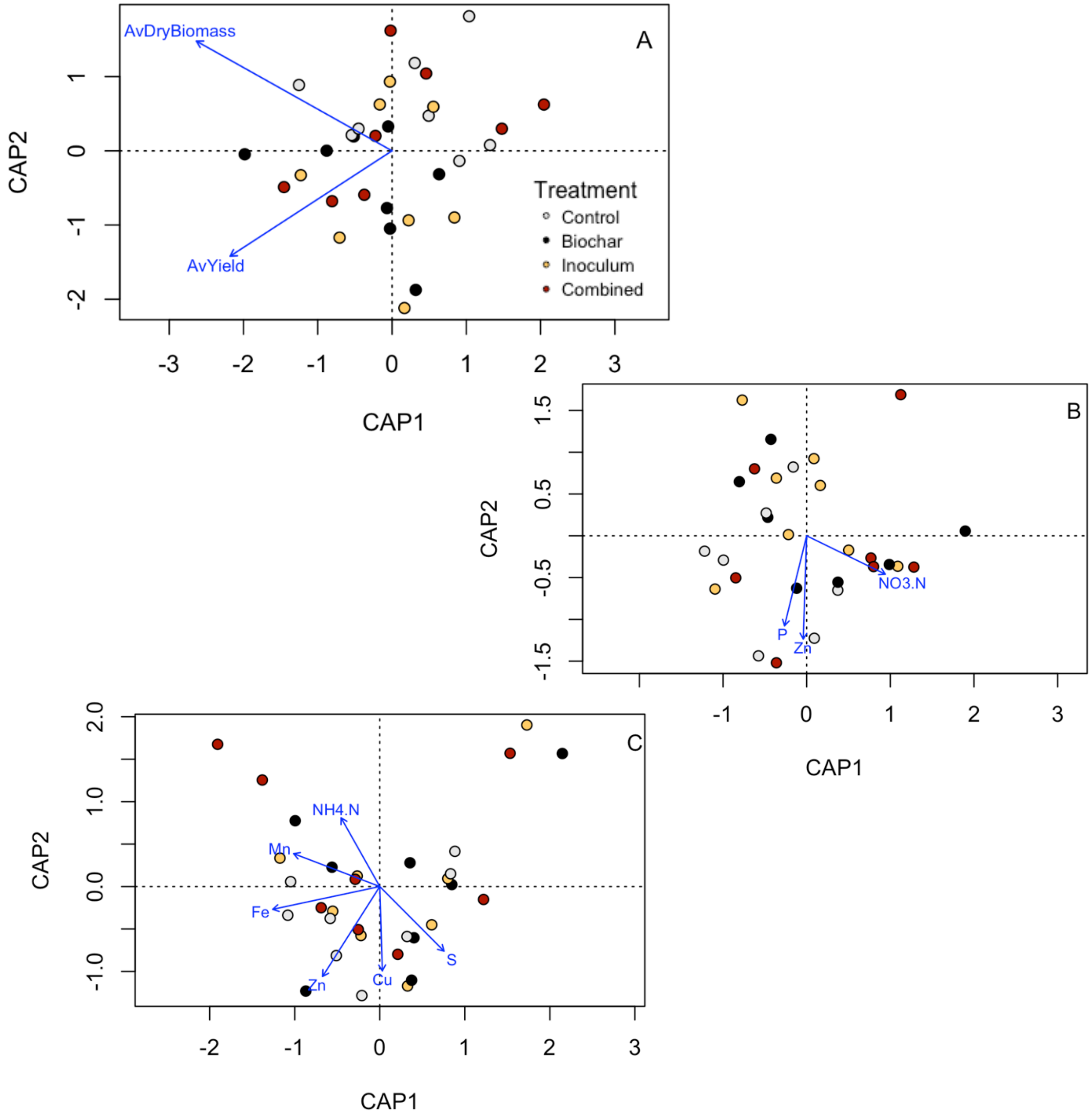

Figure 4.8A, B, and C. Canonical analysis of principle coordinates (CAP) of bacterial communities based on relative abundance of ESVs. The ordination maximizes differences between sampled communities relative to the soil nutrient data represented as blue vectors of correlation ($P<0.10$). For the whole crop response, the average dry biomass correlated the strongest with the bacterial community structure (A). Community structure correlated with soil Zn, P, and NO_3^- supply at the first sampling date (B) and with soil supply of Zn, Fe, S, Mn, Cu and NH_4^+ at the second sampling date (C). For each ordination the constrained axis explain the following proportion of inertia: 0.06 for crop yield response (A), 0.42 by soil nutrients at the early sampling point (B), and 0.37 by soil nutrients at the late sampling point (C).

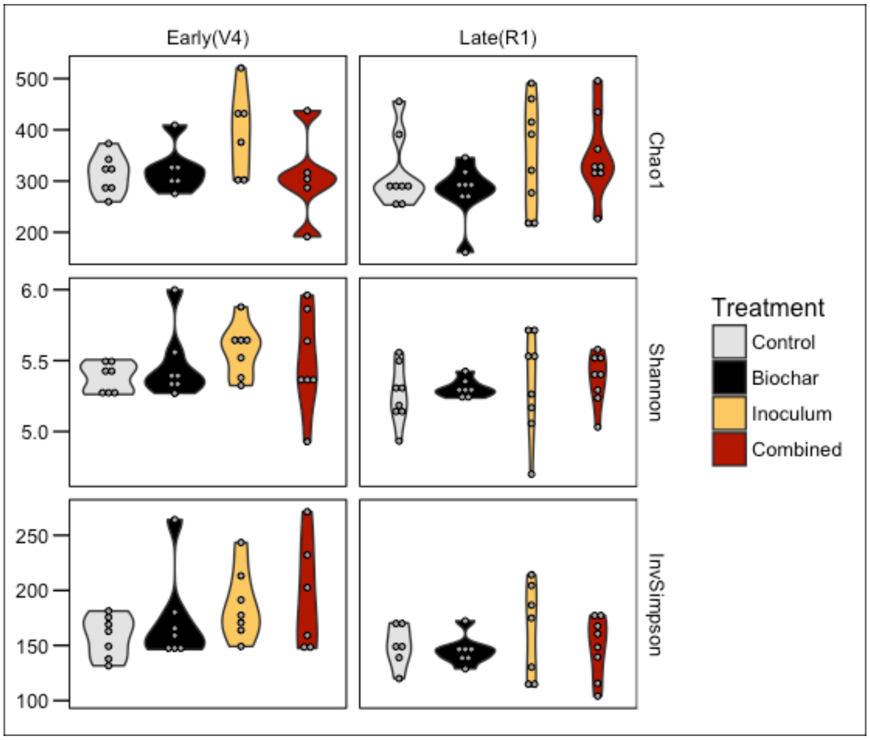

Figure 4.9. Normalized diversity metrics split by sample date include Chao1 richness, Inverse Simpson Index for evenness and a combined Shannon Index. The community diversity was higher at the early sampling date than later in the season (P =0.05). Within the violin distribution plots the gray dots represent individual samples.

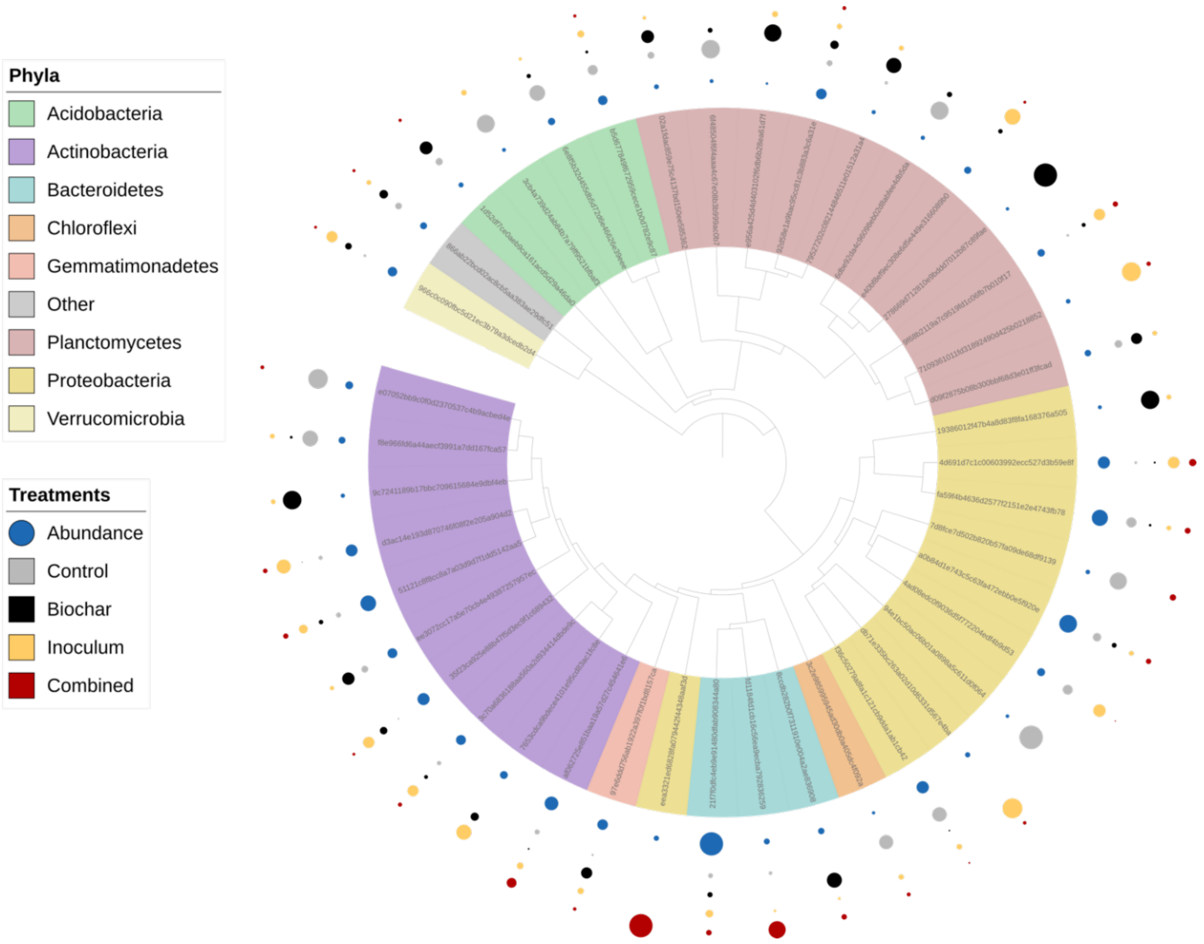

Figure 10A. The phylogenetic tree shows the 39 features that significantly associated with specific soil treatment group at the first sampling date (FDR adjusted p<0.10). Range colors highlight the unique feature names and represented the top ten most abundant phyla. The diameter of the small blue innermost circles represents the overall square root transformed abundance data. The outer layers of circles represent the specificity of that feature to a particular soil treatment, with the largest circles indicating the feature is only found in that treatment (i.e., A-statistic from the indicator species analysis). Find the full interactive tree accessible at https://itol.embl.de/tree/751662371154122215282167746.

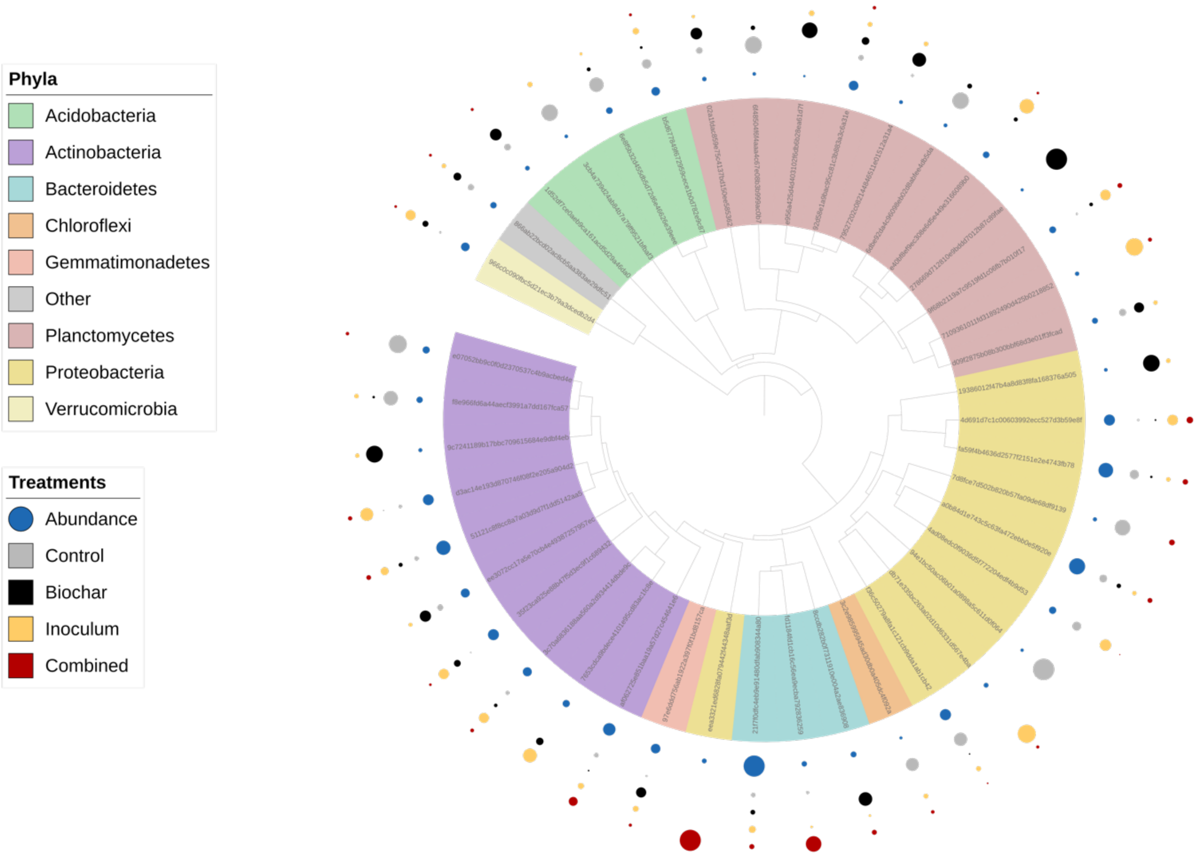

Figure 10B. The phylogenetic tree shows the 51 features that significantly associated with specific soil treatment group at the second sampling date (FDR adjusted p<0.10). Range colors highlight the unique feature names and represented the top ten most abundant phyla. The diameter of the small blue innermost circles represents the overall square root transformed abundance data. The outer layers of circles represent the specificity of that feature to a particular soil treatment, with the largest circles indicating the feature is only found in that treatment (i.e., A-statistic from the indicator species analysis). Find the full interactive tree accessible at https://itol.embl.de/tree/75166237115413961528216796.

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Chapter 5: Summary and Conclusions

This dissertation research aims to improve understanding of innovative agricultural management strategies in a semi-arid temperate maize production. The main three questions were:

1. How do manure and biochar amendments impact soil moisture and microbial nutrient cycling for limited irrigation maize?
2. Do microbial extracellular enzymes adsorb to soil mineral and biochar surfaces and impact nutrient cycling activity?
3. Can precision biochar application and plant growth promoting bacterial inoculum improve crop available nutrients and yield under limited irrigation?

The first agricultural field experiment found that within the limited irrigation maize system the impacts of 30 Mg ha^{-1} of steer manure and pine biochar differed. The manure addition increased gravimetric soil moisture by approximately 15%, total nitrogen by 10%, available phosphorus by 45%, and microbial biomass carbon by 15%. Relative to the control, biochar increased total soil carbon from 1.49% to 2.67% and altered microbial extracellular enzymatic activities. Biochar significantly increased α-1,4- glucosidase, β-D-cellobiohydrolase, and b-1,4-N-acetylglucosaminidase and significantly decreased β-1,4-glucosidase and phosphatase activities. Despite the effects on soil moisture, nutrient availability, and microbial dynamics, neither amendment significantly impacted maize yield under limited irrigation. The timing of the limited irrigation during maize non-critical growth phases maintained yield while reducing total water input by 30% approximately. We continued monitoring the yields for two additional years with no detected effects. Additionally, data of soil respiration and C stocks collected during this study will allow further assessment of the C sequestration potential of the biochar in this agroecosystem.

The near 40% reduction of microbial extracellular enzyme activities in the biochar field trial led to a laboratory investigation to uncover the mechanistic cause. The novel combination of Bradford protein assay with the fluorometric potential enzyme activity measurement at three pH levels clarified the root cause of the field results. Both extracellular β-glucosidase and acid phosphatase sorbed to pine biochar more than the lower-surface area grass biochar or soil. When immobilized on the pine biochar, both enzymes lost 75-100% of their activity relative to soil. The amount of enzyme activity responded to the interaction of solid surfaces, enzymes, and pH. This unique examination of activity of enzymes adsorbed directly to the solid phases revealed the surface type influences enzyme activity levels significantly. The results from this laboratory experiment reveal potential negative impacts of high surface area pine biochar on microbial function in soils and underline the importance of selecting a biochar type to meet specific management goals.

The final field experiment focused on agronomic impact of innovative management strategies: (1) precision application of engineered biochar with removed toxins and neutralized pH, (2) plant growth promoting phosphorus solubilizing bacterial inoculum, and (3) a combination treatment of pre-mixed biochar and inoculum. The coconut hull biochar banded directly on the seed row increased maize yield by 20% (1.95 Mg ha^{-1} over the control). In the early phenology stage (maize V1-V4) the biochar increased soil available K and in the later phenology stage (V15-R1) the biochar enhanced soil S availability. The change in soil nutrient dynamics increased grain accumulation of S, K and N with biochar addition. The overall maize biomass significantly correlated with bacterial community structure based on relative abundance data, as well as early soil supply of NO_3^- , P, and Zn and later supply of Cu, Fe, Mn, NH_4^+ and Zn. Although bacterial community structure overlapped substantially between treatments at the phyla level over time, specific patterns emerged in the early season when diversity was higher. The bacterial community was distinct under the biochar plots at this early sampling stage. Two indicator families detected corroborated previous research. The biochar treatment enhanced the family Micromonosporaceae, an Actinobacteria that exists in soils high in pyrogenic organic matter and Xanthobacteraceae family, part of the gram negative phyla Alphaproteobacteria. More detailed taxonomic resolution would further improve understanding of exact bacterial response to the interaction of soil and irrigation treatments. Furthermore, the inoculum treatment plots contained indicator sequence variants that fell within the same families as three of the four added strains. The novel use of exact sequence variants will aid future comparisons with future biochar and bacterial inoculation treatments, as well as contribute to a database of agricultural soil bacterial communities.

From the increased yield with targeted biochar application to the initial lack of effect pine wood biochar, this dissertation work emphasis the importance of field testing management strategies prior to on-farm application. Overall, the initial research demonstrates that biochar in Colorado can be sustainably sourced from bio-energy production and applied at high rates (30 Mg ha^{-1}) to sequester carbon in soils, without impact on yield. Alternatively, a targeted engineered biochar at low application rate (0.8mg ha^{-1}) can enhance crop yield. In terms of soil moisture, the gravimetric water content responded to manure treatment, but was not changed by the biochar amendment. Thus, in this research the main finding in regards to water management was that the well-timed limited irrigation can save a potential 20-30% of inputs. Finally the impact of the synergistic management strategies on bacterial nutrient cycling proved slightly negative with the original high application of pine biochar, due to sorption and reduced enzyme activity levels. The precision application of biochar and the inoculation with plant growth promoting bacteria both impacted bacterial community structure. The nuanced shifts in bacterial abundance require further study as research techniques continue to improve taxonomic resolution with exact sequence variants. Ultimately, just as the engineered biochar increased yield, with a more thorough understanding we can better engineer the soil bacterial community to target specific nutrient deficiencies.

Though agriculture today deals with many challenges, from balancing fertilizer use to soil degradation and climate change, opportunities for innovation exist. Collaborations between producers and research scientists can help to develop novel combinations of management strategies, such as biochar and plant growth promoting inoculum, to combat increased climate variably and competition for resources. This dissertation work proved that precision application of organic amendments serves as one potential solution to increase crop production. Management to enhance natural soil function can improve overall agroecosystem resilience and thus contribute to sustainable food production for the next 10,000 years.

APPENDIX

Appendix Table 1. Full taxonomy used from the SILVA 132 database within the kingdom Bacteria.

Feature ID	Phylum	Class	Order	Family	Genus	Confidence
d3f2aea09981b98b72e0984fd1d6540a	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.7925661
b019dd54338af8e51cf0d4cc28ded009	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.8526542
4e6003080077f3031e5398e343a20ae5	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.9974077
010ed69a887509acff94fcecd37c1565	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.9346029
649b3bbaf1fb5465dbe63b078ec6d3bf	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.997717
8a99025ba9415f84c3820348289ab75a	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Bryobacter	0.7873925
81b35651e52e52afd1c4ddfef00ed25a	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	PAUC26f	0.8562711
2b6b4549dca255b65da9aa45f3467946	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)		0.9730599
c3f59a1145be898d24b79fea24eaf820	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.7815388
0ef77bca16ca614be877aede3a634e5d	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9950023
3d52b03a4df244e7eac3ae64a6701e9f	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.7376993
09da4f1df5bb13e946e337696e75d977	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.905096
bc4c2b412618043fd32e27510a9ff13d	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.8760909
1d52df7ce0aeb9ca161acd5d29a46da0	Acidobacteria	Blastocatellia (Subgroup 4)		uncultured bacterium	uncultured bacterium	0.9762072
92c057f20ce3435b6d2938b220f0a86c	Acidobacteria	Blastocatellia (Subgroup 4)				0.999577
282fe7a7bd73a793a15f7e91cf030c88	Acidobacteria	Blastocatellia (Subgroup 4)				0.9300705
252aed3f9ad1326b046530350ce7a57b	Acidobacteria	Blastocatellia (Subgroup 4)				0.9607723
c5393883769a92dfa968f92563056e67	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	Blastocatella	0.8973462
911466f1c263e3f87a3b1971abf37948	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	Blastocatella	0.7418063

31bcf0a5168e76f7e320deb6bca05160	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	JGI 0001001-H03	0.9935568
02ed94d6e388e96c866405253c03dbc0	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	JGI 0001001-H03	0.9580687
3959a8dd2e3dbc39d169701e96311a4b	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	JGI 0001001-H03	0.9880471
eeaa37807c2ecde843731ca84f9903ed	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	JGI 0001001-H03	0.9854735
6ba46f2b5eac60cd35b997c34e5e1c6a	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	Stenotrophobacter	0.9758483
1c778519615057ad2f4a74d2b8457e97	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	Stenotrophobacter	0.99996
967770bc0be01782473e51be4bac4f89	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	Stenotrophobacter	0.9952678
6e4b50a611f333bfb12f3b9a4a9e8b61	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	uncultured	0.7038317
a652f496fb4f9105e6797d717c3926ef	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	uncultured	0.8927725
f533223aef7e44b298e0c71c3ffe701a	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	uncultured	0.9110395
28c9c933ef4fab3f4a31cd36416e8076	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae		0.9999976
c3de58fb570aa28d17bbfa1fb0243ff7	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae		0.9980893
a979501da8eb307fa5b86d85b8dabeee	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae		0.7862371
d8aaf978faeead23947095ec9702766d	Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae		0.9452362
c5f51cecc5146aa8e957ae7bfa3ab4d0	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.9582465
70dfcfbe632c4105839468849de6ef43	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.9173162
8127d981c6c481dd366aeb22119b97d1	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.9957257
4a7774dd046ef6de936621dd22271853	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.7428016
7e8cecd0ced894666039f5946836f2e4	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.9012971
2972b25f4f00ee57c72460049798ce5b	Acidobacteria	Blastocatellia (Subgroup 4)	DS-100	uncultured bacterium	uncultured bacterium	0.9388632
a1c4acc3169c2a95cf474a3645129d84	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.9986755
fca9ec5a6137cbf682d325c17876fb91	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.9763429
ce88479c67c424bd1b2d977d099ce325	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.7199871
73f9f40df58f53080587b3e3d73c6161	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.9994222
7b8fe6ced40068312b04832e57b94127	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.7780765
8562afaf3955423d4eda6d71b8b277d8	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	RB41	0.7382592
ed1922e5f77ee53f2ffcd590127f5f7a	Acidobacteria	Holophagae	Subgroup 7	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9999798
46b5ffa8ac0cd64106d7ecff522d1ffb	Acidobacteria	Holophagae	Subgroup 7	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.7877279

eabf84bad40d7eaacc2879c06d774598	Acidobacteria	Holophagae	Subgroup 7	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.7317737
3a72502b1bd13796dae57ff709b6ec4c	Acidobacteria	Holophagae	Subgroup 7			0.7973218
c3297668cf75ea8e774d6d9c0044cce4	Acidobacteria	Holophagae	Subgroup 7			0.7636081
c053f620077233b99b2c48075570f502	Acidobacteria	Holophagae	Subgroup 7			0.7484059
33b59ac7bf646a8a5b1129313c3cd6bc	Acidobacteria	Subgroup 11	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9252955
8aba8f68fb7a619a78035af90e29e396	Acidobacteria	Subgroup 15	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8891308
ea9453005f6b270b103f51a22ac0d0fa	Acidobacteria	Subgroup 15	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7659946
6d9c381768fd23ed621fb57c2abe51df	Acidobacteria	Subgroup 17	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9613444
d20aa3e15bf7b84b126878151a165c26	Acidobacteria	Subgroup 17	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9976844
960bd812e62ae6ff3baeee8ee7b1d194	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8092996
e35e160d3a00029666805f1782bf78ef	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9177064
28b19f2a1434a769e707c452a927926d	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999981
ebe28f5e64362aa9e064dd814ccecad3	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9845941
c345d9a034d3e3447e9659cab8a894e2	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999909
c8dab75b28b4a7e2708ec377483ecaaa	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.995568
dad55ea92d7fa141339fe68b62b04507	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8185662
8f6f4f44b539779ccadc00fd7f2c915c	Acidobacteria	Subgroup 17	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9960594
a7fc94f824b7bf5d8c7d28c0125c4e32	Acidobacteria	Subgroup 17				0.7381151
7b32f308dddb1b981af50da2c6e9aad9	Acidobacteria	Subgroup 17				0.9767407
8c558f99be44284ff308e0c8482b3af8	Acidobacteria	Subgroup 17				0.9766139
e094f1afaffee759ffd73c7ca25894ef	Acidobacteria	Subgroup 17				0.9253355
8c1079e83b69d1ca9de859c02f434a59	Acidobacteria	Subgroup 17				0.8674959
8821169f36e7de426c7a394328c4a1e2	Acidobacteria	Subgroup 17				0.99567
723d1eb62e2964c5852bf76f334408b6	Acidobacteria	Subgroup 17				0.8215702
6e2528f0f8a064171b2dbcf7e3ec73c0	Acidobacteria	Subgroup 17				0.9390386
34558e4ec1fa54c99645496195250f39	Acidobacteria	Subgroup 17				0.9999997
a3eec1066dc4d8e5c4ddfae5d2c4f9f8	Acidobacteria	Subgroup 17				0.958351
e0af83680ad03f5754696ac0a448923a	Acidobacteria	Subgroup 18	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9987002

dc3335ef3308ec570f453e4c01a22f2c	Acidobacteria	Subgroup 18	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9997772
bffeaa586bc2c11fd77bf419fbc251cb	Acidobacteria	Subgroup 22	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.8376766
3354bf218f9726426cef7d96fd6283ec	Acidobacteria	Subgroup 22	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.7407198
537dd53b6b8901bc53f10701ae63eb40	Acidobacteria	Subgroup 22	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9809476
a3e23d862a438f3870e78e70e99cbc8a	Acidobacteria	Subgroup 22	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9993786
26d8a245ef623724b10b526c4be0c2b4	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9864501
ee99bfd4ce5fb75c24bf950c16833e5c	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8012654
6f9a3638466ea6271482b01ce9cee3b2	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7872939
b0b4d96cab1748ef14f54433acbbc6a4	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8617418
19ae9738a33b9cd82c8e72b8d463bf0c	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7719623
f7fbcf1b1390828a76f5c40706f0effc	Acidobacteria	Subgroup 5	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9377727
a403a39a51ab44068caa2952fda38fc0	Acidobacteria	Subgroup 5	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.772605
a2b6fe674885d9dbadb38feee1c6d498	Acidobacteria	Subgroup 5	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7045582
b0c140b2ef121daf508fa768cc7dfa8a	Acidobacteria	Subgroup 5				0.9101605
63d2c053b5e264fd04ba0d89aba4592f	Acidobacteria	Subgroup 5				0.8032738
5068164620f2bde1b65b7765974c2bc6	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.92316
806da84a4d3359c4137830fbb8a2cf63	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9976666
06b39700f929d7f221346ca8d940d5be	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.7526278
b869c3c4a8ce0f77fd8f4ce7ccfd39af	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.8400569
97d51c3d68756e0b4353c777605c334a	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9999999
2a19a73c06d11bf6d14d021db39165ea	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.7534895
1a175ac0e06047cb76acf95378454a16	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9987612
728cf78e39c0015d6156afa47e6c4c6e	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.8964228
646cbd530199bee6857c2df9e367e889	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9981712
fd42a17506638640cdee202bbd963ff5	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9009928
f6ed1d8ae29604f751f8e54517eae730	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9222476
28caf857680612f98aecbbdca159745b	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.7494411

b34562cde151650da12aadc4b000e2f5	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.8272579
8ddd0dd07f1cb76bb98500c89075aa46	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9999994
7b7cb3581bcc51e85757bfe0cf4312e7	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.7484318
a7d793e4c9028da01a24b4e2db4136fc	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9516056
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86eca251a79873cec5eafc313b8141a9	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9975053
00d836649b55e0910427a3c99fb14733	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.9048624
7b7850a58a9360a60fd5cf319dbe7345	Acidobacteria	Subgroup 6	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9993306
b5d677849f672959cece1b0d782e9c87	Acidobacteria	Subgroup 6	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.90244
14a312c5939f1228036ad4e4c9b0157a	Acidobacteria	Subgroup 6	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.9999978
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6bd27c79f2f053d5c5f10f9d3fe0f7a9	Acidobacteria	Subgroup 6	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7049774
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d58b6cf2e9af6364330b92566e14d59e	Acidobacteria	Subgroup 6	Unknown Order	Unknown Family	Vicinamibacter	0.9919327
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81bc68b1f5ea92f5440ffab967438731	Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup 10	0.9999981

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fdfb7628622d1f8ff6e4745a5b171546	Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup 10	0.7097154
6b1489a8f98603ee677b7574ce95a8d5	Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup 10	0.725301
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c7535fa9a8bf3d56365ed4371896fc95	Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured bacterium	0.7665371
6f3ce5d1ced34ce17da79a51daf74eed	Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured bacterium	0.8510172
5f8946c3a3b4e3e1a4d031fa42510b79	Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured bacterium	0.8143008
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785e509770a3aa447fcaa0082d460264	Actinobacteria	Acidimicrobiia	IMCC26256	uncultured bacterium	uncultured bacterium	0.999485
c5403152134075e71a9bda661e0a65c6	Actinobacteria	Acidimicrobiia	IMCC26256	uncultured bacterium	uncultured bacterium	0.9616417
f963be2062b9a088c922feb4752b2de6	Actinobacteria	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	0.999943
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385b4f8ae56646e8b9c1a0f2abd56ad2	Actinobacteria	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	0.7905442
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2f08f91319b71ff9612b3d665567644f	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	CL500-29 marine group	0.854694
3a54d4e72af90b9c2fd50d7d1bb0336b	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter	0.8134935
35f23ca925e88b47f5d3ec9f1c689432	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter	0.9754072
9b38d78a8db30446a4fcdc108248eaf7	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	0.9888381
1d73584d033a3152817257e607bca19b	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	0.8957661
cc2d00709262a1ad0b9dab66b6d8654f	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	0.9518199
63fc2de8bb0a8c04e30d1c3afa4607c8	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured Acidimicrobidae bacterium	0.7696065
3b380172b2b9a7af73dcd749b6a0c33c	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured Acidimicrobidae bacterium	0.8330059
d28f578c180b1577c171f9614d6bf0fc	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured Acidimicrobidae bacterium	0.7352661
c7826f9e0cd6d8efc2c0f5833d4dd737	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured Actinomycetales bacterium	0.8923887
f03c1ff4c0f4f52f62810ed5ccf71fe1	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.7403964
16a2d9fb115749315f15eb595cb4b6d7	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.7097944
247ff633f12db0f1f827d33325f659ce	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.9039878
a09932e806ffb93969d9dcadb46b1a19	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.8198539
486337399ee28cfce1cd938314ee2c94	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.9550541
be7bdef3dcbb3b87c9ef34b4a5d77967	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.7169484
3e828479f7bb382a569b12c2830e44ce	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.9722022
529023a93455f29894d3c82b3bcb6926	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.9185676
793652baded08dcde64374c3fb845534	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured bacterium	0.9576158
44ecd7466825308b9348e53a5016edca	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured		0.8828222
4c332960b3e08bad4bbc005640907e5c	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured		0.7555685
af6002392c0fa0428fca53519f1c53cb	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured		0.925801
2a2ca739858c027fc7a1687f152ac362	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured		0.8529816
68d7c4d552a61673b0e2f0074a741681	Actinobacteria	Acidimicrobiia	Microtrichales			0.7272563
d70f4646e125726847823b43b7df085b	Actinobacteria	Acidimicrobiia	uncultured	uncultured actinobacterium	uncultured actinobacterium	0.8459398
04aad26312a2099568cba48eb37a94c1	Actinobacteria	Acidimicrobiia	uncultured	uncultured actinobacterium	uncultured actinobacterium	0.732368
6d8af7f219f9fee5bebdca626bac50c4	Actinobacteria	Acidimicrobiia	uncultured	uncultured bacterium	uncultured bacterium	0.996826

2e5798959b9b6eab12ea2710eb704e34	Actinobacteria	Acidimicrobiia	uncultured	uncultured bacterium	uncultured bacterium	0.9494957
a60e7400c19a2689dcc0b9dff7a65945	Actinobacteria	Acidimicrobiia	uncultured			0.9968636
fa49cc7f5f0ab50fffbf6f89ec8b1e1a	Actinobacteria	Acidimicrobiia				0.997914
bca92bacb095b7b7038fa9db51eecb3a	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.9977758
1fac7db9ef21a1e305bcccc863a8bd96	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.8609847
8cb4ccd83cb9625c4d095d86751ca598	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.9507484
58e1986d6ed9177ec034b5f415b6d51d	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.851981
3730ebc0f0bb5d970d53cc2d210d3b1f	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.7567851
956290465e6b3f3c2559cfd56d7a4536	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.9121427
29115e7bd8ef43044853d0193cf6f622	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium	0.9946874
afe177db68872b66bfc1a2e7c3c1a804	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Nocardia	0.997747
08bdc6c81f6b9daab3d132b54e1d45bc	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	0.9998355
f6a6d568071d44e612854548340d94c2	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	0.9953709
9f9faef726ecb7a80ef2bf8c971bfe10	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	0.7926465
ecb3d4718690efe8997f8067f99c436e	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	0.7365808
09de3dde6c465b74bcb8e6f8a478e4e0	Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	Rhodococcus	0.9999998
b8c4ed03d7d91546b9f6ad80b80135a3	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	0.9635196
f6edbcb91f18c1dcc550ce2c68333165	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	0.992901
4b1ef2044dd76e8095216de4fd4122fe	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Geodermatophilus	0.9799375
a630a15abd6f0999ffa032c69c8d0876	Actinobacteria	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	0.990257
1935b9726fc8e67ef0b72ec5208097ce	Actinobacteria	Actinobacteria	Frankiales	Nakamurellaceae	Nakamurella	0.9903789
dcece32e6721f47a5d0849ec92f722a4	Actinobacteria	Actinobacteria	Frankiales	uncultured	uncultured bacterium	0.9999238
fe9a5980704285a959aabb88f0340e75	Actinobacteria	Actinobacteria	Frankiales			0.768891
cfdf66ad8b27626f14f419a4f6c51b88	Actinobacteria	Actinobacteria	Glycomycetales	Glycomycetaceae	Glycomyces	0.9993501
eb28b1a40981d38e6a0aab251174dae1	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	0.9885863
cb2521024d70e8938204d167ae4a3df2	Actinobacteria	Actinobacteria	Kineosporiales	Kineosporiaceae	Quadrisphaera	0.9983142
d892d40bc79d0c356bd2886ce8d120ee	Actinobacteria	Actinobacteria	Micrococcales	Cellulomonadaceae	Cellulomonas	0.7680667
93a299b4f0a27d63080dedea3a7d049d	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Tetrasphaera	0.8946608
45ab7b23ee88482238e3e81f02515f68	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Tetrasphaera	0.9593417
7d60223125f03ca8acdeca2872cfec2f	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Tetrasphaera	0.9804619
a41e51ea1f8e3b3623199b24522d5cc5	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Tetrasphaera	0.9967516

225671ed33a06c9e372cb09428c37ff1	Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	uncultured	0.904863
984919ce3c93ca2b6d54479b1c165fbb	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Agromyces	0.9954811
09fcfc99232a8211fc24af58233d5f0d	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Agromyces	0.9987632
dd93a5212cf24a278d626226f6441d93	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Agromyces	0.8064262
b758cde6d5121b176c6c64b571a41b02	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Agromyces	0.8554835
ee6ee5f00eb1c192da3115ea88c2c0b1	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Parafrigoribacterium	0.8101763
702af9e944edfd5a1a7f0dce0d566376	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Parafrigoribacterium	0.9999611
453cf07d3e96e304f23fbde7b355fe70	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Parafrigoribacterium	0.9742397
e1853bf0594fadf01e5600b12fa24a07	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	uncultured	0.9977827
1dca104d96e09a385302f0e0ec8b8553	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.9612244
ca1fe70202213a0522f8b97c6d8b1720	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.998213
43f8d1ced946461f54ea0b5b7001d5d6	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.7240837
79276373456f76c2665e4b9a8c193b72	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.9928886
964f34907444dd43ed504b24f3687ff3	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.914173
c51c974c591cce75ceff90c9bd817424	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.8585022
7b7595f9b76cf1c37a9b7943d54f75c2	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		0.989888
9b4be26e7bb3a23d25e080a3bba619f6	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Arthrobacter	0.960768
3fdb30b9b5dd6a998867bd974c0a1732	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter	0.8870376
7ff346973a282aa55de296afdb5d74af	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter	0.992679
a1ed615a4ed0b08c534fcc504a4608b2	Actinobacteria	Actinobacteria	Micrococcales	Promicromonosporaceae	Cellulosimicrobium	0.8930647
594061ed4e2ea378773c474cd4803c29	Actinobacteria	Actinobacteria	Micrococcales	Promicromonosporaceae	Promicromonospora	0.9214159
c489a5dd3e6b99cbbe986a7965f907ff	Actinobacteria	Actinobacteria	Micrococcales	Sanguibacteraceae	Sanguibacter	0.9992063
fc4d567d1d0828e1fdc36916f0d53d15	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.7087881
aa980be936816779e585eb839cc05879	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.870609
e3587b94b7d9c458335ae7235bb6677a	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9994077
1c0a3725f25027e98ff6aea763fbb4d2	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.7948908
e07052bb9c0f0d2370537c4b9acbed4e	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.8126992
b3fe77bd4d27e30779be9b5fbdcd84bd	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9997331
f8e966fd6a44aecf3991a7dd167fca57	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.7642936
1cc4d0d06af05f45284b9a5bd6c8ca5e	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9778025
d569b3034acdb4c7cadb3a5fdadc6943	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9921663

70591b35ed664f271d3ccf22e9c564ee	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9996074
572b96fefec73aa11fc6628597853ed7	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.947736
40a536ceb4a09d4bd78fbe6ce5107600	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.9802551
35d20da789dde8d76e4389fd6d30cc9d	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Dactylosporangium	0.9683004
af2056250982f6c87fd28688fd3a1ad0	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Luedemannella	0.9827583
f6413cfed1e9991f4da1ee5fc1e4cbd2	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Luedemannella	0.7712469
370b9391b142205b3cc28a27b2a55655	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Luedemannella	0.750519
a7036d9a8aac1ef9c0c7553bdc3b6a45	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Luedemannella	0.7571883
199ea5c6c43f4c66996902dc771afb69	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.9016479
ce2ad9cee88a62c364579292c902bb4b	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.846756
a87b7e02daaa828c6dc11fbcba68b61c	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.8844729
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926c02fd6f6697c549ce4ddc2477372f	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.7805063
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3eec0ce64b656f27306dc84b37f150bb	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.9193237
f5bcdbab58fabf472426221c74f5c131	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.7276646
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940f95ade7361677b9fca5f5087b5919	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae		0.9868555
bcd599d42ecce5fff9170bbdca8cc097	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Aeromicrobium	0.9992912
2712c08c68a18386a5b7f18eee908d3b	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Aeromicrobium	0.8501832
f8440b4977cfe1a8e067c386098a7070	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Aeromicrobium	0.8966396
754c7c6f3b6988d240275e2f44436292	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Aeromicrobium	0.998856
1e181baaea6ea44783270cf5e6116420	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Kribbella	0.994658
a51af6f7d3369f355257160b33da3cff	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Marmoricola	0.9674291
26c10cdf8e73fae705e1f929e60f680d	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	0.7185731
7034493f95fe775db5f9eeb1aac0cad9	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	0.9972678
e4fb16123647885661750a901efa2993	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	0.7915289
6c33785c46c3fef68941d9addceaf948	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	Nocardioides	0.9225079

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e4c6c2f01a56afb89f85f101912ce3be	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Lechevalieria	0.9998764
52fd95eb476921cf2b9510888ea0cfe8	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Lechevalieria	0.8069391
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a23445cf50766c9c2f4964be5b1e882a	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Lechevalieria	0.9456125
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5725a3cf5bc2a845cf21e6f2f554346f	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	0.9176653
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171bf49d02f052e31714985f0aecef5b	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Pseudonocardia	0.9800639
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8ece70e47ce9f70bcad9297055bcb9c1	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Saccharothrix	0.9967518
bad135fbf0258fddb72f9528a47d35df	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae		0.8044386
c1d2d31236add70f9e9e3bd926eb84bd	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.9936357
db52e1be4ef9e236bbbb0f32d952ca1e	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.9999358
51121c8f8cc8a7a03d9d7f1dd5142aa5	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.9915751

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120eba657e42a11a5c29f97b90f02035	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.9994551
020a94d69ebfddc17d8e0b45d9d140ee	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.7888848
6b9753766d1381bc5574a21558e1b741	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.8604902
26b4b526e1e97e0a1322abc26264cfea	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.7181382
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65d259303d84fefd571cd6335bc2f28e	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.9751444
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2968d767d606dde4a6477e8042ccb9b9	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.7426438
9b6ed1d4f601b4bdb5e89ba85c4a46bb	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.825477
8c1c7a6066f143b1d90f8730fbd1d0d7	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.94036
350bdeaafb3f125d96d7baf5bc6ffdd0	Actinobacteria	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Nonomuraea	0.8256017
d3ac14e193d870746f08f2e205a904d2	Actinobacteria	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Nonomuraea	0.8056625
2d7a1f3bddbf3fb35fad9c7c31e95fd3	Actinobacteria	Actinobacteria	Streptosporangiales	Streptosporangiaceae		0.8989643
8687cc49cdac1adda44effe1e7a18e13	Actinobacteria	Actinobacteria	Streptosporangiales	Thermomonosporaceae	Actinocorallia	0.9670765
fcad0537b5b620597c0dd17e4bf48cb2	Actinobacteria	MB-A2-108	uncultured actinobacterium	uncultured actinobacterium	uncultured actinobacterium	0.9380116
26ae0cf6b9bf99fcd1538f0fc16ef690	Actinobacteria	MB-A2-108	uncultured actinobacterium	uncultured actinobacterium	uncultured actinobacterium	0.8021054
39adcf571c6edf2039d5a40a9db91a95	Actinobacteria	MB-A2-108	uncultured actinobacterium	uncultured actinobacterium	uncultured actinobacterium	0.7040519
954a00911aa2ca7b0b667abb1f668e97	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999492
b1c6ec51faeab3d65da38964ffa52d16	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9661586
595febefa3efae732f817d55efaa8670	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9939245
2698248357eb0c88b13e5684f963f459	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7868825
62a8e1b3e5bc78c9552474f65dc12285	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7976772
ea8a5786215c8b19a0fd5b49825d554e	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8383853
88f441ba6fd69562c7182156a41f5f3c	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9985686
62151ced275da257fb1f06daa7fd990d	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7756391
3a22176a6f33fddedcdecae67e4e0a0b	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.99951
e83f0cb9d2856454d6a7905a90419860	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999747
6fa0fe79653ac74686b1b42f941aab8d	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9982396
3760390d4943fd5176f2352156d8d53e	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9996462

af062725e851baa19a57d27c454641e6	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9998302
c7ca0630b3639d434162b1138269fe62	Actinobacteria	MB-A2-108				0.8245224
ee3072cc17a5e70cb4e49387257957ec	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.999763
89322f04a0ff844fd4be004f7def81fa	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.9978721
46e4f62d61f70e0c9b145e3abde8d747	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.8929307
d99a0b2472cd7caecdd8d63ac9cb3fdf	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.9620186
e2b032563bddf12eede3dd17e124e861	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.9746931
adf578f5313b1ae4a1cfd5885bf3f5c4	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.9916697
380dbaf8a6ad7ebdb3773b4b1157e72e	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.941587
4d39c80fbd8047adff745bcfea264952	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.974712
61c3d8e4d1400a8556a911a292791e9f	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9548429
b2e536caaeb5f4a6363b88739dd044b0	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.8449576
774f998ff49f49db70020f8ae193938f	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9999999
98db96cc99654ef243cb9136f09d14e6	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9890807
e7c2c171be5ef785791bb5a3a49fb3b5	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9996541
d921c6cbaea103ae8bbc8bb9b5f6fc01	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.998371
f968254345bd05c204aee9646945cfa0	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.7594438
dd836f10a84a311aec7b27d57a22239f	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9955148
c7d57892d6bf8efa95f97d6102d0ca9a	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.8511792
163d731c07b58f6a7f42ac3eb051748a	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	Gaiella	0.9056206
8c66a2e64ebe40d9bbccc8807494033e	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	metagenome	0.9386213
7c095f27b78b5f8660f4c8b6b45d5494	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	metagenome	0.8280306
86eda500f8e7f68c02c7315b467e87b2	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	metagenome	0.9131429
a0a26f17c680f2380076ea6891680870	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.7830536
735a34530e1dd2ede72d29fc30982807	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.7121323
38d2cfd1a81fa384e8330189c2ec3042	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.9567115
b9ffcdeb54aff2e5f169d493c73a53b3	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.8481407
55171d6a7d2a6277fcaf13baf685e8fd	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.9933864
7b930f6379e67e52f830dd7f53107a41	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.9895785
3c70a6836188aa560a2d934414dbde9c	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.8851067
35ebae74843490d505c7a299cab0109f	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.9924912

8a5061182403c027a8959595a9db0032	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.8594598
32153157f37d9f790c8e2efbaaaf2ed0	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.9871839
7653cdca9bdece4101e95cd83ac1fc8e	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.7799357
c85d1b78dc8077b2d72f6ffe73fd4783	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured microorganism	0.9893111
8c83fe5d444479bd20ab5ab54d7c689e	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.9923599
f08c2b3fe62e49d5cb9381abd5739bf0	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.9873499
964794f6e0519cc1d96d1a245b8d4431	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.9002344
225f29be80fd847f301dbad3c177ba40	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.9998835
37be7c734cda7d0bc29ca07b84b7f605	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.7508829
52e886c187eaa363d0fda554350a959d	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.9943838
c0ceaa7d4433ffd5368f7ea93321111d	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		0.7120899
26f122db8ccc99731efdb039790aad9b	Actinobacteria	Thermoleophilia	Gaiellales			0.7065326
7da83bccdeeb83a8aa9894d532911277	Actinobacteria	Thermoleophilia	Gaiellales			0.9711516
3dfef3e971e90e5c5faec3abf449848d	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9991042
f94b63f139c710222293cd7c6dffe7b9	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9999914
6727bb2c91a7a6b0489e814af3bb9cbc	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9999985
ce031f0517b6e948db55cfc34ae6279a	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9662281
3d516236a1ebf0935c73738350687477	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9895419
4dc24fa062f9520295bb4c29b91fd7d6	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9148357
d5f10ac9ff9a61e2239d9b89189a904c	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9999997
41aecb6c1c7399be7429bcd6584f823f	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9875449
9f8ed8afec9572def08f5287c80288a2	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.7482026
ee4c323e8bb93997f0b8bcb9a5efddb0	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9885697
aaf2906e85a062743c6acdc8ae0ec0f5	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9890818
89df4eba23365b3a08d774a527d7a0bf	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9930077
ab82627e3e67b1b80c7154ca2b462940	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9999922
8100d2962cb4532282d053c8239a2da1	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.7944418
daae3699c460e7d41ec585f2d1241c4f	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.8474204
210103819517329a90f0656fbf1639ec	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9973016
2460b83e646333ee1ede1a37fc8fd303	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9876874

2ef183f6797f1c77b6cde046c29442fe	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9317169
b32c31cdf2e8499f2dcf74dc1dca50df	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.9957754
bf04985fd58dcc698557f0e092e889b4	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured bacterium	0.7728851
7cc9bd23d0a81b25254d454f13cc7e35	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14		0.9960558
e4e1c7c2e9568299c4797073944234f9	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14		0.9686361
c81eb462d6200569f9453e6c11642aa1	Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14		0.7595696
ca92bdf271282ba65ab50c35dd6cad8b	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.801727
f4ca24355cdbac7181b362a21da39d70	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.9968525
9d127ac8ec1a7b03befe92229847b811	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.959702
2c2c3491e121453294c214a2d8cb6591	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.9398175
a251ae02db5ed074ffc3acb72d5fbe33	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.7252477
43fc1708be1b01002bcd51e177b07c0d	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.9927319
446bf77dde080dd65049ca9d15a47abb	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae		0.9996992
4312b429c28933c568488f8f2ccf60be	Actinobacteria	Thermoleophilia	uncultured	uncultured bacterium	uncultured bacterium	0.8126019
12c66c9f8bc4063e277e74e4c701df2a	Actinobacteria	Thermoleophilia	uncultured	uncultured bacterium	uncultured bacterium	0.7182169
7afbd06055d72ff20cb5102b3f420ceb	Armatimonadetes	Chthonomonadetes	Chthonomonadales	uncultured bacterium	uncultured bacterium	0.9999999
befb7a73fdd3d798a9050073cc027155	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	metagenome	0.9776815
038cd699389e8b93b37532dfa181f762	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	metagenome	0.7351394
5ad411756629630605e27df140de4319	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	metagenome	0.9659944
e2f9076176ff1e540345ebcf04aa708d	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	metagenome	0.9276901
506899e938bf4a7d8eb858e07c43199a	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.7565899
1b21eb2a07af7a72ef08c47f5b9ffbd6	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.9999974
8cc3697f336746bae610bd8fd5cb3af7	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.927818
a1eaa9e415ad4070a0cfa8500a0ecac9	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.8105823
ddeaa8986703f1c377c5f098396e1136	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.9978455
8249285fb88d0710da9fc50d4b68a9f7	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.9996907
32b3d3902ba0857285130a9ecacfb033	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae	uncultured bacterium	0.9930372
358b5734826e34db48d8d82bbf59da66	Armatimonadetes	Fimbriimonadia	Fimbriimonadales	Fimbriimonadaceae		0.9837388
41a58225310fd9251a2ab706b6c025ba	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.7517534
6a22f5fb8a4996c60fad93674d053757	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.9844022
48b92876940e467b73a053655396a8d4	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.9992602

7639ed933fdab652179367708185078f	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.9990941
22af6faa0d8945ad5b0ffa006fca5e18	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.9705382
fb0ed992c657f6b365fa14284524dd2d	Armatimonadetes	uncultured	metagenome	metagenome	metagenome	0.9916487
98d31ae77b22d457a9d5f9b4fa66c512	Armatimonadetes	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9710543
1a4346a2a6549d88b643eefc2b7c80ff	Armatimonadetes	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7107743
751da794f3162dbcb44c540641d1a077	Armatimonadetes	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9195011
adbbb85bea0c018e519c8cc8ddf12e13	Armatimonadetes	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9824466
ac5465521931cfe96c054125ed5122b4	Armatimonadetes	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9833609
17c50062cc0f5e32e69417b16854528b	Armatimonadetes	uncultured				0.8386951
48ef44520932fdcce4bf78053f9d4f51	Bacteroidetes	Bacteroidia	Bacteroidetes VC2.1 Bac22	metagenome	metagenome	0.8267804
92690a1ffd596e17f1397de37946ce25	Bacteroidetes	Bacteroidia	Bacteroidetes VC2.1 Bac22	metagenome	metagenome	0.9013782
0668472c2f0402114fe4a4ffa8b2d682	Bacteroidetes	Bacteroidia	Chitinophagales	37-13	uncultured bacterium	0.9923991
c50304b7aca09ede7f7162fff48de6c8	Bacteroidetes	Bacteroidia	Chitinophagales	37-13	uncultured bacterium	0.9999805
72f3162966e9357e7999a2ef8d163107	Bacteroidetes	Bacteroidia	Chitinophagales	37-13	uncultured bacterium	0.7742036
f1f9a1c7142cd57327e10673b02a2ab4	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Chitinophaga	0.9761627
e07719f4be1c88d455837c0779481019	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Dinghuibacter	0.992195
c6f064f6b89aa571205e6d7baa08a47f	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.7089623
9e79ffb1ba498e74b74093eac14e7f04	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.9989348
6f6e48b06c0175c1efdaa3413dbbac5c	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.9888567
bf8b559711beea207ee3ab2f9df87604	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.7168909
422a3c019dbe1b529c87ac238b5bafd5	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	0.9869927
9e1a84c523f0aad87e1b2d82f9720b1b	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.9688377
f716ca223786d697f2f0961c1e8ef9d1	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.983231
853f427b8c7b9896de4e3179cd7a0fbc	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.7277211
fd9566a2b963a28558617cdfa8809ca1	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.9693787
072a834e48e0ce8bb0f15eba8d80a5ee	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.9281294
517175c66a736838e6aab09855f73bca	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.8413639
af5a1564ed9de77e6cc208f83e9a15c1	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavisolibacter	0.7618981
a5aa30da0b2685c7b0c47be160249bee	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavitalea	0.7438104
d4d0332abcd8e0f165ff77ffb968a4ff	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Lacibacter	0.9562401
a8df653da66acd4d326cda1667bc2941	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Lacibacter	0.9896754

1b83dbdd6f88577a0df8ea556bd57fe3	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Niastella	0.8759134
8678dea077ece20287b950cd5bc66db8	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Niastella	0.9633006
44a3a3929c7affea0b4e857eb74a0e8f	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Niastella	0.9972926
8f095d3ea9df8f6449dc69315c77b191	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Niastella	0.9682836
55e086e0a1450201ad02b2eb33447e54	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Segetibacter	0.9602029
be99c7c7026f370dcedbab199c6581d1	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella	0.8609028
123105c60c75e8765ed7731563817ac7	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella	0.9603564
2eac72eb872b6938aedf01dfb7d7a524	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella	0.99316
598032889ed63d66f0d741697e49983d	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Taibaiella	0.9995848
971cd633ca316d4607234c1a7c3bf13b	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas	1
05810500448cc3ad7c9d8b11a497f1ca	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas	0.9855752
1f8d875146897fdad4face9b82c5b15a	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Terrimonas	0.9999044
d59668e479c38469a1b2b96494292954	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9995744
bf121ab35dfaebcac0746bb9ce8f4780	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.8361269
9cb4c858c66fd440214f6d5683bed435	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.999147
28ca720b165ff076cbba07d51ce2274a	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9657601
b8798f021bbef7ed37044d7e4152646f	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9972533
87ce875dfac48815181a86cab5e36841	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9996203
8650d50536861d275a6139d1cc04516b	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.7360593
eec9ee649c45bac516b7bc8889f401c3	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9369953
238edffed967305335229246ba46b195	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9954795
64bd319e4d15d6e8c2d76f097883303c	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9999996
9403f4687f2ec9229256404cec583646	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9998833
0cffabc501090490bf3054a8b71d9ccf	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.8328496
37bd9a54fef37f84f41dbeb09b7176dd	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.967158
25c9aa2cb09b258e40a2294aed981c09	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.8195237
7274b0e43661a8da8d18162932a02c22	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.8378237
1868d891a4197bf06083e26c27e3e2f1	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.8096431
39b05ff6a262798edf1320c52c4b1f2d	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9785654
e1fc22b820d06ee8b7924dc7020a11ec	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9999998
47f2617de53ce85d035fd4d1cc587272	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9987401

036db0b1cd0434c5d4404ff4d9ea47e0	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	0.9972195
1bfb718cd023f2763fe020fd31f1697b	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	UTBCD1	0.9823503
3a243c419f242f78d33de701e1c590d0	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		0.873407
5d9222cc7f5908b0f2cea28b5e08e040	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		0.7453439
44e2ab81e5e7cff6d965651c707b9479	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		0.9897405
5eabf7bbd88b549bb96b44adcb120fc0	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		0.9391486
ae25fa111d6b00c202e93780d18fcfa9	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9885599
8424091c988a951bf8aed8c682ebae5f	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9818408
0ab5af9a08c57a4ed3fb285507aa14d3	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9730999
b92f55404e59f086f0ced4880681b69d	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.8014927
191ea95cebce19311358c47984f90ff6	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9989501
8ccdb282b0f7311910e004a2ae836908	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9819404
d4dd9dc50722764203ad6748f34d81d8	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9968051
2e2858610adc6f89731e6dc06ce65791	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9973626
f44afd583279d391d747a00335b3ca20	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9831383
aa81949da7fe93cf8fad9ef84aee2edf	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9999303
f8e5132bc4608c1b6a95f2c83c02fe4c	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9906015
f083eb5ec074002f03d4af8f64f6743f	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.9997465
a3ffaf32a41d05b464640e4b38394fc7	Bacteroidetes	Bacteroidia	Chitinophagales	uncultured	metagenome	0.9455617
2090cf302a629954721b74b277601c06	Bacteroidetes	Bacteroidia	Chitinophagales	uncultured	uncultured Bacteroidetes bacterium	0.9801413
946177df53d41f6d31e21aa92d36ea33	Bacteroidetes	Bacteroidia	Chitinophagales	uncultured		0.997992
dce9a92a7e1afdd04e99bf340a330fc1	Bacteroidetes	Bacteroidia	Chitinophagales	uncultured		0.89308
ccf3804a82044fdba7753a04498f1e65	Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	Algoriphagus	0.9938135
092a1a506f4d1bf4b25864c9561ff471	Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	Algoriphagus	0.8904621
f433c322c396a54a90ef0ab3a903d0cb	Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	uncultured	0.9316292
4730ad44b9d01a4e32f8dc002549039a	Bacteroidetes	Bacteroidia	Cytophagales	Cytophagaceae	Sporocytophaga	0.9952731
7a67dfe0a156d6bf90195ef99a7ba2f0	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.7838426
45a5b937529debcc980ba40152dc0103	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9564943
dabc03ac078c320a402d965dcced1ee5	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.8014619
bc21eb5df115c16cb625ceb844ffc0c4	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9842565

576ffa1f764dbbc9968b25aef5824f02	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9686212
a7baa09fd673897bdbde41afbed88fde	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.853388
043c5451a5022d1abc509fa1e188ee54	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9994194
3ac4e6d2bf411194b3df70b4cf78e1bc	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9999989
fd1184fd1cb16c56ea9ecba792836259	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9999942
c824241042bd08835b8b0327ad25e597	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.7860863
7a1f78821a8093d440270f0c8733fe88	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.9829583
3725e63715d30df08b67d09db5ca80c4	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.8220252
618c56b2af5f5b410f9ba7ab6cef83a6	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	0.9665935
9b18c9fb5123370dd4a4a3b41a9cf50b	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	0.9463566
08287d26314336a22e26ab0b742b3341	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Hymenobacter	0.9998102
58eb1cfd997a834e5c799c54f4472cfb	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Nibribacter	0.9744214
2b8057f7369b4cdcd38ffb9450e3bded	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Nibribacter	0.9562825
dc0863aa6314a958198334fe1b380930	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Rufibacter	0.8801037
342d31d1260719ab243739b7b7eedbec	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Rufibacter	0.9255867
f9addd8a736ba8f99f715836c4086005	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea	0.9999661
06ac1ba7b79b5a17f8a8a8b7e5c2ad1d	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea	0.8409331
5d55a1e7677ce1d04a34cfccafdc0e17	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea	0.995556
48ccf1e2969896d59252679ec29a8aa2	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea	0.9997807
669c8f8d724c09e49dc3b239b06e68dc	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Chryseolinea	0.9946617
f185edfd09f286f5f35a6c234e217adc	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9728782
78c8ef5f1aab306298d96d8276b4cd95	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.8465743
84e12083b95641d44fa71a9e3acdbce4	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.7885968
01784452cef9e81e1814fb6423bd2acb	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9855577
4e467826a385443732b88adeaed18877	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9776825
9380e49952dccc3c2169dad4ffd0a02c	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.8561746
92391dea7a69d874040075b6362877f0	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.895972
834cc6cf02088f238ab6cc96f7e7c0f3	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9974329
0ab03766a2653a88fc64612dfb97bfda	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.7924988
97492bac8e218ca18c3dd30f0d338f91	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.7982279
c68803398878eff60e0c14498b950ccf	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9998136

9d47dc2fc394841ab61c36fc6db9aec2	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.812805
5e616c0a99413e29f72efd5e9c67497a	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9123367
028921f3d71d087dcaf8ff1a822650bb	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	0.9277799
3125694452d98013214919bea3df321d	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.8673823
ba9ecb28932826e70d43988826679fbc	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9913675
17feaac3188957685c924b2422f192bf	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9995653
efd7cd579d2f9650dc0865ab1c8431a6	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9997084
ec3bc784a3be57e9a0b20a095ac3f331	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9876121
c05ab25457f3aeda12051440a3f1a2a8	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.8977874
b8400624f2337c45aacd4beba4199e27	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9848598
ea92d90ef499d3b30b0aee203b3d7778	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9508986
39058aa84552dad1fa30dcbab6e6b1b6	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.789396
8a3d0130ff8e61dab89cc1d3b30764a2	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9932579
dac62a87167cf04f4a25f3824f9af890	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9921118
b6aa0321169856fa2d98ea9a21520b5a	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.7349692
39a936ad1211618807fccce21b8cd615	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9998169
1240af4974c64654754de53f15550c8a	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9891607
9e56d913c8bbdccb6b373fb563f06f2a	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9622488
19152387d7eed4380d5c89bd59cc157d	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9960718
a918ca60e42cff7e983b1cf412a072bf	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9867083
21f7f0dfc4eb9e91480dfab908344a80	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.99546
ac68c7c702432c26bc13677cb4c1ea8f	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9992796
405a7b562518a6528bb2b07a9e8c1216	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.9779803
6d6c23ff9cd2ca92fadd835f12a0b536	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae		0.9999997
662d2f267949dd47bcf335254b145d04	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae		0.9836096
99266b1445534b364447497bc671adcd	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae		0.9273055
bf89238446119af983b28e8e5cf2e9dc	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae		0.9867875
a35b2549d34e0cf52f2ff3b76fa35cf8	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae		0.8362995
1ebf3c81b9f872f5a309a1a08ab97d1a	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Dyadobacter	0.7720264
aee23bfb05fd3cc0ca7b392a9e2b9c4c	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Dyadobacter	0.9999992
fd1fea8e03c567c1f96fabffadb66fd5	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Emticicia	0.9998897

e38cdc0771494753c7c0e451a0fef477	Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	Emticicia	0.9806584
77adc91c43a714f1f4b8c6259e05d570	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix	0.9971931
7ed4e63bf16b983efc3e9d9166d8f4e9	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Crocinitomix	0.9669992
9ed20ed64c7d21137f69053bcb65af05	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Fluviicola	0.9991917
5882ed1cf232bf6e5b46d18b440fc0b1	Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	Fluviicola	0.9587817
77449b2ef996b44dfe0b8055790a00d8	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.7452746
d95c9b9d40850582e8fa353fcade987b	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9328367
b678a0f9073def0d5c2a1bbe81b6a091	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.8986493
c757ad670c5d796cb866c941c62c4e33	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9535604
5afec052157f7768bf459883f118a638	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.8259182
945f562bda86790338922e12f9854407	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.92504
68262884f1021c896f8e1bf7348d773c	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9344303
f9c1c7de158ab4d555ec46bec26478f1	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.892244
7dcb7f66997c6e637a9a7bd3fb8546ed	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.8897959
a9c08388f3e0b2c9d2d3626597f727c0	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9077592
75e461a26eb13b42090ccdd19074d51b	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.7310901
73019f066110de1d658b58005062df87	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9999965
34d84de5190792c421c0bda75a35a61d	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9987496
c9ff5508342adeead449b71b04f2d82b	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9999785
cb1258e334f3d12aeef6bfc5397f90ca	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.8673059
a1dd22ea95e415e80400353ad351c85e	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	0.9993323
0d24b0bf935c12edae9b2c8c6fe7c588	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae		0.8049575
ddfed0af37288c00b0a9111399962c1c	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae		0.8914741
2564c356e86a2749ce6f903a65d3b58c	Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae		0.8454187
514f3dae12651aca127fcd7c19973fdb	Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	metagenome	0.9920409
d7b021cdbacdd3a27c18e600e8a8ecf9	Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	metagenome	0.9998162
223f06920a8c3534323b310c7e0bb62d	Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	metagenome	0.9609913
fccbdff8fac6bb4a77fa3e3d96e7ec2a	Bacteroidetes	Bacteroidia	Flavobacteriales	Weeksellaceae	Chryseobacterium	0.7163636
d2863e8feaf2cb1d76a8b2191df2d9c7	Bacteroidetes	Bacteroidia	Flavobacteriales	Weeksellaceae	Chryseobacterium	0.9999693
d2a53ea9ca9f076c0dd2ee8429e01a3c	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.8466363
a9b20196d79a674490574b7c6b94ce14	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.9930724

e503457e7b38bd23a9dc6f72a98c1689	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.9054009
0d24c4ac82f283219a675ce16edae3cc	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.9222255
2dc0ef2957f4dcc2d047cd1c3ddaec9c	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.7732549
84d062305234ee51ccce4d3f5aa1e251	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.7971685
be5c37a29fe3e6368a7c6ad737fdb3ca	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.7256366
db439adc4e5abd361747b5585c15c7c6	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.7319739
20bf67d0d8d18a201e96359e574a6bed	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.8531999
e60a1585a5cdc8520377047611e127a3	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.8422122
3ed7f0996269193fa8c135cf0e015359	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	uncultured bacterium	0.725729
186350e1f25c53b8cf31ee0589293fdd	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767		0.9735384
8385823ac714efd9aa0b81485899210c	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767		0.7748035
b2e3e0899405d98a06062c7264452246	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767		0.9912955
113d31b301d63e6764e0ab48616d6166	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767		0.8397752
fcdbdfd86ca4e166582b733ef0edb40a	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767		0.9408846
22133f1add1301ec0492fac810a92019	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured bacterium	0.9957084
389e40a71572160614d6b05b05cd34b0	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured bacterium	0.9924059
5ad4ffad545af8e279101d52bd189173	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured bacterium	0.9997971
048d2fe48e627d31cf210062b56fb6c4	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured bacterium	0.8002445
fbf12440b43a76ef526640bdb9592893	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured bacterium	0.9508842
f41bdd3950eb73241667b3545c2470f0	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured Bacteroidetes bacterium	0.8945841
fea4131b8e55fe7e385e4cee00682f61	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured Bacteroidetes bacterium	0.9981567
ee4b7efb7ecab10ae61c6f2cfb03220f	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9526697
e07cab74ad970188b1f14b26c919d64c	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9843558
594e6fd1e2b2d929f910e097c7d0701b	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9769994
fe50ea60633150a924302518158a0c4e	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9994271
80a544dfe60f9418893700481372a4fa	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9922856
d5eaf9f713b35a70e2de3420eea5353d	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9790831
7e77779210b2887a074473e902da3593	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.8303128
638988e449c5653850413b5afdf0dcbc	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9689769

ce87e3c86dfc2edceefd165bad38c2f4	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17		0.9220277
0b9d4901cae1832ca539a89edab342a2	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured bacterium	0.7845838
646a1135f5b6531dc99a2a204c097658	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured bacterium	0.9899329
ad0af88866a26b48db5594012e1cd4e3	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured bacterium	0.9978973
1889e19f68bee5d791313c3110e468ef	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured bacterium	0.9875927
4a985ef668a7922b95e77b0039e9d6ac	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured bacterium	0.7559876
ce4a6faa57b9e49f98e6dcf1ea6bb591	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured Bacteroidetes bacterium	0.7417569
a53db821a39b71d23e827f8ce57f73e5	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured Bacteroidetes bacterium	0.9842527
8abd5ba6a8306130ceb7c6e609889cbd	Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group		0.9961624
c2cfee2a35df185be4dc4a8cf82724c2	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Arcticibacter	0.9998203
75f2a155feb020ca2222e164e8771fdf	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Arcticibacter	0.7531783
d15bd1dcb9de71d7452648673a59f5b8	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9861414
a099b394e1c5bf8da4ea283c5f27fd68	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9189327
0d34e514b2d0d3a14fbfa27a9717f5ae	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9999942
e6c4a7258a21cb1ee250bdb71efc5c98	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9363486
57534122b65b3942bd7294443b3e17bc	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9985625
e00254c81e0e58719fdcd510482c7e80	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9557253
b8539dd30ed5fab9dace2a776b1db440	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9772549
861c357388b498ed9ef7ef6440b4dffa	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.9867978
a609f4962f69a1032066c3e150e0c93d	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Solitalea	0.9596521
810d24ee924214144b5ce85d1626f9cd	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.9784957
10b890326e2b0b15509aefb95d0d6b79	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	0.9024881
7743c1587efe702b5362aac242c6f6bd	Bacteroidetes	Bacteroidia				0.9997636
8b6c7afd77e501aac7bd275ff2144a81	Bacteroidetes	Bacteroidia				0.7344687
420c7e53b7836569163bc23dfbae4d5e	Bacteroidetes	Ignavibacteria	Ignavibacteriales	Ignavibacteriaceae	Ignavibacterium	0.9999938
0a5d94a1538d3f5c0ce59d01043f5fe9	Bacteroidetes	Ignavibacteria	Kryptoniales	BSV26		0.9999961
dc8955ec412733aacec44476b2ee170e	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.8759817
a30b48e93c3f0fc39364db38c673d7e2	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.7980782
26a6a4b8d54159be2e2a106bd20a2368	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.9974707

4978c64b9ff08951fdaeb48202b9e88f	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.7138219
0866acfdebde7c80cdb63b297c774958	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.9997976
307d99fb97058b3a061ef36772c8feb2	Bacteroidetes	Ignavibacteria	OPB56	uncultured bacterium	uncultured bacterium	0.9894764
ee4c824fccdf97ab3de5e8b086630483	Bacteroidetes	Ignavibacteria	OPB56			0.9997698
0f6bb4a53b6f943200b7bff7e1287950	Bacteroidetes	Ignavibacteria	OPB56			0.8802803
40d53554337806f59b13c788b44e192c	Bacteroidetes	Ignavibacteria	OPB56			0.994015
25e2c52f9aaf8382287cc0326c0c661e	Bacteroidetes	Ignavibacteria	OPB56			0.7923587
4d5627d4e148f4b661176ae0500351d8	Bacteroidetes	Ignavibacteria	SJA-28	uncultured bacterium	uncultured bacterium	0.8398402
8e7aa11bcb46e64c8c9f5b09c9628f36	Bacteroidetes	Ignavibacteria	SJA-28	uncultured bacterium	uncultured bacterium	0.9207033
f53cca9d300aaa0ac067376e18d04c31	Bacteroidetes	Ignavibacteria	SJA-28	uncultured bacterium	uncultured bacterium	0.9762593
23b25f334b3fed43836dd50ee9e6fc20	Bacteroidetes	Ignavibacteria	SJA-28	uncultured bacterium	uncultured bacterium	0.9893851
b1586b7704c0452d6ac6da6d0ff1deb4	Bacteroidetes	Rhodothermia	Rhodothermales	Rhodothermaceae	uncultured	0.9032677
050718ce37435f5df6a6ec5b67c49e2b	BRC1	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9859516
8c4b449fbfb573c925735c181092ab61	BRC1	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9846415
47deb8d3de19365fbf353863c93d3a5f	BRC1					0.9868114
d1c66f9c20318aef9e05a5c38737aff9	Chlamydiae	Chlamydiae	Chlamydiales	cvE6	uncultured bacterium	0.9542416
a3d55d725735945c69818d4bbc8ca795	Chlamydiae	Chlamydiae	Chlamydiales	cvE6	uncultured bacterium	0.9248996
0e53519d30f5e9545c689eca8a5c4992	Chlamydiae	Chlamydiae	Chlamydiales	cvE6	uncultured bacterium	0.9955301
1e56e5fee04f2cc0f22f2814a7b10ed0	Chlamydiae	Chlamydiae	Chlamydiales	cvE6	uncultured bacterium	0.9292429
d7e720c6a5a79c9765de7d89d07b31e4	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	Candidatus Protochlamydia	0.9998135
9c474020e3c2eb3234c6566979c0a5ca	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	Neochlamydia	0.9714839
a6018fb2ee93ded290ca494583fefda0	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	Neochlamydia	0.9999721
70d29aaf9b0d88a9c9e3ef277f1d9523	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	Neochlamydia	0.923209
8f65c14e45d3c8ab8247a7fbc53dbe61	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	uncultured	0.9984863
2149f5adb0000be42396317da2c9e354	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	uncultured	0.7002382
b62d6cb9a17c05b207ec0b9dfdbb83d0	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	uncultured	0.9625132
9a5bd57b91efe1e1396bf0c2d0ebf270	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9077307
a2af774ae54cc013d194fa2f8cc98f75	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.7855748
71760775e67373f91814889d3c12c2e6	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.7457052
2b7bdf1293bcc9c58f6431ccd20d076c	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9736969

be80120bf884f246e05cfc4cb8263428	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9903944
2e5f7b65e3ab675c6d80c77fd09894a6	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9988703
26c937b9b6be3de8e924c544073b7d48	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9952696
0ea34d5029efd2f8f7aef8b3911a63ff	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.8884321
5580bf05f601a130d123b9c90db9edfa	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.7034224
ac7e1b70ac6df97c9a7ca7671a4e9c7a	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9887164
75b22df5f45b2a017796d205dba9487f	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9025529
fdc8876b09d30831b82f678c8d5f3fab	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.8885218
b3599d34d2579b08592a3457584367fa	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9855389
3969715871a7ed23c8862d69348cd958	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9924002
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a419ea93d8b204eb468b17ae2df831d2	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9700837
2f8864ea6bf4a35c91d91176103acef4	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9996629
ca47ca174b95861c381f51454c4ae731	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9998281
81f742444684887eafe3895c3757891d	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.8636413
5e9a06418a0934113f2f631ae4bd2e1a	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9882821
1006f89ce2f3d546af33ed2f71e2fe6a	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9965002
d7febd5b24cfa919e58d262f47e1a674	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.9518
b44d741431688b85ab939ecc1b7ec63a	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	0.7254134
02c285724d247d2d0dee023369f2a134	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	UTCFX1	0.7910831
5760a90563204c4be4a0562231be0b81	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	UTCFX1	0.7001464
4f643dedf3500af5130189938fb5de10	Chloroflexi	Anaerolineae	Ardenticatenales	Ardenticatenaceae	uncultured	0.9756326
3c2e985995945ad30db0a405dc4f092a	Chloroflexi	Anaerolineae	Ardenticatenales	Ardenticatenaceae	uncultured	0.8012369
b28cfcd79772faa9ebc457e5b5457b87	Chloroflexi	Anaerolineae	Ardenticatenales	Ardenticatenaceae	uncultured	0.7188449
12925f07a3c09cd9dfe3ec5283af9163	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.9685774
c94811a8d119639dd34a6adcad76d8b8	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.988331
3ba3248822fa59f04b1df440122e1587	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.999887
b397fa385e883d8810d28ae6294e58c4	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.95353
f9f072785364d8c834ec55c8cf9e52c0	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.983111
27a161674a5018e50478d7f681fe5cdb	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.9856671
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fe4168974e62d82878e26b4a9bf0ce06	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured		0.9833756
b957c3233f1d1842ec74638619be94bb	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	Litorilinea	0.8672059
6516754b481a8200eebec4446cc13a01	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	uncultured	0.7605461
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44ca562a768a11b1a593d8076270897d	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	uncultured	0.9414712
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4635cc6775ac4bc4ef20f8205d3fec68	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	uncultured	0.9997059
1290670dde42b3b4f7a3c0ebeed87524	Chloroflexi	Anaerolineae	RBG-13-54-9	uncultured bacterium	uncultured bacterium	0.9629492
38c1f9ab3f899c765c722668ce11bf8a	Chloroflexi	Anaerolineae	RBG-13-54-9	uncultured bacterium	uncultured bacterium	0.8227669
c6549b8f914feb6d9735b21ee2078787	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.9863619
7a4af691bca65f86212b2dbdfbbcb4e0	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.7280933
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169800d3a8f698e77df6769fe332c7af	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.9031813
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1957e9c11acfd7c687d8be39f734fb8e	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.9231874
ae52afddd6fa5fb9e036e65ebfdaea4e	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.9676728
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47f4fe5c3218aaefa88ac0265f93a117	Chloroflexi	Anaerolineae	SBR1031	A4b	OLB13	0.9922891
862bc42a125998779219ade59319e78b	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.9999996
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f80b4940b639913680c263922e1edda3	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.9785117
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4fc44eddef3545ebdb97609fa011f062	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.942312
0c78d54155b17d02c4a78956aebed572	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.7730913
3cd58f92c22c1e38b19715d424a53244	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.9282877
aac91e2dfaa20d308cab40c52e3d409e	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.7011056
a26982ed4deb49436299eac7b0f13719	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.8959996
baab976edef9d09ce72f0e11d14356ac	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.7165269
01845e99c199fb253c60d156c77c8f1a	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.9894618
90d53e77a0bf27f55eb1a0534288863a	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured bacterium	0.9980399
568c150c9aa1afdf37c3b523705dea1f	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.7995749
0f1597888071d8b38224834c74490547	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9592283
899e9fc30a2a3e200df2b2902bad7236	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9997591
fbdedfcbc53fc40942a992b6f095c610	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9998906
be8cd6c8bce331c4251e9750d05292d9	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9921925
11edee9c081d89fd6a990e890370a86a	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.8237184
c42c7eb0631795ec86e94dd157694dbd	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.8756251
cdaf4751a41c3c5c68b90721299a0c90	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9530076
ca8e8c8fdd2f859c7ab8ef12b742d93c	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.920097
47fb2a93b05eacd33de3020affa86060	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.9956174
2d0f5a39d7975b7eeff410ff84ed20fe	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured soil bacterium	0.9225031
10506b11a4bac2c3877146ee2e07a05d	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured soil bacterium	0.9844819

97a7b9f6246f987e1b427a0b4f9043b4	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9999968
e9e59f2707814784bc0d62525205c893	Chloroflexi	Anaerolineae	SBR1031	A4b		0.999436
6f2c4d4d4d87416d0d1d856624873906	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9999966
1234cf012c7ba470c846990ec0d9b167	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9985413
c488e46f1d145dec12a4cce4cf04a5af	Chloroflexi	Anaerolineae	SBR1031	A4b		0.82915
28ecfb6ee5bcb47ad766403ecdcbb5b7	Chloroflexi	Anaerolineae	SBR1031	A4b		0.7463671
49ff82b823ea0ebfd80a8eae619a1711	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9911326
e4bd6f600b250b7b68633f818ed7e92f	Chloroflexi	Anaerolineae	SBR1031	A4b		0.730188
2a3c3b1f3f256c1d5b20cc7c51f0d634	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9999211
239fe3f94b1065ab3cc08ffe85c4cb90	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9936176
89e518bfb731f754bfb9b6cb8b20c2a4	Chloroflexi	Anaerolineae	SBR1031	A4b		0.8815711
3443a946876aa9c922d9c50c6963b782	Chloroflexi	Anaerolineae	SBR1031	A4b		0.8285125
16a2fe44025bdc4ecbe352368ae74d20	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9604455
55298b1081afbdd2112c9c4b5e8e7691	Chloroflexi	Anaerolineae	SBR1031	A4b		0.9891933
c83aecec26a1788d1f06a533ca2fe4ac	Chloroflexi	Anaerolineae	SBR1031	metagenome	metagenome	0.9999993
2c730dc9fb691fc3fcda699476e6503f	Chloroflexi	Anaerolineae	SBR1031	metagenome	metagenome	0.9720955
4d2f60e755cd030a10c3f6054e719cb2	Chloroflexi	Anaerolineae	SBR1031	metagenome	metagenome	0.7467336
6085483cca55aa81aab983f524953d8e	Chloroflexi	Anaerolineae	SBR1031	metagenome	metagenome	0.8647174
f8b09aa2a3a6c1d1e3c0448279b79042	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.927285
0b20367dc3b31f404ebe42d28c9f8ee7	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9682445
4751159d8b2b7a3af6e4000ff359ab5e	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9960556
a1ee08abbde4febecacb4b6e8965c711	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9035255
869383e9c0b26042e2c7b38632cd91db	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9999679
e8bc7754b0d78f3fc6f59ec7f2df721f	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.8990707
1ded3ca181cbf288fc5ded9487a43fc4	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9683276
70e847c33552fcbc5e9009665117d359	Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	uncultured bacterium	0.9231109
98d4b25ebbef4105c92b84193b75c42a	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9535436
aab285c4e608dda774dbe747cbaff732	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9999839
4779015380aff50982d3ab653b9bcd6f	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.7634134
15a0ea0b07df0ad179e0df478f07dc83	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9440408

556ee236f3fa817b9504f8debcfdede7	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.7854576
6b0c0aae5476c870b298969c20c6f6bc	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9994941
03cb5f2fd2fcc716a74a77934bd2d636	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9995468
3f7509ccc77d2ee249d8b1d187c62f8e	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9837415
766a8137bec5f1e8e572328db7ef7268	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.7016981
97c830155caeeff5786884b6f32f730d	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.9998657
1284f51b6ee13750d739478053ef7de0	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.8611196
136d26befe3fe2e91dbed196707e76a5	Chloroflexi	Anaerolineae	SBR1031	uncultured soil bacterium	uncultured soil bacterium	0.7289515
206e1c33da40dfdfaf2f1d4d91fd4e5b	Chloroflexi	Anaerolineae	SBR1031	wastewater metagenome	wastewater metagenome	0.968265
1abfd002e1cac900a13edcc864e30d1f	Chloroflexi	Anaerolineae	SBR1031	wastewater metagenome	wastewater metagenome	0.7381571
2b0487f05aff5a01e90192f438ddb372	Chloroflexi	Anaerolineae	SBR1031			0.9674557
9446b2f91904bbc524c69d58e25edf73	Chloroflexi	Anaerolineae	SBR1031			0.9955568
3feb3539d9f0a1e77b8eeb0ff8d27727	Chloroflexi	Anaerolineae	SBR1031			0.8752543
d90576a6de9fc7d993ab4b7a8d7edb8f	Chloroflexi	Anaerolineae	SBR1031			0.993059
6b84c87c4c1f659ccac740bd6bdded57	Chloroflexi	Anaerolineae				0.9468639
7efe66d5685109893da085cf9e35df01	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	Candidatus Chloroploca	0.938919
eab017d9066bfef763ed1a4a6b62cfe3	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	Candidatus Chloroploca	0.9296938
19249332d8a7a57eccacd945db020575	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	Candidatus Chloroploca	0.9337293
a012ab2b87713cf3e8c9d705e87434c8	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	Candidatus Chloroploca	0.9995958
6631126838cb98ec2800beebac288be4	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	FFCH7168	0.9997684
bc46ccb9d506482fcd4dd3050bc4ab4f	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae		0.9985988
85e600c70874ff6ee9f7728967075674	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon	0.8738802
4c4f26de6f86a581df2582441675e24a	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon	0.9418332
465529781648a1aa9d70c9cd564356d4	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon	0.9999958
28c695bf00589f05d01812c28de8e76e	Chloroflexi	Chloroflexia	Chloroflexales	Herpetosiphonaceae	Herpetosiphon	0.9837431
03b2d709d676f9a3d9123ce648f91bcd	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9756834
6d96c1f1595f8aca90c4735dca89653d	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9466774
7be1aec38fa53c1388a73bef7642c161	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9959212

08cfc176d3fb079b5c285952780d60ec	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9972483
b3f406f163eaab28a7fbbdac20a6d03d	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9997064
d3ccd53c7825390a637468b2b3a54668	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9999997
27c14f5e1db4a0d6563fff04079273b9	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9120647
9dbfdd233f751f570901cc823f989f58	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9855173
26975930ded9411405eecc6b51d27734	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.7605795
d2a51f5984325efed7d8cb0fd55b6116	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	uncultured	0.9972409
5d52997561f49f62fa0d3a85c403b0a1	Chloroflexi	Chloroflexia	Kallotenuales	AKIW781	uncultured bacterium	0.8781867
277f2d9644d7a29c7c2cf2d89408cf19	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	uncultured bacterium	0.8099988
75de48aed253d360fdf934e5c6ba9840	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	uncultured bacterium	0.9998835
31d0e02fe7dea959901edd22ed875e11	Chloroflexi	Chloroflexia	Thermomicrobiales	AKYG1722	uncultured bacterium	0.8691504
358653c8ce0e7c1d8475afd42a10d238	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	metagenome	0.9473858
6c21bedfa10c3cac7e5d7cdcaa9a7777	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	metagenome	0.7125662
f1be300df01babcf1897e6103507179f	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	metagenome	0.9046485
b2a41deb1b1e720d0e16a3d9c33f7c38	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9999475
e84f141e50806d74f2e46162ed0c552f	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.7358075
d8598bd4995349ea6ea88e1a59cbe211	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9581613
b5a75ee30645cb947ad835d87d6cfa11	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9178248
d4bad34b58a761bbc81ab892e1c98021	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.7577535
6110c9636e4e563ac05833108a9fe60e	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9877519
923248831a8e803f26825c2d63c14806	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9946688
5b5fc41e4def55055e7e165fecdfc4f1	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9989055
ac803d472c9358ac07b5e6ecb0f7c0a9	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.8429051
24314e521e9a2d31b0b12954f43cdd9e	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.7561231
d7908dc6c0579582a988f385854ef9ea	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9926428
77da1d31adb235bcbb1ce6f1016bd1a7	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.9997408
0cc1ec2f2c99505b4a13e6917f97051b	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.8683375
7c1a9cbd620c9e19b03125f275f23416	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		0.9998176
5bcb07cbbd189b61fa15cb2833a2ce31	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		0.9941184
79b3b6c751c001ddeb49b14eb3cba615	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		0.9963696
0a6bfb8ab9fb9f91375f6aa3f41c8b61	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.987017

db0e4473672a468dd8ee9ca6aed1b83e	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.9999992
659dfaa4139ab68506c87e2ec192d4e6	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.9392425
5a48a9f38da8f975620c0b26820aa482	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.9976985
1d4f12fc5956ec762599e169befd6cbe	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.9552985
560859414b86c10a44c3ec7dc1b85c8e	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.8194451
6b2a83d37dc7fb15874799a975326bec	Chloroflexi	Dehalococcoidia	S085	uncultured bacterium	uncultured bacterium	0.9804735
e6633f62777f58f902a3cd0c50ea2b36	Chloroflexi	Dehalococcoidia	SAR202 clade	uncultured bacterium	uncultured bacterium	0.9463485
112ff08a9588eb4602901a4082290513	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9811401
980e3497839d16ad77ffede708c5497b	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9805633
d63e3ee111f0d41a61942a4d040b4d1a	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9987238
d488cf3858f9027aab1ce1f5a0f92091	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999316
cb5c3bee2fedf8c1be504fbcd06c0d2c	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9334587
1845147963cd510356415ead4dd51a54	Chloroflexi	Gitt-GS-136	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.737711
10ec46957e2deb10b791f6ae4ba994ee	Chloroflexi	JG30-KF-CM66	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9614239
f31ae34e64f8cd73ee6cb4179ff40266	Chloroflexi	JG30-KF-CM66	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9990296
6e3c17e666e9ea225da4cafafa2e47e3	Chloroflexi	JG30-KF-CM66	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7918855
203e2c1008a3e27919c4a1d5f8d14b09	Chloroflexi	JG30-KF-CM66	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.773155
3971e1cf77a6e587385acb27e7cc40a8	Chloroflexi	JG30-KF-CM66	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	0.9987024
a09866bd0a8a9eb09d730fff1bc63e7b	Chloroflexi	JG30-KF-CM66	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	0.9878125
9e425cadb3671f9bcc1986f6b1dd8d7a	Chloroflexi	JG30-KF-CM66	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	0.9589779
1cf585b9c88ac26a6016f8293bb95568	Chloroflexi	JG30-KF-CM66				0.8587587
8aaaa8d82e84f0578c2ed71c52346da9	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.987019
cfdaf415dbb3f3f62e4dd4ed4168aa89	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9936056
36bdece87e7773ea8d1356f21d5caa25	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7322443
b579a69b7c1f7201186e170872137da6	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9579497
9bc95c55fe902227e2a20785f2b93f25	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9921938
c39e15de7f8295ecfed0969cd53b2126	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9934874
582f4394a735cad73896520fdb2dc3de	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9982294

bffd6e7320d0aa746feb22974f1388eb	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9868822
25648685986d7c6c59055298cc1f672b	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8142927
0cc8d7b27904e0aa70657f6ffe144890	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8246713
96cb78b4e0ff3c2b00953987d32c6f9c	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8364145
dbcd6540c9df7bb310d55bb3d3350d2b	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9112835
214732244e8dee3386f41ad165f711da	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.948952
b2d56adc5bc2d8ac7ecd881523ba5f43	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9817245
0dc604ec0afb867721bec814b50999ae	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8396998
32dd60b013160e742b295c60b010be0f	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9295619
58ab4257cbdb7c2021a954410d08ff84	Chloroflexi	KD4-96	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	uncultured Chloroflexi bacterium	0.9072582
cf65e84b310d3ee6f0ba66e35acc93fb	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.9821684
6c9d0db73329b0e2aba443f37c8dd960	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.8584006
db09aecebfb20e1176fe07a736dadf2c	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.9768342
2a5d8998c0e8548285c05818513a88a7	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.9619334
f4ae778bd03ed3b2b9a2066f62c5172f	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.8835417
8413c208cd202bc5df988c40ecd48e0f	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.8704852
2bba80577889fbe78e867c6a21e90a24	Chloroflexi	Ktedonobacteria	C0119	uncultured bacterium	uncultured bacterium	0.9193725
5d0a8aa11fa36f25a991a3c4c36c7dfb	Chloroflexi	OLB14	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9762423
8fc741ae4b93c88527163b77fd80c4a8	Chloroflexi	OLB14	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9079034
a6a8ad96c9374e85f15b4bc1dec2c662	Chloroflexi	OLB14	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9931461
117b512d767ae270dd4d244965b855e8	Chloroflexi	OLB14	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7530278
71a5753d4ed729be6a99181a1a8b2af3	Chloroflexi	OLB14	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9923596
f798d7c74da01177a5a0740d3f811d88	Chloroflexi	OLB14				0.9374627
4240cbdefb886ef8e0b16e50862861b4	Chloroflexi	TK10	metagenome	metagenome	metagenome	0.9426228
85b30e8129e162e37f17dcf6f835caf1	Chloroflexi	TK10	metagenome	metagenome	metagenome	0.9998254
5fa0ee1758403a8cc21cc38a5a1021cf	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8288547
4443296b5cbb3ee846e7cf4256e7cf9b	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9998897
6db6524d57e9c4ea840d7626a3e0b893	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8767448
ed747edf937dcda2641f02af3683ea7a	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9934391
98bea40298289d741ed9313473bca7ac	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8370138

40235c357bb85cef927162c89c4c1c62	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9932568
c678a9d231f5168b51b105f6d82d72cc	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8939286
8b49e37e3c87b34b3cf8fa98e87b9e56	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9749865
e8c2f46cc66e411d4e3449f2115b9a26	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9986632
1a0db85f8cd3acf8f51934e333fb073d	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8628367
0482d026ded9fcdb059fc22bd533d5a2	Chloroflexi	TK10	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8102539
7455e6194aea7e49be7d1ba815429968	Chloroflexi	TK10				0.9919668
05244bb385efa9f7ca304f011ab59ddd	Cyanobacteria	Melainabacteria	Obscuribacterales	metagenome	metagenome	0.9106877
8232bf1c5ba53cb969f190bab044e49c	Cyanobacteria	Melainabacteria	Obscuribacterales	uncultured bacterium	uncultured bacterium	0.8246022
0b95de0e43a3e4c87341ce6625c37107	Cyanobacteria	Melainabacteria	Obscuribacterales	uncultured bacterium	uncultured bacterium	0.7240291
a697c575aa674cf1c483cb803507426c	Cyanobacteria	Melainabacteria	Obscuribacterales	uncultured bacterium	uncultured bacterium	0.8673497
49e5db0cd88c44dea715cb58d76a8382	Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured rhodophyte	uncultured rhodophyte	0.9147995
f1212845293be73b88dc58e1c449b027	Cyanobacteria	Oxyphotobacteria	Chloroplast	Virgulinella fragilis	Virgulinella fragilis	0.9895966
cd65a72253c3003d9b9bfbba6a7b1618	Cyanobacteria	Oxyphotobacteria	Chloroplast			0.7104991
7911816f5e81f650f769aba0d5c708cb	Cyanobacteria	Oxyphotobacteria	Chloroplast			0.9984239
a7a95741e067e16bb997ca28e2aec879	Cyanobacteria	Sericytochromatia	metagenome	metagenome	metagenome	0.9299346
c313546707d7360a4b412406c8afe5d3	Cyanobacteria	Sericytochromatia	metagenome	metagenome	metagenome	0.9129743
514deb1294de0a7d421cc444d93f533b	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9991681
fd7873dd1761be8d94a32b7eb2f75d16	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9742479
65b6d9cd9cbc23b2c2ae60da203fb6ba	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9533563
30a8a9fbeb4a6e09fa542ef3b744ce11	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999752
426e6dbcaa7d82da0499975943909460	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9998496
f9ecc1982e42debf950b2c434bd1198f	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9299573
aa052466a45eadff3708d1704aa64ec8	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7800459
5d5342817478609e084f225ca389089c	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9888946
c0014b9aefdc5e6ec2ed8c0bdc702925	Cyanobacteria	Sericytochromatia	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9814733
498fad6f3c3814c46c48fbf080ae521d	Cyanobacteria	Sericytochromatia				0.9984748
331f60e039fc2803a4a80ee39c065ca3	Cyanobacteria	Sericytochromatia				0.9676592
5a9829dba02745b6cdea944d2aed2968	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera	0.9546421
1c21ae20343c91f94860cf738bf1437b	Dependentiae	Babeliae	Babeliales	Babeliaceae	uncultured bacterium	0.9782735

9edf586025e90b397c5ba2af74edaa71	Dependentiae	Babeliae	Babeliales	UBA12409	uncultured bacterium	0.9351347
9c38e01be35dc87656d6504a253c8364	Dependentiae	Babeliae	Babeliales	uncultured bacterium	uncultured bacterium	0.7457595
5f6ff87e781e0881f8c963ddd084f5a0	Dependentiae	Babeliae	Babeliales	Vermiphilaceae	metagenome	0.9926402
2032b96f74eed68a09b4fa9d195c9aa7	Dependentiae	Babeliae	Babeliales	Vermiphilaceae	uncultured bacterium	0.960113
a50b1c39b588f442eba3172ed1e02eb4	Dependentiae	Babeliae	Babeliales	Vermiphilaceae	uncultured bacterium	0.9978527
c58a2959e3768e54afc2fd3e5b7666e2	Dependentiae	Babeliae	Babeliales	Vermiphilaceae	uncultured bacterium	0.8445655
b7ad1c99fa90fab1498b85f4a82e35ca	Dependentiae	Babeliae	Babeliales	Vermiphilaceae		0.9912983
b101a5ba23c86c4e040a27b7bc916af6	Dependentiae	Babeliae	Babeliales	Vermiphilaceae		0.9999531
9ae5ac30a77f54d542288d57a6f194a7	Dependentiae	Babeliae	Babeliales	Vermiphilaceae		0.8723393
478f3e25c5b11f8e14f2e484c88712db	Dependentiae	Babeliae	Babeliales	Vermiphilaceae		0.8927433
de71223e7d1380d393010aff9860b3e4	Dependentiae	Babeliae	Babeliales			0.963575
d4ed868de86969d3cbfb7861fac8f1e3	Dependentiae	Babeliae	Babeliales			0.9986414
d5b4757d11e37b8b09b78e5d458e548f	Dependentiae	Babeliae	Babeliales			0.9957005
6b363e17654d24efd74adb6d9fb89bfd	Elusimicrobia	Elusimicrobia	Lineage IV	uncultured bacterium	uncultured bacterium	0.9957188
4bce85d76ddfdd2fb2381b9ef8ff9ff3	Elusimicrobia	Elusimicrobia	Lineage IV	uncultured bacterium	uncultured bacterium	0.9990764
68ccc41d90b73126badb7e31f05f38ac	Elusimicrobia	Elusimicrobia	MVP-88	uncultured bacterium	uncultured bacterium	0.999944
fa0fbb67ae81ee3d6c40c72a5ef7e82d	Elusimicrobia	Elusimicrobia	MVP-88	uncultured bacterium	uncultured bacterium	0.7496914
d23ac7aceabd2203a0aab602674c04c0	Elusimicrobia	Lineage IIa	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9984967
2cd6f17f618b3d74d2cb7e69c90b480f	Elusimicrobia	Lineage IIa	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8100741
1977edd421ed3250ad3af793b892aec4	Elusimicrobia	Lineage IIa	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8638595
76e6b9060de420cbf4cc2a047cd97013	Elusimicrobia	Lineage IIa	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9401685
da02828e2119768a4d2d17d15c90fb57	Elusimicrobia	Lineage IIa	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8498946
524d41108c50198a654864345782d24c	Elusimicrobia	Lineage IIa				0.9999409
fb994548844e464cd4e0ee2fbbb6e0c6	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9974277
8ec5214dfddca9b6081e4772809b5ac1	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8441519
f42edc033031fdf45306be2eef8f2f3a	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9944578
db6f30809c543038ea21b418f7274fd6	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8566925
8c11f7978898d5d36331a4fdcb3241bb	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9478067
075389283f8260b6a31c23f5eada67de	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999084
06092dde56e99e184d17d00385c0acd2	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9996054
a1e90c9656ad199ffcaa3a6c9f18afb9	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.80542

ff69709624c6b612e008ca21d0d48477	Elusimicrobia	Lineage IIb	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.895768
850929696009bfbaeb74f4f68f74c161	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.9998517
7d8deb60b09e33f29185603c7f59267a	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.9997647
84a8d5b2d6ec9307f0acafdfd5a023f9	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.9040542
d9947ee3ee3e4f5e0b639a9e5289a80c	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.9983692
750732f0c019bd508aa28712fe687b0b	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.9347961
5d461854cb85eb9e4f841027a1964236	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	uncultured bacterium	0.9999991
31f6bf08aba82b3789b3d423c8263d35	Euryarchaeota	Thermoplasmata	Marine Group II	uncultured archaeon	uncultured archaeon	0.9652099
cfbbf3ba7281dc4603525c562e10d508	Euryarchaeota	Thermoplasmata	Marine Group II	uncultured archaeon	uncultured archaeon	0.9744527
e8bbbf019a91b7e9752768c21b5f1e65	Euryarchaeota	Thermoplasmata	Marine Group II			0.9925101
0089c64a706c99a0c1e2ae85bb84382c	FBP	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9906862
d89a8ee718ffd0865a529db6448d5cb1	FBP	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9337104
4d0f83c489fe7e60aa1653e1221ea8c5	FBP	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	0.7314816
6564cfb915b0f0019e6996489715b64c	FBP	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	0.9297096
7eef654b39a956677039f6e8cfba9f7f	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.8960334
76a0a5dca6892ad6664ede7b6376ad55	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.8604517
964f345aa73bd1f5d6a6e27398098261	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.9999996
08e3afea5ca22a6e7a83dafc0c5a22a1	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.9999839
50e38e093467db77e25a1d54d38c9414	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.9958544
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b1f67f024db0bca893aaf0a81ff013e0	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.8134144
f81b9ca9dee5cb51c7b0a1a7de657cd4	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.8947457
14bbad56a53b35d6b78e67d9544c9ade	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.9176381
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5d62a115a6080afb2bc3d37d729aea72	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.8922662
3b7a8abb8c9e79d8a9279bc340d382a3	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.7598313
34f767132d46e8366ddb0d73de9d9e25	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.9998398
93f8d28139be91da38fc73f86f32b5c2	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	0.7491597
d746d67afb3018f615c290203c9523b1	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus	0.9893845

83661624915dc313386333b36e2146f4	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus	0.8782238
c55df6cd40166d06b25d3a327bfb9dd4	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus	0.9996894
90af6ea2ff9602e8700d7ce624d08164	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Tumebacillus	0.9957792
7d88cb85b80e0024b54a61e7a6da3bf0	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.861905
83e948f389f9d97b0c975afc880989e8	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.8455194
bdf8a26094624622d68509a87fa75ba7	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.9944125
26005dfb7ad2e8cdbb139846af329663	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.9154354
e9b70570f6e642a8721db4312e0b2763	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.9999804
ad4cba5280fb47cbebea01e7031af61c	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	0.8501769
25fe23e989514e818f4bc1f680ad6da1	Firmicutes	Bacilli	Bacillales	Family XII	Exiguobacterium	0.9722176
d79cccd83fbc9154ad7e4dfd3cbf2e75	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Ammoniphilus	0.9999993
70eae3f0af7c1ad7350c1a3189b6766b	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.9732203
b5d0821c7524008340ea6afd6e5a15d5	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.8827702
8091dbdd5a2c2e3b93f49fa03eb13433	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.9964224
8281b52dfbde95b71865fd7fab8ffc20	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.9768373
9f04d4582c00cc1372a4a536aaa64d65	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	0.9284155
77e8c011ba49812b2d8c2085785afe8a	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina	0.7890631
295b4fc52bbe62488fad64135cf9b995	Firmicutes	Bacilli	Bacillales	Planococcaceae		0.7070127
a3898f84eed2d7c59a9d18efba21d2cb	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	Kroppenstedtia	0.966618
2134d6bc753b919665382b03869f155c	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	Novibacillus	0.9907894
c475b7d0a0ea94c4fc5e7f2f4190de5b	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	Planifilum	0.9955602
fd1098cd571337c869bc804919b0f630	Firmicutes	Bacilli	Bacillales			0.7907019
1763dbd2ac5b6c96acebc480d8bcc4a2	Firmicutes	Bacilli	Bacillales			0.9795947
4083b7c2ab82927b37378ab6df413f9d	Firmicutes	Clostridia	Clostridiales	Clostridiaceae 1	Clostridium sensu stricto 1	0.9973034
d8147479a31fc5a28e4f606c34ce2627	Firmicutes	Clostridia	Clostridiales	Clostridiaceae 1	Clostridium sensu stricto 13	0.990655
1a4f8fdcd62393f7bb42c420906015cc	Firmicutes	Clostridia	Clostridiales	Clostridiaceae 1	Clostridium sensu stricto 3	0.8342184
f29b098a073a46c72bd36f8dceb54798	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae	Gracilibacter	0.968898
bdb904685433e5c698a6596abf15f3a5	Firmicutes	Clostridia	Clostridiales	Heliobacteriaceae	Hydrogenispora	0.9999999
7d0d1128850e28ffeb3067dabecee9ba	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae		0.98759
ef6210f9cbec27ef76e5f08bcff84e48	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Paraclostridium	0.9961695

b6d8f4e790858dc122499a6d7d14567a	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Anaerosinus	0.7203046
55029eb3203db2aeed060a861b60f60f	Firmicutes					0.8145281
d3150e6b8394a1d01fe87f2bb1fba050	Gemmatimonadetes	AKAU4049	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9737989
f9c97adffa7ac976f53976a689e9885c	Gemmatimonadetes	AKAU4049	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9957276
d763ea326cee9cf5ef9e9e5f23687112	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.8878217
6191f3fd089658b8c0d51d6460481f71	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.8677699
5534202fd5edd1319865b6bac7603c84	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.8454239
133d2c4f26c58f8ba5669efb7a0d7c87	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.9998723
629251956186124b2d4411d62301a61b	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.7448131
0d0e8586c6af61fb6dc02feab9d98e17	Gemmatimonadetes	BD2-11 terrestrial group	metagenome	metagenome	metagenome	0.7292647
9fc993e631c99d1c5f02b1aa0d5702af	Gemmatimonadetes	BD2-11 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9523141
d86d7c14ce5223fca6c27264da4392f4	Gemmatimonadetes	BD2-11 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9660431
ad0ae13c06b27a514a194e72535a3c28	Gemmatimonadetes	BD2-11 terrestrial group	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	0.7570304
97e6ddd756ab1922a397f0f1bd8157ca	Gemmatimonadetes	BD2-11 terrestrial group	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	0.8205075
fe03ebbad5801eb8a0df15d1820edbb6	Gemmatimonadetes	BD2-11 terrestrial group	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	0.7892328
910bed6fbcaeb795569ea53db319bf05	Gemmatimonadetes	BD2-11 terrestrial group	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	0.9714017
93c9fb56479fdeab47d4f5a2bbd652bf	Gemmatimonadetes	BD2-11 terrestrial group	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	0.8537339
9d4cba2f1c79ac198a697d0da96bedd9	Gemmatimonadetes	BD2-11 terrestrial group	uncultured soil bacterium	uncultured soil bacterium	uncultured soil bacterium	0.7645174
91f658cd8db900d0f52f570bc2a2e95e	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.9509421
2ba7c6c11a74c57f9cc6e605a95160b3	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.9999194
dad7efbb3d538972f9974a88ffb3e064	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.8418971
5995dded96d941ae9d71d27494a28a9b	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas	0.9690495
7470c0b2985a3554663ba20290a98e1f	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9964592
89e20d04310c7fc5eb6a8c3f8d065d4a	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.7431093
6864292234931b89e9c4e8a1a1ffe250	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9588406

1e41fd1927dc5d8754b0f3d8d77bf60b	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9427388
c4802bcb41820984125be513362920c8	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9871551
4b1ebe0ffa937bdd5bc956a43116efcd	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9991321
53aad8b96133a70c5422baba7cc21aca	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9998219
772f2cbffdea1af524bae25a97da2380	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9537336
717b3849b1e71f76e5cc6276c176430b	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.999684
85498157e1903a4b33ab0c96c1ff4e11	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9579898
56a9efd16fd60e131688c58977c16e8b	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9691469
a1fd4ccb126657836ad68b541d41e421	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.871855
1ba88e448032b8389f537bd7ca21ed7f	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9609403
7470aa288f38596d297d1bb272976354	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9981796
75c27a4cf562485367383dce2865bbd8	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9241072
e3b59aaff00d632db524ccf1aba30069	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.8819726
7dca8966c5bd1ffb4aeb4f44bd68586f	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9985125
feca81a7fe343c148a92304ce19b0084	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9773281
2a1e1aaa1f226c26ec65fe4f49d654c1	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9996196
9b3ee17f02daecf4b2b2dbb06056c930	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9867804
63614a9c783518a4fe86b741c64f8a43	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9378664
a2e2234d0c2e68f66d2146e031782589	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.9987368
fcb44a5cdcd7b1aca552aebbc386d9b9	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	metagenome	0.9663378
cdc72a808d7b019c5dcdfa31afddc317	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.7808153
bd9c1b669bcd3a0207acb00e8a6e3d54	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.9993633
1b9bc8ecf96dbfc09c6b508545ef4271	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.9985391
ca3a8c023d8c6f3f700ae70190875f4f	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.9495741
0e18a6bc90dceab51ae4e0dc0e0ff6d5	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.7854357
ece6d96c54505a21e515ac418d9c2125	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.9951885
87f76a945b7961833b9917007959a3df	Gemmatimonadetes	S0134 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.999737
12685c5c242962f0158f7f5098b40221	Gemmatimonadetes	S0134 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9617873
b2d868ee8026b7db5104c98b0c42defe	Gemmatimonadetes	S0134 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9692035
4e25c60b3feeb8a9a5d6fd2ee12fdf4f	Gemmatimonadetes	S0134 terrestrial group	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9964723
e36bb4268ac52a9f32b836f53f3ccd7e	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	metagenome	0.9121076

6ef2bd1bc2936843782163d4261ac7cf	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	uncultured bacterium	0.99635
4a6e637cb215e7c82c7516aaa763d94a	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	uncultured bacterium	0.9677133
048bc41210b42c401e6ce57cb9124a43	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	uncultured bacterium	0.974898
aecaf6424447f5d7aee16c670b92a3d6	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae	uncultured bacterium	0.8496497
4d2d08ec423bece5f7ee8e0b5b8f0a7d	Hydrogenedentes	Hydrogenedentia	Hydrogenedentiales	Hydrogenedensaceae		0.9995846
92db3e30fa077eb88fa9ca80903bb7ef	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.9932413
9233b698ddf03c2a407576841e9794c1	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.7116017
867f62cefe09804d0b803cc3d30d2d09	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.96667
a12aee5c389ca6a135cd6f748b4c4b43	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.8401024
e430265371da3790a6b8a544e660bba2	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.9750111
a22c544ea39f71cc02cb01365c1fdf71	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	0.9777148
f1cdcfa07eb5fb27178178650b5c9b7e	Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae		0.8751344
5a70f90b9f368a5a457c6e71ef4cd0d7	Latescibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9964206
aeb6bbaaf2a9a122dffd8bb22e4a0362	Latescibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9991932
45bdd24b81b9a4ed791efe55f698a230	Latescibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9968938
5e7e7af7a604d31b88358e98bea45991	Latescibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8186633
7db0fe087f5e3cf2518b05c7b1ef4f06	Latescibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.86076
2a24ba26332e5e380405bed040506eee	Latescibacteria	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	0.7515643
770f6d40306b14f30101bf45337bdecb	Latescibacteria	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	uncultured Latescibacteria bacterium	0.9999858
a72b76f7636ab3ba68a151c6bf450121	Latescibacteria	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	0.7571314
ba1999fb0e906b50ff35aad339b35b9a	Latescibacteria	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	0.9997976
f344c3f60ac05a695b5a911e506bb1c2	Latescibacteria	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	uncultured Pelobacter sp.	0.9917363
240cb198d85c29eec395af1ec1f55fea	Latescibacteria					0.9988552
1e14fad3befec76b8c22dcf0422f57e5	Latescibacteria					0.8415462
40a76f2b2c15a89a9747c612f3d3607f	Latescibacteria					0.8931682
1cdeee9229d1e79749df3aa6f8b3c9cc	Lentisphaerae	Oligosphaeria	SS1-B-02-17	uncultured bacterium	uncultured bacterium	0.9727266
4c687e9abe11199b993e2ab668384d5c	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.9999081
49f375fede0ed446a93d78b44b509d2f	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.9999997

d03b56bc04454a6e25c7a5f5613bd818	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.9625044
e4bf762a482b91fa74906919d19054a4	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.8592356
320ff3c16dbe3990acc5be779a159e51	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.9296651
f0e2f066b40af6b9116c22dad5a54c13	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.9190318
3289bf742c0d3dda50dd7887639ac63b	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.8795517
dba5c048a47e252d5557efaaef56efdc	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.995408
0ac5e2e931f0d753129b5ab826493c4a	Omnitrophicaeota	Omnitrophia	Omnitrophales	Omnitrophaceae	Candidatus Omnitrophus	0.9817474
a087a43be79298d6fe27a01522b60b22	Omnitrophicaeota	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8282016
947ac0ff561580ce32b1c7795a2a6a5c	Omnitrophicaeota	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9788775
ed0198e6c51111a9a518048a0242007b	Omnitrophicaeota	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9832231
1274934c30e867990c3776aee754c339	Patescibacteria	ABY1	Candidatus Magasanikbacteria	uncultured bacterium	uncultured bacterium	0.9519368
9b7f16086c482f617b8a9b9172847c85	Patescibacteria	ABY1	Candidatus Magasanikbacteria	uncultured bacterium	uncultured bacterium	0.9999803
52c3562b3978c4a6801d4145c0e678b7	Patescibacteria	ABY1	Candidatus Magasanikbacteria	uncultured bacterium	uncultured bacterium	0.9663577
3aa566463a9c32d72000b921001dc2c2	Patescibacteria	ABY1	Candidatus Magasanikbacteria	uncultured bacterium	uncultured bacterium	0.9995717
85cf7b4083440cb78f7084dd86f23319	Patescibacteria	ABY1	Candidatus Uhrbacteria	uncultured bacterium	uncultured bacterium	0.9999996
cdee81654e3e901a7babfdf150489a0b	Patescibacteria	Berkelbacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.915015
6fdae826c8c33e78d9162902ca5fe42b	Patescibacteria	Berkelbacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9040655
6146035edc255969a227e19a5eca0387	Patescibacteria	Berkelbacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999824
8130a99ae0ca2d6295862ae018e74077	Patescibacteria	Gracilibacteria	Absconditabacteriales (SR1)	uncultured bacterium	uncultured bacterium	0.7880733
b908844466f157f7564955ae5522395b	Patescibacteria	Gracilibacteria	Absconditabacteriales (SR1)			0.9998511
becbd09e60b8247e6f7442be53a8ff37	Patescibacteria	Gracilibacteria	Candidatus Peregrinibacteria	metagenome	metagenome	0.9875702
a70957d1e85a96f69b7d68555f86f5a3	Patescibacteria	Gracilibacteria	Candidatus Peregrinibacteria	metagenome	metagenome	0.9289567
f9a7519a76b1186878c9420ee9ea328b	Patescibacteria	Gracilibacteria	Candidatus Peribacteria	uncultured bacterium	uncultured bacterium	0.9999254
c6d3be4a653f60cf0d1b02c8e8f1067d	Patescibacteria	Gracilibacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9410559
b24bfe18f8bace41a5268d1aa29cbdd3	Patescibacteria	Gracilibacteria	wastewater metagenome	wastewater metagenome	wastewater metagenome	0.8181643
fca91d31374e4cb1eb5bfe5d3e8413fc	Patescibacteria	Microgenomatia	Candidatus Woesebacteria	uncultured Microgenomates group bacterium	uncultured Microgenomates group bacterium	0.8881629
11c279cbf97b5d37895e2a71c0118b1b	Patescibacteria	Parcubacteria	Candidatus Azambacteria	uncultured bacterium	uncultured bacterium	0.996929

263c1a4f8bfb6c916318c0022de2a7e8	Patescibacteria	Parcubacteria	Candidatus Azambacteria	uncultured bacterium	uncultured bacterium	0.9737393
65c0d7ed212b35797e66f84c60b5b24b	Patescibacteria	Parcubacteria	Candidatus Azambacteria	uncultured bacterium	uncultured bacterium	0.9305271
54abec405d0fd81280c0af93d6feb43f	Patescibacteria	Parcubacteria	Candidatus Doudnabacteria	uncultured bacterium	uncultured bacterium	0.9848012
d897007412277148eb37999860abcc53	Patescibacteria	Parcubacteria	Candidatus Yanofskybacteria	uncultured bacterium	uncultured bacterium	0.8062113
7d1173cd5f0d05654c356616bb8cf693	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8225924
1729e93018d6a831d18bc3da3be6839e	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9468281
8cb707c5bd1b7d0ea1be4cb307ccec35	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9043937
4964bffad918c6125e2b0a7039142768	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8794201
c937bea79328266c05166c562fde7c96	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9799538
c4d78737a90afe3d04edfc3255ac2361	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999604
9fdbed90f58a5ddf43a19eff4d1f9a01	Patescibacteria	Parcubacteria	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999905
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36278cf6888724bb7d7b836816aac85f	Patescibacteria	Parcubacteria				0.9943287
f072a764fb6fed1bc28cda3e79b6f3ed	Patescibacteria	Parcubacteria				0.9999439
94a91d88a99226792eb8c3c34638227e	Patescibacteria	Parcubacteria				0.7534344
4bad82bb96b226ca89047b09078ad84a	Patescibacteria	Parcubacteria				0.9820103
43adaea62852219260585b202ad85e49	Patescibacteria	Parcubacteria				0.9918629
755c880b2a8c0b96e8f5ddc799fbe286	Patescibacteria	Parcubacteria				0.984094
0b4657e8c7685e558ed8541f2337da1e	Patescibacteria	Saccharimonadia	Saccharimonadales	uncultured soil bacterium	uncultured soil bacterium	0.9999994
f3ae1da67eacb9be74ab33afe15731a7	Patescibacteria	Saccharimonadia	Saccharimonadales	uncultured soil bacterium	uncultured soil bacterium	0.9655215
800fad52ba89c922b3f94df3a846a6c0	Patescibacteria	Saccharimonadia	Saccharimonadales			0.9328465
c00e03bce000f5a7e2d35110c2ca5b71	Patescibacteria	Saccharimonadia	Saccharimonadales			0.9916186
5ea9b25e6f5cc9e915bce9cc1fe0d86c	Patescibacteria	uncultured	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9971502
257df219e67f9021dcb49ab40a601772	Planctomycetes	OM190	metagenome	metagenome	metagenome	0.9997759
37db27274d1534b5ff701cfe737c1803	Planctomycetes	OM190	metagenome	metagenome	metagenome	0.9888429
59915850ecc67e5aaacdcaf96c04ea03	Planctomycetes	OM190	metagenome	metagenome	metagenome	0.9999998
369d7a3d5d1bed10e8d756c6a5691b1b	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8432514
bbee411695b8f23df77794dde524a070	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9549015
64daff1e5b6f45a9003b6c1752298150	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9090396
1ccd81b882efc7b0bf8a4769f88b9d9a	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8499155

4d55d05ea287212226b7966224136453	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9770251
7cad4489002a9dc9c7a985711052bd19	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8410429
34aebfbe99e0dac3f9e12a1b25ac91b6	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8226105
e5a8313329c6761ee1d20547d38aa1dc	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7284701
2716723ef97aee656ee8c05fdefed0cb	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.997281
5b05457a1d894beb0f6546e0785943e9	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9996919
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5e2ed3673277435aa9eec447b27617d1	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9998061
60f87573453e614875560b08c9bd26b0	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9821629
610b296c4bf98fc3c6fa1c59413939a1	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9734626
c5f9563ca074dc876a98a92169d1829c	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999089
65f50d067782cb049864029211fe6b76	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999997
dedfeaa11821ed2a5852692338d696ad	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.856322
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56d54ba1b9bc0942561fe254ae95975b	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7548757
a42a0d2bedbe21efc498e8781c8bafa6	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.999871
02a1fdac859e75c4137bd150ee585362	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9631924
ef8471af916f51d8c5768ab0103b74e4	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9956219
928257c53baccf384cdc22f39d4d473d	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999435
f10908b9820bb834ca72bd94e2124939	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.8217967
023f80aa6a8adc49a5890cd3a9a2ccb3	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7253827
7d14078031a159ee086f916fc5fc19f1	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9794045
aee1f5a59f963946ee96b206766adc93	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9928591
693c515f8ec76e7b7a9bc165c76d3e69	Planctomycetes	OM190	uncultured microorganism	uncultured microorganism	uncultured microorganism	0.8563749
c28adf165260f37cbb807f3cd053becd	Planctomycetes	OM190	uncultured Planctomycetales bacterium	uncultured Planctomycetales bacterium	uncultured Planctomycetales bacterium	0.9907208
b50bd7a9349ab54eb233e5ec0c496319	Planctomycetes	OM190	uncultured planctomycete	uncultured planctomycete	uncultured planctomycete	0.9368826
b42ab8d3a383dde596bdff7be38257e8	Planctomycetes	OM190	wastewater metagenome	wastewater metagenome	wastewater metagenome	0.7233306
939a8228d5bab5f9c136a37a7a8ddcd4	Planctomycetes	OM190	wastewater metagenome	wastewater metagenome	wastewater metagenome	0.8587882
a15a8d44040b8373572b5da426ed914c	Planctomycetes	OM190				0.9667472

81e4c91b52a983585db1bed912aee7a8	Planctomycetes	OM190				0.9682662
42ffe15bd27ceedb37ed5547b11bea38	Planctomycetes	OM190				0.8416504
e8a83ef47f5d1e4cd8e3efc7db82bab9	Planctomycetes	OM190				0.9372969
b226c18a4141aab3db0876e0f9aa765e	Planctomycetes	OM190				0.9999817
59c479c64fa7c29dab851363b0343a8e	Planctomycetes	OM190				0.8226264
c404718e2bd915327438ec63f3d8ac2e	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	AKYG587	0.9929544
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71738d4cdf79de18607734c961bd09b6	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	SM1A02	0.9993442
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46ab7d3435738705a65caea2777abf34	Planctomycetes	Phycisphaerae	S-70	uncultured bacterium	uncultured bacterium	0.9683857
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13d1cfc4d9e9e4ecf14df5181107cac7	Planctomycetes	Phycisphaerae	Tepidisphaerales	uncultured Planctomycetales bacterium	uncultured Planctomycetales bacterium	0.781846

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9833abc0d78b49fb15ffa77c4e651242	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.907549
1b52b99711650b202fb1730322860f0b	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.7275211
32f306fe2b1e4bd7feec9a26ec4f4cd0	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.7605503
6535e9ba0170aa1887d0426dca67c6ef	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.9684613
8ef26d8df1349ad526ea283bc14144dc	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.9892664
e59b24d992f653658aaccc1c4f3c3174	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pir4 lineage	0.9993826
00719cbe864d173ec2a221b09796dd9c	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9991736
9beadfb4b51f2318844cf228459dc9a7	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9539975
c394ebce70c6329f57134b3e88f94f26	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9999723
ff3198ba694f132175b53c66bc189b17	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9971319
07525d8b6db4f71e15746b9fe58f1c21	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.8038246
aca3f4001070fb0604d1a7dfb4b877c5	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9108222
ba1ec6062ff9a13cbdbc758452d8ebee	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.7279311
c9282e30c804d5bba4d401b0cd3651e0	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.7515837
76cb225b455ad99fb8ff065f8efe4e05	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.8024139
79bcac3acb05547d1ebb1def99bb972f	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.7570505
7109361011fd31892490d425b0218852	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.8348083
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93e3ca341ebc6b79571ca8fea5abf671	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.8676108
e583a6322876ce1206f953353e2675a6	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.9343265
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71e5e8a3f253eb09b97dc991f02b7b51	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.920686
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a8854fc9a325c7e54a9caa4480217ccc	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Rhodopirellula	0.9769379
2249d5bdc5de72a95bb98cd0b47838f2	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Rhodopirellula	0.7837282
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3b71f57bb92c50b2397cb3fc5443c9c7	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Rhodopirellula	0.7431676
e795e6320527bdda6cf73297e7fd75cd	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	uncultured	0.9517851
51b28e8efcec063c9f7299fbfb3bb43b	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	uncultured	0.9363646
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013a93b86b97d99f0546aa9d767eeed0	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae		0.9993697
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8feb7349b9627e920f2130f96ec5be33	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae		0.9592442
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8d14df5ce8ea21e46633a1f51708a4dd	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	Planctomicrobium	0.9692185
919250877ef03c315730c7b4df29795c	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.7455568
dcada3dab45da4a886fa9f9951f85388	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.8507259
3d254eae6330c3af118ad55d15587525	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.8852922
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929e8450daa3418e6311c0a70f6aae0c	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.9108203
686f03da5e8e525f57e34baeb0101f63	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.8685112
872c53931d63b9d2383382d800bbb467	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.9940859
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ddcbac686a3b8cf283f16c94358545ec	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.9874085
0668e8d95b17b10cf40e28029cbd04d4	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	SH-PL14	0.7581434
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0ade20498a5f6bbe7df3683610166bb4	Planctomycetes	Planctomycetacia	Planctomycetales	Rubinisphaeraceae	uncultured	0.9093836
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3554a67983718506aec741cf5f5c4ac1	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	metagenome	0.9696722
e075269fffd3522b91d34135e1076a2d	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	metagenome	0.971542
e27c3062c3ebfd305447410c7c7ca1ea	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.7708866

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bc7537620a3659626b9b26cd03b9b3f3	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.9260433
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9f68b2119a7c9519fd1c06fb7b010f17	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.9993831
b166affe9c69a63660c21211b72251b6	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.9549694
266682b8e1c660f4afa3e859e49d52d7	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.9999923
68272991438b211c4b9f653c55a25651	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured planctomycete	0.9999733
5521e8f3ea8551e31c7decca2e27714e	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured		0.8918738
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d318bdf9671b16967d5ea5137d5c1d86	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured		0.9606513
7f42070ef49d3f8527aa5ab8d1322fef	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured		0.9979635
53bad4fb84c65f7ef987cdb65ecd30cd	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured		0.9980415
8d6807d98572bcae2ca1e01f5c48899c	Planctomycetes	Planctomycetacia	Planctomycetales			0.8243765
edb7ef516e4462daa9aba8fd10e617fe	Planctomycetes	Planctomycetacia	Planctomycetales			0.9880486
8de5a5c5b2383912fd97e26fedf51ddc	Planctomycetes	Planctomycetacia	uncultured	uncultured bacterium	uncultured bacterium	0.9048097
374d1d91c9d7e3b242c40a3e60d5c1ca	Planctomycetes	vadinHA49	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9277698
79751a67a635bc0084b12dbb618a95af	Planctomycetes					0.9104507
7a8122cc6b81cfca7101d7ec0df4a194	Planctomycetes					0.9999275
8f79b861569d02d195045aa966e18d77	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas	0.7851997
ca062221b62b696374ab9857e0e08144	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.902501
d1f677a61cd89adfff6327a4518e5880	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.7837966
c43ccad8f58430e360c76332e20e3172	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.8831013
0fa9b44d52836d2f173f4ac532f8a013	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.8568446
0a023b056a85b92a1ca8214e78a9c45a	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.9917548
3f16b1327105d19bca9cde53b9f60197	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.9537534
aa958be264f7eee3c2251f0820892b8c	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.994464
bb740c10ad31d5779e628bccffdb5015	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.8793231
bc84c01dbfc576927c9a43ad8a4fbf8f	Proteobacteria	Alphaproteobacteria	Azospirillales	uncultured	uncultured bacterium	0.7369774

6cd521d4f7f2f49c4c86e06f49e576d8	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.9999238
ad72127c01dac114c005c83404612b5d	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.9398904
fa96cbd7b2df953f48e159b78c51527d	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.848006
2dd9e191a81b91117b77df5eac7e6048	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	0.9252117
79029fa983ec4eda60117a273a52cfc0	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	0.9969778
594557dbc9dc0721b0db36189252c953	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.9575892
6de8fff163b98c8aa71aeec462c52f49	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.9371287
2173ff99b55e25f3178d3943d534facc	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	0.8164607
2a079227fdd4c1dc045b7c458a6b5149	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	uncultured	0.7515504
0f5eb1819e343c392f814e2f5b07071d	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	uncultured	0.9987332
f4187519563396c7822f6d064020c4cb	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.7136965
68e646344c898152b98df4c22e51cda7	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		0.9692878
ef3ada26c21f2f3a2a1f3547cdc660eb	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia	0.9714758
3e150ccbf8dc11e57339f9b03a2975eb	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia	0.9935369
a2129306ce778f0ae10be9cbeba2601b	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	Hirschia	0.9999832
d23a98ab18bd13238a0c9e416e220dc2	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02	0.9999629
8814d2c1cde559e401e01e137944aabe	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02	0.9995355
4acbe51867850c532a8e23d89e6eafa5	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02	0.8407665
fd7a29a224c0789cd1cd690a83fe9054	Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	SWB02	0.9392436
af66fe25a99bfb12a2849d20d408ccb5	Proteobacteria	Alphaproteobacteria	Caulobacterales	Parvularculaceae	Amphiplicatus	0.8542333
d46765c55b861a8eafe1d194a8fc7cea	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.7380537
6afa5a7346c82bbb1ba23d7a308e76d9	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.7848543
a206cc680cb24a8575d7c26e9d73b6ce	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.7573409
03524904486e37bcf799e02a7f899cc0	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.7912156
46ec2c6b98436105173275f7ef73b5c0	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.7102294
f120d43d6fcd4e8c2ff09268fcc41e4e	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.8489512
d307989ba946e193aa888362a15df355	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured	uncultured bacterium	0.74297
3562db1d345723d60bd7eab0868ab18e	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured	uncultured bacterium	0.9709309
4275cd03dc7fec34fd1f1f87ae1ca331	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured		0.8151278
fcefebd3172dbd28897b36be9ebab4f1	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured		0.9131417
80b4ae10cd6f13931f75385802d1541e	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured		0.7015302

f6620bb3020c1f5f6056df0c427c28ab	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured		0.9995701
e1035d0f36e6230f903b31c0e268ed1e	Proteobacteria	Alphaproteobacteria	Elsterales	uncultured		0.7925166
9c36aef21b75b737f3a30f64145d055e	Proteobacteria	Alphaproteobacteria	Holosporales	Holosporaceae	uncultured	0.9974078
997349b1e79a9009d63384d3b0c2cb4a	Proteobacteria	Alphaproteobacteria	Micavibrionales	uncultured	metagenome	0.9878811
f6450e60e8a0f1c9146a3fb61791e19e	Proteobacteria	Alphaproteobacteria	Micavibrionales	uncultured	metagenome	0.9998364
d122c4a88fbb99522c52735ccb3335ab	Proteobacteria	Alphaproteobacteria	Micavibrionales	uncultured	uncultured bacterium	0.9999998
1b01273444eafee8d9136f8046543fc7	Proteobacteria	Alphaproteobacteria	Micavibrionales	uncultured	uncultured bacterium	0.9999999
9e6c74996690d3c5e03f3c1ab168a2b9	Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae	uncultured	0.9999995
78160eab3afa23fb208aee5ed00b5934	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus Paracaedibacter	1
5875355989b2074a5419c484120efff3	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	Reyranella	1
151f25319c8715bb49632a77fb021ad5	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	Reyranella	0.999991
019a8e93cde9dfce660c99097f2bc8ef	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	uncultured	0.7985229
dd50423a79ae013068897e14b5688744	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	uncultured	0.9999997
e5096bcc6d25cb64a6385c07bb1c8972	Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	uncultured	0.9986076
d18a3f61d369a215398fef61c725c098	Proteobacteria	Alphaproteobacteria	Rhizobiales	A0839	uncultured bacterium	1
4473ac847f597164696bc96da74ca753	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Bosea	0.9999349
b5403e3d3e7f5a219e1fbe3cceee2261	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Microvirga	0.9995653
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0412cc24e1ad6b835e85b3f45da4b27d	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Microvirga	0.999998
691849d2d09ff0dc91cdd3bb95292dc8	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	uncultured	0.9818841
7cbf318a351889e6ea3311913d1cf8d9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	uncultured	0.9983264
52cde3121930654ac3de59ce3870bca7	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	0.9866238
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30e75521586b534e02c33b48d7b6bb55	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	0.9998024
57856408be3a5dbe085de255f1ca2234	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	1
17e562606dc747dd9f950ce27d3eb95a	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	1
38673ed4d11a008f2d196cc692be2f3e	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	0.9995581
8abc38d4338376e837e00dd7b58d814e	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	0.9997347
1c2b8892a0d7f828d72808cd01cfd199	Proteobacteria	Alphaproteobacteria	Rhizobiales	Devosiaceae	Devosia	0.9999988

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bc532a44bd64a244fb62185276c54b2a	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	1
4bc2853b48494b7dd698fccb74a67f56	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	1
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b3d99500a196f8deeff625c44f1fe837	Proteobacteria	Alphaproteobacteria	Rhizobiales	KF-JG30-B3	uncultured bacterium	0.9999976
e83d6e9d8887338da699e1c7da86ccf6	Proteobacteria	Alphaproteobacteria	Rhizobiales	KF-JG30-B3	uncultured bacterium	0.9986867
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b408bfd98bbc4822ec3477d519ed37e9	Proteobacteria	Alphaproteobacteria	Rhizobiales	KF-JG30-B3		0.998729
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32a9882804579c3c33c4d29e6db07e16	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	Methyloceanibacter	1
41b269824f02f78229e19e91590c7b2f	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	uncultured	0.9999701
e1464539879868d4c7719804c23ac0e6	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	uncultured	0.99986
053c09f43a8ca677723e10f2650f95aa	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	uncultured	0.9887401
fc6622c636a5210293fb2873fc4761d9	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.9548583
c130baecd35f08a8f79bdfbdc0abb6c0	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.9969751
9ac6a4f21c1269ddef77a85d63272b7f	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	1
4ba6bad752253e930876e8c688e4d9fb	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	1
2653f9a6e90d957c951070035e6edeea	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.9999953
e1c7d97fe13e9127d225d76a1feb8c78	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-	0.9663856

					Pararhizobium-Rhizobium	
5073eb042f1600783fe65118c8151bc3	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.9999999
791905e09a4afe910bbfdefe781e04e4	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	1
15d56c1957f615a428b92ab2d5f3e1ee	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	0.9999933
9bd4bf5557b0e1a63f89669e39f6f1be	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	1
de3d0e440533123bef372ef43c19f3aa	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	0.9999989
223c5f90b35263bc56813fd8e68bd1f2	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	0.9337314
64a36d894db90cba3328c4b611bed241	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	1
1dc3a7cd36625f81a603740de6b3160b	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	0.9053202
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c509dd0911225930ed1761cf2653cc63	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae		0.9996457
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1bc625bd6d3510d38f0b5b3f460bdc50	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodomicrobiaceae	Rhodomicrobium	1
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6330f064ff038966c3611d20e13f49b0	Proteobacteria	Alphaproteobacteria	Rhizobiales	uncultured	uncultured bacterium	0.9985763
87cf92be932197570d27e7c4d38fb5a1	Proteobacteria	Alphaproteobacteria	Rhizobiales	uncultured	uncultured bacterium	0.9997196
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229f76e5c4491c2f3c4077ff8bdf52ae	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys	1
97a87d2b578c367b43f90d2ca6b4cb4e	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudorhodoplanes	0.9999687
76e02e78bfb4c55bbb24125506c3d440	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Rhodoplanes	0.99668
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c3d0625bd39bdd32db19c74e00af42f8	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	uncultured	0.9837818
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1d145835e7f0188562322f4eefb02657	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	uncultured	0.999996
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35aef3a8a6fb15d9c302ef6f7e3791fa	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	uncultured	0.7927997
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0c4931a61fd1fce4b2cfee8c1914503b	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	uncultured	0.9892142
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aa007d7086843b5aea4e17ebd5ef39ac	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		1
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b4b55462fc87503bdabeb19518353ef9	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae		1
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ca004eb3af4e4a7392c67822f8fa6e99	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospiraceae	uncultured	1
da29a4058ab0336db2ccbbc328b0c02e	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospiraceae	uncultured	0.9917102
45bec90d5434e68213368156261bcdae	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Acanthamoeba sp.	1
8f7b46b9b511b86e73bca09f66d71609	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Acanthamoeba sp.	0.9999998
81827fc8b5dd693269d62da55d299804	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Acanthamoeba sp.	1
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284534bd2b7bbb214eadd8eaf05acb26	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Pseudogymnoascus pannorum	0.9999091
344bc639e11f289ef226e0a4a886fc91	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Pythium insidiosum	1
9565b80a0b0185518ba628d3daa57eba	Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	Pythium insidiosum	1
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93a8856b6b76b6c1f4b6591a099bec9d	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	uncultured	1
5bacc68959ff977fe7ad80ddaabad2d3	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM2D12	metagenome	0.999989
286912d297e75fdbc32c6824ef0dd37e	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM2D12	metagenome	1
a518865b40e4d7502c2696aed08dcddf	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM2D12	metagenome	0.9886153
497ff78b1af27abcdd91e8b2401f7f5c	Proteobacteria	Alphaproteobacteria	Rickettsiales	SM2D12		1
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0e399248b074e726fcaa5d5fe355c925	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter	0.9998156
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bf7be24884994a6cdc679ec3980aeb8f	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter	0.9998921
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2937de446e4e066a11138ce9b029a7d8	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter	1
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26c4413eee52cf2a9fa86eafcc3453e4	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Altererythrobacter	0.9999377
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31fece52bf330bddd3a1d29c7273f088	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Ellin6055	0.9999762
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99fee6617d20f02a0e0641f4d5a57916	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.9999185
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227b7a4c194ea39cf3686d285a93541a	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.999998
e526b7bcb6bcc4067b9f0430c5399489	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	1
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2d6ad2917f65c316c1c4a36ac1492bb2	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	1
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1ea02703d3515609bff8d36fd136f68c	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9999999
f229bc8757981ab84ae78a847d2bcabd	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9999899
83bdc0f979ca81d8286c40e4bd27cca1	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.7400167
04295b1b33cab6843a6707dedcd23b6c	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	1
135308925565172b275b0fb8164a7b7b	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9999343
9b678a1ed5fc7f8d61f246f6927c0d1d	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.993036
11cbfd2a4163315d40fd3a2a70044885	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9997413
c9727f4d0827510e267a22c12e320949	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.8210106
e988aa13f1f68214ed8773f9f0c23f4b	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9999993
a050b7b059f690483a4a60e389722e2c	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	1
e74b7b191577fd73d006b86a9ea013cf	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.7211108

903ffc35a09fc0ccef9815bcae58a517	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	1
9fbee25316ce2d9f90b98daa8dd4c315	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9966374
046d51f3063acfbc93d82e74aaf4bb6d	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9999169
aa46161e445867a97a17e37f464b26f3	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9983018
67ee5b631e8da81d3a65a8558efa7b72	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.9995167
4ab34a3a97d2e0a6c9594ef441c06208	Proteobacteria	Deltaproteobacteria	Myxococcales	mle1-27	uncultured bacterium	0.9963323
4d0f571b520a2c703e5c32d47f2cc822	Proteobacteria	Deltaproteobacteria	Myxococcales	mle1-27	uncultured delta proteobacterium	1
23c6b816b5afe99feb3321a212a22627	Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	Myxococcus	0.9977236
84d7066856418ded4120bbbd4c37140f	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.9999491
22dd186f9c5a53fc7ba2e12ecede351d	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.9999998
d365c951036e3ae4415dabca5c5faf35	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.9999986
de56bdfdd060eaab768517f665182eb9	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	1
90899885ea6c8c5d270c1a0e0761cf29	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.9999921
dc149baad02dadfd9e1213267d97758f	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.954653
c9f9355d32e264f6bc060415332587bb	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	1
856c418beb012bad07f9db0bfa07e148	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	Nannocystis	0.9879752
9748bc05c9d6cd206ee07e5502466dd9	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	uncultured	1
ead651b71834df61a9ccb659c1d9d31f	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	uncultured	1
b3195d6d2448933e7ce7efe886528ea6	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	uncultured	0.9995143
380a71542a98c4bef2605836d705d81c	Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	uncultured	0.7796585
14ca30b13e73729af8fc74729bda7e15	Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42	uncultured bacterium	1
196e942c5ac46baae7e407656c399a32	Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42	uncultured bacterium	1
d3ac69f71fff868f44f1e93fb5bae998	Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42	uncultured bacterium	0.9955881
13801e7bc71636162780bd7b6d06bf65	Proteobacteria	Deltaproteobacteria	Myxococcales	Phaselicystidaceae	Phaselicystis	1
e7009dac7d1e7f76f1b04f4a91987a85	Proteobacteria	Deltaproteobacteria	Myxococcales	Phaselicystidaceae	Phaselicystis	1
80df1b5032ddc9acfe6b028b577869e1	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Pajaroellobacter	0.9987699
62db4cd61b405e3678a59876416a85cc	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Pajaroellobacter	1
b6cd6eebf58a64774443c82596adee7c	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Pajaroellobacter	0.999987
e8246466fe381d8a8d5c10cb90640eb3	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium	0.9999988
518e628e6d5047093f971c9573e040d1	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium	1

41d2baffd2ae6a8339d93a4c29e8d8a6	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium	0.9827859
af5adc6bf4a35ba30bdd347d1a85c6c6	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Sorangium	1
35ed22e9fa79ab018326b68bd06b3bb0	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	uncultured	0.999709
9666d7dd642b71cb7082141a70b15971	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	uncultured	1
f83ebaafef912c247212c36183775d6a	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	Sandaracinus	0.999999
e7e934a1f316883b99763726a84cc2cd	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	1
1aaeb074752193618c7f76698ce5704f	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.9999988
a0e1aa43524c2518755bca3197227c09	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	1
42f17aa0b5cc8471fd3f8f20108ae2a9	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.7305094
0adff9f8d713645f601df7ca2c2b6f3e	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	1
e1983c3a422f49d7a4776a453848d317	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.9999984
4ad08edc0f9036d5f772204edf4b9d53	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.9999994
6cad158df7966582e3719c3822c427f6	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	1
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2c688e1a28ab22a2d83c529bdc6d5bd3	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.9999999
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f1c53cd45aea51b2b01fd88e2234ec39	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.9993225
c4c068c5bb913a90c594ee60acfa557b	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.9998529
8470362fab9b39cb1e85d6b20d4523ed	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.99265
c9558ceda5c7472d1a04bbe7f78d3deb	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.9998981
d6a62118a591295481c301790a75e9e2	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.9999999
a0b84d1e743c5c63fa472ebb0e5f920e	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.9973272
9aa345045968b607280afc718ff20193	Proteobacteria	Deltaproteobacteria	Myxococcales	Vulgatibacteraceae	Vulgatibacter	0.9999995
c30e31af9e812dbb05b4c4f89ad51b52	Proteobacteria	Deltaproteobacteria	Myxococcales			0.9760854
3750c7035c15b6d4594c0f6f62caa5df	Proteobacteria	Deltaproteobacteria	Myxococcales			0.9414307
1e8bb5183d54ade7232423026ed85a4c	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	uncultured bacterium	1
daebf4a7f72782c739fc1fecc3f6da31	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	uncultured bacterium	1
2c4f42b48c742df353244d8008b1a29a	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	uncultured bacterium	0.7161579

82bca39b16949d4e6d50354d7ffb82ca	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	uncultured bacterium	0.9999992
1270da80cc0e29e38d735c7f38a145a3	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	uncultured bacterium	1
768b643d6bb2ab8f2ce0a33671cee8ef	Proteobacteria	Deltaproteobacteria	NB1-j	uncultured soil bacterium	uncultured soil bacterium	1
97a85ea73abea0bcdff3c6817e138177	Proteobacteria	Deltaproteobacteria	NB1-j			1
5058ed1d765e0771f97a2762ce80395a	Proteobacteria	Deltaproteobacteria	NB1-j			0.9995298
139f9d2eed23248403f54a40db2a523e	Proteobacteria	Deltaproteobacteria	NB1-j			0.9999999
73ee45247f008545aa2b0e89b054537d	Proteobacteria	Deltaproteobacteria	NB1-j			0.9999475
d492c07ecd9680e67f2b77f0e02b8e08	Proteobacteria	Deltaproteobacteria	NB1-j			0.9999555
53ad8d70075d427dc13e9cfec4b93e70	Proteobacteria	Deltaproteobacteria	NB1-j			0.9999469
e0c4d683dd6907eac4c0675fe9967bbd	Proteobacteria	Deltaproteobacteria	Oligoflexales	0319-6G20	metagenome	0.9848108
ab1d8786e4ca8f0246ca0b2071e4c9d2	Proteobacteria	Deltaproteobacteria	Oligoflexales	0319-6G20	uncultured bacterium	1
9a3bc31f03e25f369ab789c99ded433b	Proteobacteria	Deltaproteobacteria	Oligoflexales	0319-6G20	uncultured bacterium	0.9783758
77191edf017a621b5774568c1ce30b35	Proteobacteria	Deltaproteobacteria	Oligoflexales	0319-6G20	uncultured bacterium	0.9999992
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596b563acc8dfe58b5cd6013a3957dd7	Proteobacteria	Deltaproteobacteria	Oligoflexales	0319-6G20	uncultured delta proteobacterium	0.9999986
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d14368ceff3dfd711843aee819334418	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	Oligoflexus	0.9999966
e34b206a83dca76555cc2a05ad1b9f5e	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	Oligoflexus	1
9105c4062f5e404c6c9b3e9ac6536112	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	0.9999934
3272998c80e55cda11e2c4477c10e911	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	0.9999985
48515a65c7c527d807928682a52abe6c	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	0.9999919
c3fe938752170066d90b2640fbcd59bb	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	1
30c87bbe9af7968fee8b553da7231765	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	0.9999742
89021922421c772576a1d1e5f38f1e48	Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	0.9975828
54724b5d3d7472a56d5452263175a78f	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	uncultured	1
f2e69997ea44f310ae794df85b375aeb	Proteobacteria	Deltaproteobacteria				0.9979978
132ffe9a542685a423a59236950b46b0	Proteobacteria	Deltaproteobacteria				0.9998424
f53cb9609a8dd4b0830033481a0a03b1	Proteobacteria	Deltaproteobacteria				0.9999998

021d915da90c213fe3ba1d3e2028b810	Proteobacteria	Deltaproteobacteria				0.9998889
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ae3c08efd8363704a8032cec0aa38ab9	Proteobacteria	Gammaproteobacteria	Arenicellales	Arenicellaceae	uncultured	1
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20b3df08cd5fac2be26a2928155bab69	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Achromobacter	0.9999085
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7117984c22f21c4c62eadf27cf65ab16	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Massilia	0.9988025
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4f31fc43bb2ba611fa37c25e788fecf7	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Ramlibacter	1
f36c50279a8fa1c121cb9dda1ab1cb42	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Ramlibacter	1
dab1160ee7a4ecf9945086ff09f99528	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter	0.8281814
a669eb6ad9a74b0022af57efee724096	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter	1
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e5116b23d071580eb1022380655098ac	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter	0.9988029
7224b1f7fa7d6d2bade90064b7b33e18	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter	0.997481
45a703c3d46ed9731722d03c72be9069	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured	0.7843661
c1dfa382eef43fd5f92771aa57552dc7	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured	0.9998071
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68e3bbe1d66df04b0b9e842c4a12e782	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae		0.9999385
5747e5f586c92b5428dc631872e6c0c9	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae		0.9909229
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acccb7cec4d146864bc11d37da55dcd0	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Methylophilaceae	Methylotenera	0.9984467
fc6b1ee638725dbf2be878f146ac1fa4	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Ellin6067	1
840da214791d4f4a6f3f743366731c59	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Ellin6067	1
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f3b163580cea29af310e7210d107fade	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	MND1	0.9998665
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7684072284024ca2b426a6bdd04c45f9	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	MND1	0.9808561
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48c62702595216dd0c3af82f7f70fafe	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	MND1	0.9739556
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b8f64099026ffffde7cd2c6aa4642240	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Nitrosospira	0.705654
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265f0ed6b3f8dbe0916726ff8e9c0c77	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	SC-I-84	uncultured bacterium	1
62a31f4bb442c6c6cdcf4deae651f3cd	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured bacterium	0.9959519
d65eba8da9f472c30a9f63f61ce1df62	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured bacterium	0.9999999
24c153463453ac3f9ca4dfa84b8e1962	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured bacterium	0.9976176
38de8bf60c1f649e377e1f74e4bb2d8b	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured bacterium	0.9998487
9135c9b64f73599b35c6321fbff7036a	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured bacterium	0.9361434
274e1a441b97bacbcc8b549ded93512e	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20	uncultured beta proteobacterium	1
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09aef7f63dfb9ce6ce5a8fc236729041	Proteobacteria	Gammaproteobacteria	CCD24	uncultured bacterium	uncultured bacterium	0.9979293
b129908a3d7a6d0da381e0720f649f59	Proteobacteria	Gammaproteobacteria	CCD24	uncultured bacterium	uncultured bacterium	0.9827615
15f46f18b0361890a512aec4f5517a58	Proteobacteria	Gammaproteobacteria	CCD24	uncultured bacterium	uncultured bacterium	0.9172747
bad02fb4b97f30182ffe6e934f54ad5f	Proteobacteria	Gammaproteobacteria	CCD24	uncultured bacterium	uncultured bacterium	0.9999967

354b4d2bbedce16d1a4f778f6770c61d	Proteobacteria	Gammaproteobacteria	CCD24	uncultured bacterium	uncultured bacterium	0.9999996
62dfdd481f414b8b1efc59c28d843fd6	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Cellvibrio	0.9981876
8e6a3fe26cefc539638ed3d8ca50da13	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Cellvibrio	0.9993227
6112d362565c5797eb555106a550d353	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	Cellvibrio	0.9994231
1e2094de687f5461d4f3815e124674a5	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	uncultured	0.9999999
27b64e66ea49d4f903e6520f0b4ab47f	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	uncultured	0.9999987
dc14c48293ab127111619ca42e985bde	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Cellvibrionaceae	uncultured	1
1cabc767637eea0d8fee45d1445ea3c7	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Halieaceae	OM60(NOR5) clade	0.9304523
c06350a9c4427385d5bf910c5dadfc3c	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Halieaceae	OM60(NOR5) clade	0.7176856
c36bd8f2fd540d0355d28c38b88ef861	Proteobacteria	Gammaproteobacteria	Cellvibrionales	Halieaceae		0.9999999
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85eee8b95d580fab3641a7c814920216	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	0.9996292
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84a26df5be570526a1dc0f43fb9a2ad1	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	uncultured	0.9806283
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cc761daf51f27c423da57f3f1f0ff5cc	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	0.9967145
3481fa43fe5fba6aecdc7f9aae6ed9c0	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	0.9292905

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cdcd895a508fdc0b34ce68fd0abb3f4f	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae		1
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7f123a3d0a70fc75dfdbacb656c282ff	Proteobacteria	Gammaproteobacteria				0.9997434
01fa5957c5c8928703fe23fbb0bb85df	Proteobacteria	Gammaproteobacteria				0.9999997
21a0b7eac468be9ac18c36080aaa1810	Proteobacteria	Gammaproteobacteria				0.999362
4327a4e0670df2843eae4bdca5e4d3f1	Proteobacteria	Gammaproteobacteria				1
50279dcfa8950528dd30465e8e2c46d7	Proteobacteria					0.9996565
70e97bcefa938b2d83b03b65d4793e16	Proteobacteria					1
c44c8b47ef06c40a4570bce759f7e10e	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	1
e5b8aa4e9ca9b255a6e1e7ea5f0c576e	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.9999981
6571967f27f2fa6b370aa7e4ba7502d7	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.7134427
299a62d625ea2060f6135eeb19d34dae	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.9988975
11c18457aeb0716245485fc46fcf6d0d	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.9994967
d554f717d25d5f90590ec252d3c67d0d	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.7355781
987908f833dd6a4d43a48cfc6186d1b4	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.9997797
b38f1c5064027eebd53d58050d20a067	Rokubacteria	NC10	Rokubacteriales			0.9999993
abb84e2d67b4893105bee050b0c8c4ab	Tenericutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	Candidatus Lumbricincola	0.9994292
bc3676c17839094c4fa8e33268905268	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrocosmicus	0.9988184
95b0d4f1aee6d2f42602026d5c634276	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	0.9999985
e42d6ed4bcbff0c1730d82c4b0b63803	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Candidatus Nitrososphaera	1
1427435456d4da78e4d4f36902b0a273	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	uncultured archaeon	0.9957914
ed3d7020f31a64a765244b28d6ca4be7	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		1
3ab9af3e9d29ebb0b244558ddab132ed	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		0.9971166

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cbeb331b838ac67aa049f01247965fb8	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		1
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7347881ef3980ea60fc95285a8b34495	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		0.9999894
2d51eee954d47bb2f71665bd2691bb94	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus Udaeobacter	1
c282c5b44744fe719e7edd27a8470f72	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus Udaeobacter	0.8698494
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9f72141feaa897f97c0cb1ab1a7b06c4	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus Udaeobacter	0.999995
cf30d8a623ac604ae24a85e86dfccceb	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter	0.9875918
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59c034937293c06f8ceb6dd84cfc5ef5	Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	uncultured Verrucomicrobia bacterium	0.9999743
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47856ad208b14ee27a8db4107cc70e06	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	uncultured	1
5fdca08e0ec389a1e1812023915a903e	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	uncultured	0.9999721
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ac1d196d7bce207625a8189bf58722a8	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Verrucomicrobium	0.9982856
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71b9607a402057dae797a78265abcbac	WPS-2	metagenome	metagenome	metagenome	metagenome	0.9975426
a18c46de0d6de855ecf173184997590a	WPS-2	metagenome	metagenome	metagenome	metagenome	0.9992219
38c73e82ee6b144f24083f330555e5e3	WS2	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.9999676
46fd336d831784c1b83a905bfe09cd17	WS2	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.7279131
4e84f8fa56e69de89897fc8bb56dc8f6	WS2	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium	1
3dbc0dacdeb99683b68f58ea01ffe52a						0.9999998
6bc2c58b30fd32e6b0ebef25720ad0f0						0.9998795
faa1a2ee4ed2c921739cb9a63880a9de						0.9310897
4d104737bb9e14bfe2d1459f36667a5f						0.9898049
334ca43ac246f4f961da7b739704bcb6						0.985232
a1fe70fb377a743c1da07b5cbce83197						1
ecda17946975d446ffb25c69493fc282						1
866ab22bcd02ac8cb5aa383ae29dfc51						0.957645
0eb922798aa4543f66d66073afc05e3e						0.9964542
32e30e57bdf13799ab2361e631f66094						0.9999951
1203335b5f473266a3621ea02a89f8ae						0.999968
0b8d64eb7fa84cb2b125aa12363fc567						0.9973853
0c6e268bcb5c7cc1486909b122ab981d						1
d3174762eb33a1a7c5951ff6434f3872						0.9999999
3939ef6c0d585bdab00972ebf79b2374						0.9999982
ecab19bd64116ff2d8b37fc64b2c990c						0.9999831
cc413511cd3a4ad0b434ba1b645c6591						0.9999981
58026d1098162d178f365a6aeb16b881						0.9991436
92b9a2999a6f81497c8c072f364d9b79						0.8981476
5810a0412fb9b49b09bb1693e5e2b289						0.7073774

7ed5b232344d34a5223773682696fd44	0.9999857
4f5b82d0d26b15082b85ee554b66c3b8	1
679ed2b430ccae5e76b3e194fa7792b9	0.9997943
0c9d1c071cb3bcd532f86c1fa327471e	1
57c3b0cc4abd71c1bf4436c9aa05e4f7	0.8529054
35effe970760b20ec6aa78df52e4437a	0.9999729
e0234d1ade443508bac3670a851ad6ba	0.9999972
238966487f2bdced77a308599c1bba3c	0.9593563
e5332548ad4c0b161e6090b98a3859f8	0.9720903
e52e0cb3e38bb2bf01aba6f323ad1a38	1
08bba2b13f77afcdadc48cb743847e2f	1
e81dd216997021c96847a5979e180d2b	0.9999327
b8b32fc01a1ceb2d1782181b53973acb	1
b689aa49148ff6a14ff50b56d0e691bb	0.7092086

Appendix Table 2. Full list of indicator species. Statistic *A* represents the specificity or probability that a sample belongs to a treatment group from which it was found, so that if *A*=1 the bacteria was only found in that treatment. Statistic *B* represents the fidelity, or probability of finding that bacteria within the treatment, so that if *B*=1 the bacteria was detected in every plot of that treatment. The indicator bacteria were examined for each soil treatment (Control, Char = biochar, Inoc = inoculum, Comb = Combined) and sampling date and results are reported at α<0.1 significance level.

							Sensitivity Statistic *A*				Fidelity Statistic *B*			
Date	Feature.ID	Phylum	Class	Order	Family	Genus	Control	Char	Inoc	Comb	Control	Char	Inoc	Comb
Early(V4)	866ab22bcd02ac8cb5aa383ae29dfc51						0.14	0.37	0.21	0.28	0.57	1.00	0.75	0.86
Early(V4)	1d52df7ce0aeb9ca161acd5d29a46da0	Acidobacteria	Blastocatellia (Subgroup 4)	43428	uncultured bacterium	uncultured bacterium	0.14	0.55	0.00	0.30	0.14	0.57	0.00	0.29
Early(V4)	b5d677849f672959cece1b0d782e9c87	Acidobacteria	Subgroup 6	uncultured Acidobacteria bacterium	uncultured Acidobacteria	uncultured Acidobacteria	0.14	0.13	0.30	0.43	0.29	0.29	0.63	0.86
Early(V4)	3cb4a739d24ab84b7a79ff9521bfbaf3	Acidobacteria	Subgroup 6				0.00	0.00	0.24	0.76	0.00	0.00	0.13	0.29
Early(V4)	6e8f5b32d455db5d72d6e46626e39eee	Acidobacteria	Subgroup 6				0.00	0.19	0.14	0.67	0.00	0.14	0.13	0.43
Early(V4)	35f23ca925e88b47f5d3ec9f1c689432	Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	Ilumatobacter	0.13	0.32	0.48	0.07	0.29	0.57	0.88	0.14
Early(V4)	e07052bb9c0f0d2370537c4b9acbed4e	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.17	0.00	0.00	0.83	0.14	0.00	0.00	0.43
Early(V4)	f8e966fd6a44aecf3991a7dd167fca57	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.00	0.12	0.21	0.67	0.00	0.14	0.13	0.43

Early(V4)	9c7241189b17bbc709615684e9dbf4eb	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.00	0.80	0.20	0.00	0.00	0.29	0.13	0.00
Early(V4)	51121c8f8cc8a7a03d9d7f1dd5142aa5	Actinobacteria	Actinobacteria	Streptomycetales	Streptomycetaceae	Streptomyces	0.23	0.19	0.38	0.20	0.71	0.43	1.00	0.71
Early(V4)	d3ac14e193d870746f08f2e205a904d2	Actinobacteria	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Nonomuraea	0.20	0.04	0.60	0.16	0.57	0.14	0.75	0.57
Early(V4)	af062725e851baa19a57d27c454641e6	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.42	0.08	0.28	0.21	1.00	0.71	0.88	0.71
Early(V4)	ee3072cc17a5e70cb4e49387257957ec	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteriaceae	Rubrobacter	0.00	0.53	0.18	0.28	0.00	0.71	0.38	0.43
Early(V4)	3c70a6836188aa560a2d934414dbde9c	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.18	0.17	0.47	0.18	0.43	0.14	0.75	0.29
Early(V4)	7653cdca9bdece4101e95cd83ac1fc8e	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium	0.00	0.36	0.64	0.00	0.00	0.14	0.50	0.00
Early(V4)	8ccdb282b0f7311910e004a2ae836908	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	0.24	0.64	0.12	0.00	0.29	0.43	0.13	0.00
Early(V4)	fd1184fd1cb16c56ea9ecba792836259	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	0.74	0.00	0.12	0.15	0.57	0.00	0.13	0.14
Early(V4)	21f7f0dfc4eb9e91480dfab908344a80	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	0.24	0.23	0.33	0.20	1.00	1.00	1.00	0.86
Early(V4)	3c2e985995945ad30db0a405dc4f092a	Chloroflexi	Anaerolineae	Ardenticatenales	Ardenticatenaceae	uncultured	0.17	0.00	0.23	0.60	0.14	0.00	0.13	0.57
Early(V4)	97e6ddd756ab1922a397f0f1bd8157ca	Gemmatimonadetes	BD2-11 terrestrial group	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	uncultured Gemmatimonadetes bacterium	0.15	0.48	0.27	0.10	0.43	0.86	0.50	0.14
Early(V4)	02a1fdac859e75c4137bd150ee585362	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.00	0.55	0.15	0.29	0.00	0.71	0.13	0.29

Early(V4)	79527202c082144846511e01512a31a4	Planctomycetes	Phycisphaerae	Tepidisphaerales	WD2101 soil group	uncultured bacterium	0.00	0.65	0.21	0.14	0.00	0.57	0.13	0.14
Early(V4)	6f48504f6f4aaa4c67e08b3b999ac0b7	Planctomycetes	Phycisphaerae	Tepidisphaerales	WD2101 soil group	uncultured planctomycete	0.00	0.21	0.00	0.79	0.00	0.14	0.00	0.43
Early(V4)	92d58e1a9bac95cc81c3b883a3c6a31e	Planctomycetes	Phycisphaerae	Tepidisphaerales	WD2101 soil group	uncultured planctomycete	0.16	0.36	0.23	0.25	0.71	1.00	0.63	0.86
Early(V4)	e956a425d4d403102f6db6b28ea61d7f	Planctomycetes	Phycisphaerae	Tepidisphaerales	WD2101 soil group	uncultured planctomycete	0.00	0.74	0.26	0.00	0.00	0.29	0.13	0.00
Early(V4)	e40bf8ef9ec308e6d5e449e3166089b0	Planctomycetes	Planctomycetacia	Gemmatales	Gemmataceae	Gemmata	0.13	0.20	0.68	0.00	0.14	0.14	0.50	0.00
Early(V4)	278669d712810e9bddd7012b87c89fae	Planctomycetes	Planctomycetacia	Gemmatales	Gemmataceae	uncultured	0.00	1.00	0.00	0.00	0.00	0.43	0.00	0.00
Early(V4)	6dbe92da4c96098eb02d8abfee4db5da	Planctomycetes	Planctomycetacia	Gemmatales	Gemmataceae	uncultured	0.00	0.23	0.00	0.77	0.00	0.14	0.00	0.43
Early(V4)	7109361011fd31892490d425b0218852	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.19	0.00	0.81	0.00	0.14	0.00	0.63	0.00
Early(V4)	d09f2875b08b300bbf68d3e01ff3fcad	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.00	0.47	0.20	0.33	0.00	0.71	0.38	0.43
Early(V4)	9f68b2119a7c9519fd1c06fb7b010f17	Planctomycetes	Planctomycetacia	Planctomycetales	uncultured	uncultured bacterium	0.23	0.18	0.49	0.11	0.43	0.29	0.75	0.14
Early(V4)	6afa5a7346c82bbb1ba23d7a308e76d9	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.11	0.00	0.00	0.89	0.14	0.00	0.00	0.43
Early(V4)	19386012f47b4a8d83f8fa168376a505	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys	0.00	0.79	0.21	0.00	0.00	0.29	0.13	0.00
Early(V4)	4d691d7c1c00603992ecc527d3b59e8f	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.31	0.09	0.50	0.11	0.71	0.29	0.88	0.29

Early(V4)	fa59f4b4636d2577f2151e2e4743fb78	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	0.26	0.11	0.21	0.42	0.57	0.29	0.38	0.86
Early(V4)	eea3321ed6828fa079442f44348aaf3d	Proteobacteria	Deltaproteobacteria	Myxococcales	bacteriap25	metagenome	1.00	0.00	0.00	0.00	0.43	0.00	0.00	0.00
Early(V4)	7d8fce7d502b820b57fa09de68df9139	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.27	0.00	0.00	0.73	0.14	0.00	0.00	0.43
Early(V4)	4ad08edc0f9036d5f772204edf4b9d53	Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	0.05	0.00	0.53	0.41	0.14	0.00	0.63	0.57
Early(V4)	a0b84d1e743c5c63fa472ebb0e5f920e	Proteobacteria	Deltaproteobacteria	Myxococcales	uncultured	uncultured bacterium	0.23	0.21	0.20	0.36	0.71	0.86	0.63	1.00
Early(V4)	f36c50279a8fa1c121cb9dda1ab1cb42	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Ramlibacter	0.08	0.07	0.23	0.61	0.14	0.14	0.38	0.86
Early(V4)	94e1bc50ac06b01a0898a5c611d0f064	Proteobacteria	Gammaproteobacteria	EPR3968-O8a-Bc78	uncultured bacterium	uncultured bacterium	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.43
Early(V4)	db71e335bc263a02d10d6331d567e4ba	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.15	0.00	0.85	0.00	0.14	0.00	0.38	0.00
Early(V4)	966c0c090fbc5d21ec3b79a3dcedb2d4	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus	0.18	0.46	0.20	0.15	0.29	0.86	0.38	0.29
Late (R1)	bffeaa586bc2c11fd77bf419fbc251cb	Acidobacteria	Subgroup 22	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium	0.00	0.00	0.60	0.40	0.00	0.00	0.63	0.13
Late (R1)	4fbbbe7148d8ec0b18e6731be1e2b8ca	Acidobacteria	Subgroup 6				0.13	0.17	0.40	0.30	0.50	0.50	1.00	0.75
Late (R1)	6e8f5b32d455db5d72d6e46626e39eee	Acidobacteria	Subgroup 6				0.00	0.00	0.80	0.20	0.00	0.00	0.38	0.13
Late (R1)	fd42a17506638640cdee202bbd963ff5	Acidobacteria	Subgroup 6	metagenome	metagenome	metagenome	0.23	0.07	0.48	0.22	0.50	0.13	0.75	0.38
Late (R1)	d9727162db66dbffac8ca727a81c7182	Acidobacteria	Subgroup 6				0.43	0.22	0.19	0.17	0.88	0.63	0.50	0.38
Late (R1)	12c69e5e0036ed5b242874f1a54a3d3c	Actinobacteria	Acidimicrobiia	Microtrichales	Iamiaceae	Iamia	0.19	0.20	0.26	0.35	0.63	0.75	0.88	1.00

Late (R1)	63fc2de8bb0a8c04e30d1c3afa4607c8	Actinobacteria	Acidimicrobiia	Microtrichales	uncultured	uncultured Acidimicrobiidae bacterium	0.13	0.17	0.20	0.50	0.38	0.63	0.63	0.88
Late (R1)	b8c4ed03d7d91546b9f6ad80b80135a3	Actinobacteria	Actinobacteria	Frankiales	Geodermatophilaceae	Blastococcus	0.19	0.21	0.25	0.35	1.00	0.88	0.88	1.00
Late (R1)	cfdf66ad8b27626f14f419a4f6c51b88	Actinobacteria	Actinobacteria	Glycomycetales	Glycomycetaceae	Glycomyces	0.23	0.00	0.00	0.77	0.13	0.00	0.00	0.50
Late (R1)	984919ce3c93ca2b6d54479b1c165fbb	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Agromyces	0.17	0.24	0.23	0.36	0.75	0.88	0.75	1.00
Late (R1)	1cc4d0d06af05f45284b9a5bd6c8ca5e	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.11	0.18	0.58	0.13	0.13	0.25	0.63	0.13
Late (R1)	fc4d567d1d0828e1fdc36916f0d53d15	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	Actinoplanes	0.11	0.14	0.21	0.54	0.25	0.38	0.38	0.75
Late (R1)	11f16b8be0d91194999ed0585ae1866f	Actinobacteria	Actinobacteria	Micromonosporales	Micromonosporaceae	uncultured	0.10	0.63	0.17	0.10	0.13	0.50	0.13	0.13
Late (R1)	6fa0fe79653ac74686b1b42f941aab8d	Actinobacteria	MB-A2-108	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.00	0.25	0.25	0.50	0.00	0.38	0.38	0.75
Late (R1)	5e616c0a99413e29f72efd5e9c67497a	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	Ohtaekwangia	1.00	0.00	0.00	0.00	0.38	0.00	0.00	0.00
Late (R1)	e00254c81e0e58719fdcd510482c7e80	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	0.40	0.10	0.25	0.26	1.00	0.38	0.63	0.75
Late (R1)	c94811a8d119639dd34a6adcad76d8b8	Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	0.19	0.00	0.67	0.14	0.13	0.00	0.38	0.13
Late (R1)	1957e9c11acfd7c687d8be39f734fb8e	Chloroflexi	Anaerolineae	SBR1031	A4b	metagenome	0.13	0.20	0.59	0.09	0.38	0.25	0.63	0.25
Late (R1)	899e9fc30a2a3e200df2b2902bad7236	Chloroflexi	Anaerolineae	SBR1031	A4b	uncultured Chloroflexi bacterium	0.00	0.58	0.42	0.00	0.00	0.50	0.25	0.00
Late (R1)	6110c9636e4e563ac05833108a9fe60e	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	uncultured bacterium	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.38
Late (R1)	79b3b6c751c001ddeb49b14eb3cba615	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45		0.04	0.12	0.18	0.66	0.25	0.25	0.50	0.63
Late (R1)	560859414b86c10a44c3ec7dc1b85c8e	Chloroflexi	Dehalococcoidia	S085	metagenome	metagenome	0.20	0.40	0.24	0.17	0.38	0.88	0.50	0.38
Late (R1)	84a8d5b2d6ec9307f0acafdfd5a023f9	Entotheonellaeota	Entotheonellia	Entotheonellales	Entotheonellaceae	Candidatus Entotheonella	0.00	0.08	0.34	0.58	0.00	0.13	0.63	0.63
Late (R1)	76a0a5dca6892ad6664ede7b6376ad55	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	possible genus 04	0.17	0.68	0.15	0.00	0.13	0.38	0.13	0.00

Late (R1)	fd1098cd571337c869bc804919b0f630	Firmicutes	Bacilli	Bacillales			0.34	0.00	0.07	0.59	0.38	0.00	0.13	0.50
Late (R1)	75c27a4cf562485367383dce2865bbd8	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	uncultured	0.07	0.17	0.15	0.61	0.13	0.25	0.25	0.50
Late (R1)	1b9bc8ecf96dbfc09c6b508545ef4271	Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	0.00	0.00	0.85	0.15	0.00	0.00	0.38	0.13
Late (R1)	64daff1e5b6f45a9003b6c1752298150	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.25	0.00	0.00	0.75	0.13	0.00	0.00	0.63
Late (R1)	7d14078031a159ee086f916fc5fc19f1	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.00	0.00	0.88	0.12	0.00	0.00	0.50	0.13
Late (R1)	c5f9563ca074dc876a98a92169d1829c	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.23	0.21	0.36	0.20	0.88	0.88	1.00	0.88
Late (R1)	86472a9b63b23f90dac6bd16791d7357	Planctomycetes	Pla3 lineage	uncultured bacterium	uncultured bacterium	uncultured bacterium	0.43	0.15	0.24	0.18	0.88	0.75	0.75	0.50
Late (R1)	50f5770b153dee704683ac37c2b9dbd4	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.10	0.21	0.09	0.60	0.13	0.25	0.13	0.50
Late (R1)	f11495619eb77d3472fe0d2c6f847db4	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Pirellula	0.86	0.14	0.00	0.00	0.38	0.13	0.00	0.00
Late (R1)	c43ccad8f58430e360c76332e20e3172	Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	Skermanella	0.21	0.09	0.18	0.51	0.38	0.13	0.25	0.75
Late (R1)	a206cc680cb24a8575d7c26e9d73b6ce	Proteobacteria	Alphaproteobacteria	Dongiales	Dongiaceae	Dongia	0.15	0.00	0.39	0.46	0.25	0.00	0.63	0.75
Late (R1)	4bc2853b48494b7dd698fccb74a67f56	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	1.00	0.00	0.00	0.00	0.38	0.00	0.00	0.00
Late (R1)	f8b6d2a553f0df1c667529b281cdac3f	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Pedomicrobium	0.07	0.20	0.13	0.60	0.13	0.38	0.13	0.75
Late (R1)	1dc3a7cd36625f81a603740de6b3160b	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Mesorhizobium	0.20	0.00	0.80	0.00	0.13	0.00	0.38	0.00
Late (R1)	f229bc8757981ab84ae78a847d2bcabd	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium	0.00	0.28	0.72	0.00	0.00	0.25	0.50	0.00
Late (R1)	c6e9c9fe9159441c4ffe44947875236a	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Rhizobacter	0.00	0.00	0.20	0.80	0.00	0.00	0.13	0.50
Late (R1)	945184b6386c192c0066e0a98a154780	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae		0.07	0.00	0.00	0.93	0.13	0.00	0.00	0.50
Late (R1)	7210fe57b610755efbfdf2a6efb7e197	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria Incertae Sedis	Unknown Family	Acidibacter	0.22	0.00	0.00	0.78	0.13	0.00	0.00	0.38
Late (R1)	ab4a316f6ef641a7a161c3e95a8420c8	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria Incertae Sedis	Unknown Family	Acidibacter	0.00	0.25	0.64	0.11	0.00	0.25	0.50	0.13

Late (R1)	5bc2d5bea3cb6de680da2fe29cce055c	Proteobacteria	Gammaproteobacteria	PLTA13	uncultured bacterium	uncultured bacterium	0.22	0.21	0.23	0.33	1.00	0.88	0.88	1.00
Late (R1)	e08e23d2a89132c6e4adadb351a1e783	Proteobacteria	Gammaproteobacteria	Steroidobacterales	Steroidobacteraceae	Steroidobacter	0.00	0.75	0.25	0.00	0.00	0.38	0.25	0.00
Late (R1)	6571967f27f2fa6b370aa7e4ba7502d7	Rokubacteria	NC10	Rokubacteriales	uncultured bacterium	uncultured bacterium	0.21	0.20	0.21	0.38	0.75	0.88	0.63	1.00
Late (R1)	4c87523f07695269d1e32dc3c5acbdd5	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter	0.09	0.24	0.00	0.67	0.13	0.25	0.00	0.50
Late (R1)	cf30d8a623ac604ae24a85e86dfccceb	Verrucomicrobia	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Chthoniobacter	0.16	0.75	0.10	0.00	0.13	0.38	0.13	0.00
Late (R1)	110af1a25622d25331ad5a80e9996fe3	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus	0.71	0.00	0.29	0.00	0.50	0.00	0.38	0.00
Late (R1)	966c0c090fbc5d21ec3b79a3dcedb2d4	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus	0.13	0.29	0.48	0.11	0.13	0.38	0.88	0.38
Late (R1)	75d13fe7dd2705511c9e83734f27d6b8	Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	uncultured soil bacterium	0.00	0.00	1.00	0.00	0.00	0.00	0.50	0.00