Shrub-Crop-Microbiome Interactions: A Novel Rhizosphere Alliance to Mitigate In-Season Drought in the Sahel

Dissertation

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By

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Abstract

The Sahel of W Africa is a vulnerable eco-region where soil degradation, and recurring drought now seriously reduce agricultural productivity. Erratic rainfall, exacerbated by climate change, causes in-season water deficits that contribute to on- going and future food insecurity in this region. The staple crop, millet (*Pennisetum glaucum,* pearl millet), is grown during the rainy season by subsistence farmers without fertilizer or irrigation. Increasingly erratic rainfall is thus a major threat to crop production. However, it has been observed that where farmers intercrop with an indigenous shrubs *Guiera senegalensis* and *Piliostigma reticulatum*, millet drought resilience and yield under drought is dramatically increased**.** One proposed mechanism for this phenomenon is hydraulic lift, the redistribution of water via the shrubs' deep tap roots to shallowly rooted crops. Additionally, the moister, carbon-rich soils under the shrub canopy harbor a distinct and active microbial community. Research in other semi-arid environments has identified rhizosphere microorganisms that promote plant resistance to drought, and preliminary research has shown that these shrubs harbor some of the same microbial genera in their rooting zone. This work describes the effect of *G. senegalensis* on the structure and function of the soil microbial community across three nested scales: a landscape level study across a rainfall and soil type gradient in actively farmed fields the Sahel, a long-term field experiment (the Optimized Shrub-Intercropping Study, OSS),

and a growth chamber mesocosm experiment using soils from the OSS but decoupled from the effect of the living shrub. Across all scales, a significant shrub impact was observed on the microbial community structure (at PLFA-, OTU-, lineage-, and genome-resolved levels) as well as the potential community function and presence and activity of genes related directly to PGPR activities. Notably, shrub presence in actively farmed sites along the rainfall gradient comprised a larger portion of community variance in the lowest carbon, lowest rainfall sites, while millet biomass at these sites remained the same as those in increased C and rainfall sites. This indicates that there may be a climate or soil type threshold after which the shrub has a greater impact on the microbial community and millet yields. Soils in the Sahel are typically low in organic matter, and subsistence farmers in this region typically coppice and burn shrubs before planting, depriving the soil of much-needed OM. However, in the OSS, shrub residues are returned to the soil, dramatically increasing soil C, presumably impacting the structure and function of the microbial community, as observed in the growth chamber experiment. Here, soils with a history of either +/-OSS management were used to grow millet without the effects of the living shrub (ie HL, root exudates, and fine root turn over) under an imposed drought. An OM amendment treatment of *G. senegalensis* residues was also imposed on both +/- OSS soil mesocosms. This OM treatment had a significant impact on community structure and function, and in some cases, explained more of the variance in the community than the history of intercropping. The OM amendment may have had an ameliorating effect on soil drying and supported a community both distinct in taxonomic and genetic composition pre- and post-drought. The strong impact of OM on both +/- OSS soils

provides ample support for incorporating OM in agricultural management practices in this region. Further, 263 metagenome assembled genomes (MAGs) were recovered for the from the OSS field study and growth chamber experiment. Many of these were either taxonomically related to PGPR or contained genes related to PGPR function, and were enriched under +shrub, +OM, and + drought conditions, indicating their likely role in increasing millet drought resilience. These MAGs also represent a huge leap forward in the genomic data gathered from semi-arid cropping systems in general, and the Sahel in particular. This region is ecologically important, environmentally and economically vulnerable, and highly understudied, so results of this study serve as a foundation for future 'genes-to-ecosystems' research in a larger campaign for food security and climate-smart agriculture in the Sahel and in semi-arid cropping systems globally.

Dedication

For Verna

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Vita

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FIELDS OF STUDY

Major Field: Environment and Natural Resources

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The Sahel is a semi-arid, ecologically fragile semi-arid, region where the staple crops are grown in the absence of irrigation and with little or no inorganic fertilizer (Belton and Taylor, 2002; Food and Agricultural Organization, 2015). Since the 1960s, productivity of crops such as millet remained unchanged (Food and Agricultural Organization, 2015). Yet at the same time, the population has increased by >250 % with a future prediction of greater dependence on international aid due to on-going population growth (UN, Department of Economic and Social Affairs, 2016).

The lack of crop production is related to soil degradation (Dai, 2013; World Food Programme, 2023) due to the loss of soil organic matter (SOM) (Lal, 2008). Low levels of SOM cause a reduction in soil structure, making the soil more susceptible to wind and water erosion (Bationo and Buerkert, 2001; Dossa, 2007). Another factor for this region is long-term, climate change, which is occurring about 50% more quickly than other parts of the world (IPCC 2018). This will exacerbate the ecological and agronomic challenges of the Sahel, further aggravating food security in this region (World Food Programme, 2023). Climate change is also a factor of desertification for the Sahel, which leads to loss of plant biodiversity and vegetative cover (D'Odorico et al., 2012). This loss of vegetative cover triggers negative feedback on rainfall, soil quality and a further decline in plant cover (D'Odorico et al., 2012).

The large population growth of this region has resulted in the reversal of traditional practices that remediated soils in the past, such as loss or shortening of fallow periods and adopting sedentary agriculture on smaller tracts of land (Buresh and Tian, 1998). Soils in sub-Saharan West Africa have high sand content and low biomass productivity, making SOM maintenance difficult. Furthermore, the high soil temperature leads to rapid rates of decomposition, further decreasing SOM pools. To compensate for low productivity and to feed the growing population, agricultural Sahelian populations by expanding geographical cropping by greatly reducing fallowing and notably increasing the area under cultivation (Food and Agricultural Organization, 2015). However, the latter is no longer possible as all arable land is now under cultivation – thus, putting the region at risk for a major famine (Food and Agricultural Organization, 2015). Thus, both soil degradation and desertification are in part due to cropping intensification, overgrazing, lack of water conservation, scavenging for fuel-wood, and human-initiated bushfires (Lambin et al., 2014). Lastly, another factor that affects crop productivity is that more than half of the people living in this region are subsistence farming households who directly consume the main carbohydrate crops of sorghum and millet (Belton and Taylor, 2002; Food and Agricultural Organization, 2015). These farmers have largely not adopted Green Revolution technologies in Sub-Saharan Africa due to economic constraints, supporting infrastructure, and limited agronomic performance of these technologies (Evenson, 2003; Godfray, 2010).

Thus to address the Sahalian ecological, agronomic and socio-economic challenges, local and biologically-based systems are needed that can remediate degraded soils and buffer against drought stress (Poppy et al., 2014; Prokka et al., 2021).

Agroecology, a potential solution for the Sahel (Elagib and Al-Saidi, 2020), embodies ecological principles to design and manage agricultural systems for greater sustainability using local, biological resources (Altieri, 2009). For millennia agriculture in the Sahel was based on these concepts and indigenous knowledge, which promoted biodiversity and resulted in domestication of crops (e.g. millet) well adapted for low rainfall and drought prone environments.

An ecological framework is being implemented in the "Great Green Wall" (GGW) program that was established in 2002 among 11 Sahelian countries (Puiu, 2019). The objective is to plant a 15-km wide forested band that spans from Senegal to Djibouti, along the East-West, southern border of the Sahara Desert. The GGW is being developed as a natural barrier by breaking desert winds, stabilizing the soil, and preserving structure of Sahelian ecosystems (O'Connor & Ford, 2014; Vetaas, 1992). However, this is an approach to stop desert encroachment and only affects a very small area of the Sahel and would not affect the on-going degradation of soils and low crop productivity of this region.

The agroforestry parkland system of the Sahel, where crops are grown next to scattered trees and shrubs, is a form of agroecology that has developed naturally over millennia and is the predominant agricultural system in the Sahel (Bayala et al., 2015; Pullan, 1974). This came about because some woody species survive or are preserved by farmers after fallowed fields are slashed and burned to grow crops (Bayala et al., 2014). The incentive for farmers to preserve certain trees and shrubs is that they provide animal fodder, marketable products (e.g. fruits, firewood) or medicinal benefits (Sinare & Gordon, 2015). In a comprehensive review of parklands plant species, Pullan, (1974)

reported there were four dominant trees species in the Sahel: *Andansonia digitata* (baobab), *Faidherbia albida* (winter thorn) *Vittelaria paradoxa* (shea), and *Parkia biglobosa* (locust bean). Although each of these can have economic or social benefits, only *Faidherbia albida* (Del.) A. Chev., favors crop production because of its reverse phenology. Its only value is firewood, typically has low densities of 30 trees ha^{-1}, is slow growing and crop yield benefits take 4 to 6 years after seedling establishment (Sanchez, 1995; Stoate and Jarju, 2008; Garrity et al., 2010). However, trees as mentioned above have limited capacity to remediate soils and increase crop productivity in the Sahel due to issues of shading and low densities that leave the soil in the intra-tree space unaffected by trees (Bayala et al., 2014).

Native evergreen shrubs (Pullan, 1974; Wezel, 2000; Tappan et al., 2004) until recently have largely been overlooked as a beneficial resource in the Sahel (Lufafa et al., 2008). Recent research has shown native shrubs, especially *Piliostigma reticulatum* and *Guiera senegalensis*, have great potential to both remediate degraded soils and increase yields of rainfed crops in the Sahel (Bright et al., 2017, 2021; Dossa et al., 2012; 2013) Advantages of shrubs over trees are: higher densities, limited competition for light, and prevention of erosion by entrapment of windblown sediment leading to higher fertility soils (Sinare and Gordon, 2015).

Optimized Shrub Intercropping

Woody shrub species have potential to deliver ecological and agronomic benefits on all cropped land of the Sahel (O'Conner and Ford, 2014). Shrubs reduce wind speeds, increase soil humidity, and stabilize soil nutrients, allowing other plant life to flourish in surrounding areas (Gómez-Aparicio et al., 2005). The two main advantages that shrubs

have over trees are a faster growing rate and the ability to reach maturity within a fraction of the time compared to trees. Furthermore, in areas where plant life has been removed, shrubs are often the primary pioneer species and typically establish years before tree species (Dalling and Hubbell, 2002).

The spatial patchiness of trees and shrubs in natural desert and semiarid environments has long been recognized in creating "islands of fertility" (Schlesinger et al. 1996). Shrubs in particular create soils beneath their canopies that have higher C, N, and microbial activities, and improved microclimate and water availability (West 1991; Gallardo and Schlesinger 1995; Schlesinger et al. 1996; Kieft et al. 1998; Van Miegroet et al. 2000; Kizito et al. 2007). However, until fairly recently it was largely unknown whether shrubs played an ecological role in cropped fields of the Sahel.

From a practical perspective, OSS, using G. *senegalensis* or *P. reticulatum*, is well-suited for subsistence farmers of the Sahel. This is because these shrubs are locally available, indigenous, widely distributed establish quickly (Seghieri and Simier, 2002, Hiernaux P, et al., 2009; Herrmann andTappan, 2013;, Hänke et al. 2016), and are infrequently grazed by livestock (Lahmar et al., 2012; Lufafa et al., 2008). These shrub species are naturally found throughout the Sahel (Lufafa et al., 2008) and typically the primary species in farmers' fields with *G. senegalensis* dominating in northern (drier conditions 200-600 mm annual rainfall) and *P. reticulatum* in southern (wetter 500-1000 mm). *G. senegalensis* and *P. reticulatum* are found randomly spaced at low densities (~130 to 350/ha; Lufafa et al., 2008), are unmanaged (but have other uses such as fencing, fuel, and medicinal) except that aboveground biomass is typically coppiced in the spring and often burned, depriving soils of organic inputs. Under OSS, however,

shrubs are coppiced, and the residues are incorporated into the soil before planting (Dossa et al., 2012, 2013). This serves to both increase N, P, and C in the soil and to reduce further C emissions to the atmosphere through burning. Shrubs are also grown at higher densities (1200 – 1500 ha^{-1}) than in farmers' fields, and work is being done to characterize the effects of shrub density on crop yield for application in subsistence farming.

It has been observed that crops receive more benefit when grown near shrubs (Kizito et al., 2006; Mason et al., 2023). Despite this, little competition for resources has been observed between the millet and shrub plants and greater in-season growth has resulted (Bright et al., 2021). It may also be that millet tends to use water at the surface. The shrubs tend to use water deeper underground or a that millet and shrub growth, and associated rainfall use is temporally off-set with millet plants using more water in the early rainy season and shrubs using more water in the late growing season (Bright et al., 2017; Kizito et al., 2006).

Finally, shrubs are very deeply rooted, and this provides physical benefits the surrounding soil ecosystem (Kizito et al., 2006). Shrub root density, diameter, and biomass all increase with depth, and soil moisture increases surrounding the shrubs' roots. Soil temperature beneath the shrub canopy is about 5°C cooler than outside of the canopy, resulting in reduced evaporation and increased soil moisture (Kizito et al., 2006). The shrubs also perform hydraulic lift (HL), which moves water from wet sub-soil above the water table to dry surface soil through deep tap roots (Kizito et al., 2012). Recently, Bogie et al. confirmed HL water was directly transferred from *G. senegalensis* to adjacent millet plants during a simulated in-season drought (2018). The authors used δ^2H

labeled water irrigate shrubs and found the ^{2}H-tracer in the tissues of adjacent millet plants about starting 12 hours after application to shrubs, confirming the direct transfer of water from shrubs to millet.

However, the amount of water transferred to inter-cropped millet was not enough to sustain millet productivity. Another very curious finding of the simulated drought experiment was that the soil in both + and – shrub plots became severely dry and by 12 days after the water was stopped the water potential was -3 MPa, well below the permanent wilting point. However, enough water was available in the presence of *G. senegalenis* for intercropped millet to reach maturity and produce a yield, which did not happen with sole-cropped millet. This leads to the one of the fundamental questions of this work – how can such small amounts of HL water be delivered so efficiently that millet is able to keep growing? It has previously been hypothesized that a microbial community, supported by the shrub, is the driving force behind the dramatic yield increases observed in intercropped millet. In fact, research has shown that optimized intercropping with *G. senegalensis* can increase microbial diversity and promote a distinct microbial community (Diedhiou et al., 2009; Diakhate et al., 2016). Debenport et al. (2015) also showed that the +OSS plots enriched for potential PGPRs, including members of *Bacillus*, *Chitinophaga*, and *Actinobacteria* species, which have been shown to produce plant growth-promoting and pathogen suppressing compounds, as well as other mechanisms of plant growth promotion (Egamberdeiva et al 2017; Pal and McSpadden Gardener, 2006; Sharma et al., 2013; Shirinbayan et al., 2019).

Microbial mechanisms of drought stress mitigation

Microbial mechanisms that are known to directly reduce water stress in plants include: (a) production of plant phytohormones (Dimkpa et al., 2009; Kang et al., 2014); (b) production of antioxidants to protect against reactive oxygen species (ROS) which are produced during water stress and damage plant DNA; (c) degradation of an ethylene precursor and thereby diminishing plant senescence (Lim and Kim, 2013; Mayak et al., 2004); (d) the production of osmolytes (Dimkpa et al., 2009; Hare and Cress, 1997). Soil microbes also contribute to soil function by improving soil structure through (e) excretion of exopolysaccharides that stabilize the soil and aid in water retention (Czaczyk and Myszka; Liu et al., 2013), and (f) C sequestration, N fixation, and P solubilization (Bright et al., 2017; Cardon et al., 2013; DeForest et al., 2012; Dossa, 2012; Rodríguez and Fraga, 1999; Vitousek et al., 2010)

Direct Microbial Mechanisms of Drought Stress Mitigation in Plants

The microbial community produces phytohormones, directly regulating host above and below-ground plant morphology and metabolism in response to drought (Egamberdeiva et al 2017). Common phytohormones for plant growth are produced by the microbial community and include cytokinins, gibberellins, and auxins (Egamberdeiva et al 2017; Vurukonda et al., 2016; Yadav et al., 2020; Zarei 2020). Cytokinins are hormones involved in stomatal opening, cell division, and growthmand a decrease in their concentration is typically observed under drought (Bielach et al., 2017; E et al 2017; Osugi and Sakakibara, 2015). Cytokinin-producing species, including members of the genera *Arthrobacter*, *Bacillus*, *Azospirillum*, *Pseudomonas*, and *Halomonas*, have been shown to stimulate root development of plants (Egamberdeiva et al 2017). Under non-

stressed conditions, gibberellins also control cell growth, but under drought stress function to increase belowground growth, allowing for more uptake of water (Colebrook et al., 2014). Auxin amendments, like indole acetic acid, are produced by microbes and can cause a decrease in ROS production, induce root growth, improve absolute and relative water content to improve drought response in mature tissues. Example organisms include *members of Actinobacteria, Arthrobacter, Azotobacter, Pseudomonas, Bacillus, Mesorhizobium, Rhizobium, and Streptomyces* (Sharma et al., 2013; Egamberdeiva et al 2017; Shirinbayan et al., 2019).

The microbial community can also produce phytohormones that activate pathways involved with increased drought resilience including, abscisic acid, salicylic acid, and ethylene (Egamberdieva et al., 2017; Vurukonda et al., 2016; Zarei 2020).An increase of another phytohormone abscisic acid signals stomatal closure (Egamberdeiva et al 2017). Under drought conditions, an increase of abscisic acid is typically observed in plant roots and leaves, followed by a decrease in stomatal conductance that allows plants to retain water, and therefore tolerate stress better (Pospisilova et al., 2005). The production of abscisic acid can be stimulated by the microbial community directly or indirectly (Liu et al., 2013), and example organisms include members of *Azospirillum, Klebsiella, Phyllobacterium and Proteus genera* (Arzanesh et al., 2011; E et a l 2017; Vurukonda et al., 2016).

Salicylic acid has numerous roles in mitigating drought stress including the degradation of ACC-deaminase and the lowering of ROS production in the host cells (Egamberdieva et al., 2017). In the presence of different microbial communities, the antioxidant response by the host plant varies. For example, *Pseudomonas spp*. strains

namely (*P. entomophila, P.stutzeri, P. putida, P. syringae, and P. montelli)* have been shown to decrease overall antioxidant production in maize (Sandhya et al., 2010), but other combinations of *Pseudomonas* increased leaf content of antioxidants in rice (Gusain et al., 2015). When stressed, plants produce reactive oxygen species which can damage plant tissue and DNA. Microbial symbionts, as well as their plant hosts, produce antioxidants to degrade, or "scavenge", these reactive oxygen species (Vurukonda et al., 2016). Universally observed antioxidants include ascorbate peroxidase and catalase, which reduces hydrogen peroxide to water, superoxide dismutase which reduces superoxide to hydrogen peroxide and oxygen, and glutathione peroxidase which destroys toxic peroxides.

Ethylene, a hormone produced by almost all plants, displays a wide range of effects on plant growth. Decreased ethylene content has been associated with root elongation and decreased sensitivity to drought stress (Danish et al., 2020, Zaheri 2020). The microbial community can control ethylene content by regulating by producing ACC-deaminase. Phytohormones salicylic acid, indole acetic acid, gibberellins, and auxin, also regulate the production of ACC deaminase. This is important because AAC-deaminase degrades 1-aminocyclopropane-1-carboxylic acid (ACC) through deamination (Egamberdeiva et al., 2017; Vurukonda et al., 2016; Zaheri, 20202). Microbes can also produce ACC-deaminase directly (Vurukonda et al 20216). Previous research has shown decreased ethylene levels in inoculated plants compared with uninoculated plants, implying that the presence of the microbial community increased the plants' fitness under stress (Mayak et al., 2004). Therefore, a degradation of ACC decreases the amount of ethylene available in the cell and increases tolerance to several stressors, including

drought stress. Microbes responsible for the direct production of ACC deaminase include *Azospirillum sp., Pseudomonas sp., Bacillus sp., Rhizobium sp*. (Egamberdeiva et al., 2017; Garcia et al., 2017; Orozco-Mosqueda et al., 2020; Zarei, 2020).

The microbial community also plays a role in the production of osmolytes, compounds that increase a host plant's ability to tolerate water stress in drought. These include proline, which mediates and regulates water concentrations inside and plant cells and scavenges free radicals (Hare and Cress, 1997). The microbial community can stimulate proline production in the plant (Vurukonda et al., 2016). Elevated proline can be found in plants the presence of abundant plant growth promoting rhizobacteria like *Burkholderia* and *Bacillus* under drought-stressed conditions (Dimkpa et al., 2009). Soluble sugars (Zarei 2020) increase under drought and help maintain water content and turgor pressure in the cells, and soluble sugar content can be modified by members of the microbial community such as *Pseudomonas fluorescens* (Zarei et al., 2020). Other common osmolytes include choline and trehalose, which are by the microbial community and taken up by the plant where each can stimulate a stress response pathway (Chandra et al., 2020; Orozco-Mosqueda et al., 2020; Vurukonda et al., 2016).

Indirect Microbial Mechanisms of Drought Stress Mitigation in Plants

Soils in the Sahel are sandy and characteristically low in soil organic matter; however, OSS has been shown to dramatically increase percent total C and POM (>3700 kg ha^{-1}). This increase can be attributed to the incorporation of shrub residues (Dossa et al., 2008; Bright et al., 2021) and root exudates and fine root turn over which acts to promote aggregation and improve soil structure and water holding capacity (Panchal et al., 2022; Bayala et al., 2022). Soil C can also come from microbially produced

exopolysaccharides (Sandhya et al., 2009). These high-molecular weight compounds are produced by a wide range of microorganisms, including *Bacillus sp., Pseudomonas sp., Bradyrhizobium sp*, and many others (Naseem & Bano, 2014; Naylor & Coleman-Derr, 2018; Deka et al 2019; Farias et al., 2022). Exopolysaccharides are major components of biofilms that allow for root colonization and increased water retention, as well as improve soil structure (Sandhya et al., 2009, Deka et al., 2019), all of which are linked to increased plant biomass under conditions of water stress (Naylor & Colemann-Derr, 2018; Naseem & Bano, 2014). Improving soil structure and storing C are also key factors in slowing soil degradation in the Sahel, a major challenge to maintaining future crop productivity (Lahmar et al., 2012).

In addition to increased soil moisture and soil C storage though production of exopolysaccharides, soil microbes contribute directly to soil function, and thus indirectly to plant health, by fixing N and solubilizing P (Bright et al., 2017; DeForest et al., 2012; Dossa, 2012; Vitousek et al., 2010). In the Sahel, Dossa et al. (2009) found lower P sorption for soils under the *G. senegalensis* canopy and greater N, P, and C retention with fertilization. Dossa et al. (2012) showed an increase in P and N in biomass upon showing a greater capacity for nutrient uptake in intercropped systems (Dossa et al., 2012; Zarei, 2020). Improved water holding capacity, combined with hydraulic lift, can be linked to enhanced N fixation and the solubility of nutrients (Cardon et al., 2013; Zarei, 2020).

Finally, it has also been observed that OSS shortens the time to maturity for millet and peanut (Bayala et al., 2021). Shortened time to maturity may allow for farmers to grow and harvest their crops in times of erratic rainfall. The microbial community's ability to produce phytohormones or other signals may be the cause, (Vurukonda et al.,

2016), and further metagenomic inquiry will allow us to better investigate this phenomenon.

Conclusions

The Sahel is characterized by erratic rainfall and vulnerability to climate change-induced drought (Dai, 2013). The growing Sahelian population will increase food demand and insecurity in the coming decades, given that most of the population depends on subsistence farming. Therefore, a locally based and economically feasible means of food production are needed. Previous research has shown that the OSS increases soil N, P and C and moisture (Bogie et al., 2018; Bright et al., 2017; Dossa, 2012; Kizito et al. 2012), as well as significantly impacting microbial community composition and diversity (Diedhiou et al. 2009; Debenport et al., 2015; Diakhaté et al., 2016). However, little is known about the presence or absence of microbes that confer drought resilience nor the mechanisms by which they confer it to intercropped millet. This information is critical to inform on best intercropping practices. The global objective of this dissertation was to investigate soil microbiome dynamics of the Optimized Shrub-intercropping System in mediating drought resistance in pearl millet in the Sahel.

The specific objectives were to:

1. Determine microbial community and functional shifts in pearl millet root zone soils with *Guiera senegalensis* intercropping along a rainfall and soil type gradient in the Sahel.
2. Characterize organisms, community compositional, and shifts in potential function in an Optimized Shrub-Intercropping System at lineage-, gene-, and

genome-level resolutions with particular attention paid to potential PGPRs and PGPR functions.

3. Characterize organisms, community compositional, and shifts in function of active and total microbial communities in a growth chamber mesocosm study using soils from the OSS long term experimental site, decoupled from the presence of the living shrub and under an imposed early season drought. Particular attention will be paid to PGPRs (via OTUs, lineages, and metagenome assembled genomes) and PGPR functions (via gene content in metagenome assembled genomes and protein clusters).

Globally, understanding the effects of drought stress is a critical component of maintaining food security for a growing population. the Sahel region of West Africa is a vulnerable ecosystem that is predicted to experience enhanced effects of climate change compared with other regions (Elias et al., 2016; Steele et al., 2018). Elucidating the relationships between plants and microbes and the roles their interaction play in drought mitigation will become a critical challenge in food security for major cash crops (Xu et al., 2018). With this knowledge, we can logically propose agricultural procedures that restore currently degraded landscapes and help develop effective and sustainable agricultural systems in the Sahel and with implications for semi-arid regions world-wide.

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Chapter 2. Microbial community shifts in pearl millet root zone soils with *Guiera senegalensis* intercropping along a rainfall and soil type gradient in the Sahel

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Abstract

The Sahel of West Africa is a vulnerable biome that is experiencing rapid population growth, agricultural intensification, and soil degradation that threatens food security. A potential solution is intercropping with the indigenous shrub, *Guiera senegalensis*, that coexists with crops to varying degrees in farmers' fields throughout the Sahel. Previous research of the Optimized Shrub-intercropping System (OSS) *with G. senegalensis* (high density of ~1200 1500 shrubs ha-1 with annual incorporation of coppiced residue) has been shown to dramatically improve pearl millet (*Pennisetum glaucum*) yield; attributed in part to improved soil quality, nutrient availability, water use efficiency and harboring a distinct and active microbial community that may confer benefits to surrounding crops. Whether this microbial response is consistent over a climate and soil type gradient in farmers' fields has not been investigated. Therefore, the objective was to determine the microbiomes and metabolic pathways of millet root zone soil in the presence or absence of *G. senegalenis*, sampled along a north-south soil and rainfall gradient in farmers' fields. The experimental design was a completely randomized 3 X 2 factorial (2 landscape replications) with the following treatments: three rainfall (450 to 750 mm per annum)/soil type gradient sites north to south in the Senegal Peanut Basin and two sampling location treatments (millet root zone soil within and outside the influence of the *G. senegalensis*). *G. senegalensis* shifted certain predicted bacterial metabolic pathways

and enriched certain bacterial and fungal genera, some of which are known to have plant growth promoting properties. These positive shrub effects were most evident at the northern site that has low rainfall and low organic matter soils.

Introduction

The Sahel is a semi-arid, ecologically fragile region where the staple crop pearl millet (*Pennisetum glaucum*) is grown with limited or no inorganic fertilizer and no irrigation (Belton and Taylor, 2002; Food and Agricultural Organization, 2015). This region is also under threat of soil degradation, desertification, and food insecurity, which will be exacerbated by climate change (Dai, 2013; World Food Programme, 2018). This increases the likelihood of conflict and mass migration from the region (Brown, 2008; Lambin et al., 2014). In Senegal about 47% of the population is already food insecure (World Food Program, 2018), and the United Nations estimates a nearly 600% increase in population by the year 2100, potentially forcing this country to rely substantially on international aid to meet its food needs (United Nations, 2016).

To address these ecological, agronomic, and socio-economic challenges, local and biologically based cropping systems are needed for the majority, subsistence farmers who grow food crops such as millet. Agroforestry where woody species are interplanted with crops, and sometimes referred to as "parkland agroforestry" in this region (Bayala et al., 2014), has potential to deliver services that can be utilized by rural communities in the Sahel. One such system is Optimized Shrub-intercropping Site (OSS). This system intercrops the native shrub, *Guiera senegalensis* at increased densities (3 – 4 times the densities found in currently in farmer's fields: ~1500 shrubs ha^{-1}) where coppiced biomass is annually incorporated into soils. Previous research on OSS has shown that this

approach dramatically increases millet crop productivity (Dossa et al., 2012, 2013; Bright et al., 2017; 2021).

G. senegalensis is widely found in Senegal and throughout the Sahel but at relatively low densities in farmers' fields (200-350 shrubs/ha) (Lufafa et al., 2008). The absence of mechanized agriculture enables these native plants to co-exist with crops in the Sahel. *G. senegalensis* is well adapted to drought conditions and does not compete with millet for water (Kizito et al., 2006). Currently, farmers do not manage these shrubs except to coppice in the spring and unfortunately burn this residue, depriving soils of organic inputs (Diedhiou et al., 2009). The OSS is based on the ability of *G. senegalensis* to be a companion plant in cropped fields (Dossa et al., 2012; 2013). Extensive research has shown that OSS increases nutrient content and organic matter of soils and increases the microbial community diversity and activity (Dossa et al., 2009; Diedhiou-Sall et al., 2013; Debenport et al., 2015). OSS has also been shown to increase crop biomass and yields, and buffer against in-season drought (Dossa et al., 2012; Dossa et al., 2013; Bright et al., 2017; Bogie et al, 2018; 2018; Bright et al., 2021).

In part this resistance to drought can be attributed to the finding that *G. senegalensis* performs hydraulic lift (Kizito et al., 2012) that Bogie et al. (2018) found could "bio-irrigate" adjacent millet plants. However, the amount of water transferred to inter-cropped millet is relatively low. None-the-less, yield responses to OSS with *G. senegalensis* over sole cropping have been nearly 900% (Bogie et al., 2018) to as high as 2600 % (Bright et al., 2021) in the absence of fertilizer application in long-term studies. This suggests that there are additional mechanisms of drought resilience conferred by shrubs. Given that there are microorganisms known to promote plant growth and drought

resilience (Vurukonda et al., 2016), this could be another mechanism conferred by OSS, but is entirely uninvestigated.

There is very little information on the influence of shrubs across soil types and climate moisture regimes within farmers' fields on soil microbial community dynamics. Therefore, the objective of this study was to determine shifts in millet root zone soil on microbiomes, predicted metabolic pathways, enzyme activities and extractable nutrients in relation to millet growth, due to the presence or absence of the shrub, *G. senegalensis*, along a rainfall/soil type gradient of the Sahel W Africa. Specifically, use of amplicon sequencing was done to determine whether shrubs harbor beneficial microorganisms known to promote plant growth as a further mechanism that contributes to the yield response of OSS.

Methods

Site Description and Experimental Design

The study was done in the Peanut Basin of Senegal, (14.70°N, 16.00°W) in a semi-arid savannah with vegetation consisting primarily of shrub land with scattered trees which is known as the Parkland system. The mean annual rainfall is 540 mm, with the majority of the rainfall occurring between August and October (Lufafa, 2008). Between 70 and 80% of the soils are sandy Ustipsamments classified as Dior with less than 1% soil organic carbon. The remaining soils are generally the Deck soil classified as Psammentic Haplustalfs, which has a higher quality than the Dior soil and only found in depressional, low landscape positions (McClintock and Diop, 2005). Shrubs and trees are the dominant vegetation in this savanna. *G. senegalensis* is a dominates in the north and *P. reticulatum* dominates the southern part of the Peanut Basin.

All sites were in fields under the management of separate farmers and have been managed in a peanut (*Arachis hypogea*)–pearl millet (*Pennisetum glaucum*) rotation for over 50 years as reported by collaborating farmers. The typical practice is that shrubs are coppiced in May and early June and burned. Prior to crop planting (~late June for Southern sites to late July in Northern sites) fields receive shallow (0-10cm) sweep tillage and during the growing season are weeded with an in-row cultivator by animal traction and some hand weeding. Crops are planted with animal drawn small planters with the on-set of the rainy season. Regrowth of shrubs during the growing season is coppiced and laid between cropped rows. Little or no commercial fertilizer is used with small amounts of animal manure applied every few years (Badiane et al., 2000)

The experimental design was a 3 X 2 factorial with the following treatments: three rainfall/soil type gradient sites; two shrub sampling location treatments (inside and outside the influence of *G. senegalensis*); and five replicates. Within each rainfall/soil site, there were two spatially separated landscape-level replications. The three rainfall gradient sampling sites were chosen along a north-south rainfall gradient in the Peanut Basin of Senegal which were: 1) Louga (Northern - 15.28° N, 15.53° W), 2) Theis (central - 14.78° N, 16.90° W), and 3) Kaolack (Southern - 14.18° N, 16.25° W), which have average annual rainfall regimes of 450, 550, and 750 mm, respectively. The soils were sandy being 95, 92, and 86 % sand for Northern, Central and Southern sites, respectively. Each field site was on a different farm. The two soil sampling location treatments were: 1) two millet plants within the influence of the *G. senegalensis* (<1 meter from the center of the shrub); and 2) two millet plants outside *G. senegalensis* influence (>4 meters from the shrub center) based on Dossa et al. (2010) who showed

little or no influence of the shrub at 3 m.

Sampling

Soil samples were obtained for soil chemical analyses and extracellular enzyme activity assays in 2012 and 2013 and for microbial DNA extraction in 2012. The two millet plant treatments were sampled across the sites over a two-week period from last week in August (Southern Site) through second week of September (Central and Northern sites) in both years. Both years, soil cores (0 – 20 cm by 2.54 cm dia.) were taken through the center of the millet root zone, stored in Ziplock bags, and transported on ice. In 2012, samples for microbial DNA extraction from the rhizosphere soil were placed in a plastic Ziplock bag and stored at -20º C without sieving. All soil core samples for enzyme and nutrient analyses (2012 & 2013) were passed through a 2-mm sieve and gravimetric moisture content was measured prior to analysis.

Millet plants were harvested at the time of soil sampling both years. Notably millet plants under the influence of *G. senegalensis* were consistently in late stages of tillering and early panicle initiation whereas millet plants outside the influence of this shrub were in earlier stages of tillering. Two millet plants were harvested at each sampling location, and the aboveground fresh biomass was weighed and then averaged to give g plant^{-1} biomass.

Soil Chemistry

Soil pH was determined using a 1:2 soil:water slurry and a glass membrane electrode. Total C and N were measured using a Carlos Erba Elemental Analyzer (Milan, Italy). The nutrients PO_4-P, SO_4-S, K, Ca Mg, B, Zn, Fe, and Cu were measured on a Melich 3 extraction procedure on 2 g of air-dried soil as described Melich (1984),

followed by Inductively Coupled Plasma Atomic Emission Spectrophotometry analysis. Ammonium (NH_4^+) and nitrate (NO_3^-) were determined calorimetrically by flow injection analysis as described by Mulvaney (1996). NH_4^+ and NO_3^- analysis was done by extracting soil with 1 M KCl, passed through a glass fiber filter and extract determined by the salicylate-nitroprusside and the hydrazine-sulfaniliamide colorimetric methods, respectively.

Enzyme Assays

Activities of acid phosphatase (EC 3.1.3.2 orthophosphoric-monoester phosphohydrolase), and ß-glucosidase (EC 3.2.1.21 ß-D-glucoside glucohydrolase) were determined as described by Tabatabai (1994) with the following adaptations: acid phosphatase were determined with *p*-nitrophenyl phosphate as the substrate in a modified universal buffer (MUB) (pH 6.5) where the reaction was stopped with 0.5 *M* NaOH after a one-hour incubation**.** β-glucosidase activity used the substrate *p*-nitrophenyl β-D-glucose in a modified universal buffer (MUB) (pH 6.0) and *Tris*-hydroxy aminomethane (THAM) (pH 12) was added to stop the hydrolysis reaction. *N*-acetyl-β-D-glucosaminidase (EC 3.2.1.30) (chitinase) activity was determined as described by Parham and Deng (2000) with the following modifications: 0.25 g field moist soil was added to p-nitrophenyl-N-acetyl-β-D-glucosaminide substrate in a acetate buffer (pH 5.5) solution and reaction was stopped with 0.5 *M* NaOH. No toluene was used in these assays because of the short incubation time. All assays were incubated at 37º C for 1 hour. Following incubation after stopping the reaction, the solution was centrifuged for 5 minutes at 10,000 RPM and the supernatant was collected and color developed of the product *p*-nitrophenol (ρNP), was measured using a spectrophotometer at 410 nm

(Ultrospec 3000, Pharmacia-Biotech). Final concentrations of all above assays were determined in reference to a ρNP standards curve at 0, 5, 10, 15, 20, and 30 µg of ρNP. Controls were performed with each sample where the substrate was added after the incubation period was completed by killing the reaction, to account for color not derived from hydrolysis of substrate in the presence of soil. Enzyme activities are reported as µg ρNP g^{-1} dry soil h^{-1}.

Urease (EC 3.5.1.5 urea amidohydrolase) activity was determined following the buffered procedure as modified by Kandeler and Gerber (1988). To account for color development not from the urease enzyme, controls were treated with 2.5 mL of 0.72 M urea solution after incubation. Enzyme activity was recorded as µg N g^{-1} dry soil h^{-1}. Results of enzyme activities are reported on an oven-dry-weight basis, determined by drying soils for 24 hours at 105°C.

Analysis of Microbiomes

The overall data generation and analysis workflow flow of the 60 samples is summarized in Figure S1. Bacterial and fungal DNA was extracted from 0.25g millet rootzone soil via the MoBio PowerSoil DNA kit per the manufacturer's instructions. Agarose gel electrophoresis was used to confirm adequate genomic DNA, which was then used as a template for the polymerase chain reaction to amplify two gene regions: the 16S rRNA gene V3 region, for bacteria and archaea, and the internal transcribed spacer (ITS) 2 region, for fungi. Briefly, PCR master mix was made of 5x GoTaq Flexi Buffer (Promega Corporation), 2mM MgCl2, 2mM dNTPs, PCR water, GoTaq Flexi Polymerase, RNAse ONE, Illumina forward and reverse primers + individual adapters for multiplexing (Table S1), and 1 µL genomic DNA. The ITS2 and 16S rRNA gene V3

regions were amplified using Illumina F and R primers as follows: 16SrRNA gene primers 341F (5'-CCTACGGGAGGCAGCAG-3') and 534R (5'-ATTACCGCGGCTGCTGG-3'); ITS primers ITS3 (5'-GCATCGATGAAGAACGCAGC-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'). The 16S rRNA gene V3 region was amplified with the following thermocycler protocol: 95°C for 5 min, followed by 20 cycles of 95°C for 1 min, 50°C for 1 min, and 72°C for 1 min, with a final elongation protocol of 72°C for 7 min. The ITS2 region was amplified with the following: 94°C for 3 min, followed by 35 rounds of 94°C for 45 sec, 50°C for 60 sec, and 72°C for 90 sec, with a final elongation step at 72°C for 10 min. PCR success was confirmed via 0.7% agarose gel electrophoresis visualization of amplicons. Amplicons were gel purified and sequenced on the Illumina GaIIx platform at the Molecular and Cellular Imaging Center at Ohio State University. Raw reads are available at NCBI under accession number PRJNA856249.

Bioinformatics

Raw reads were prepared for analysis using QIIME 2-2019.1 in 2019 (Bolyen et al., 2019), within which denoising was performed via Dada2. At the time of denoising, raw reads were split into 16S V3 reads and ITS reads based on alignment to the 99% SILVA.132 database. Quality control steps determined that forward reads were too degraded to provide much useful data, and so they were discarded, and reverse reads were used. Operational taxonomic unit (**OTU**) clustering was performed at 99%. Taxonomy was assigned via the 99% UNITE (fungal) and SILVA138.1 (bacterial and archaeal) databases, and OTU and taxonomy tables were exported for further analysis.

OTUs that were significantly enriched or depleted in either the presence or the

absence of shrubs in at least one site were then determined via Linear Discriminant Analysis Size Effect (LEFSe-1.1.2) (Segata et al., 2011). Within LEFSe, a factorial Kruskal-Wallis test determined differences in the presence and absence of shrubs across all sites site communities ($P < 0.05$), and pairwise Wilcoxon signed-rank test was used to verify this enrichment in the Northern, Central, and Southern sites respectively. The threshold LDA score for discriminative OTUs was log (2). Using the SILVA138.1 16S database, OTU identity was confirmed to the genus level for all but two bacterial OTUs. The 99% OTU UNITE database and the SILVA138 18S database were used to determine further resolution of the fungal OTUs, but only one was identified beyond the phylum level (Quast et al., 2013).

The PICRUSt2 pipeline was then used to predict the functional profile of the bacterial and archaeal community based on the reverse complement 16S rRNA gene amplicon profiles generated by seqtk1.3 (Li, 2018). The PICRUSt2 pipeline uses phylogenetic context relative to physiologically known references to predict metabolic gene-family copy numbers (Douglas et al., 2020). Predictions were classified by the Kyoto Encyclopedia of Genes and Genomes (KEGG) Orthologs (KO) database, Enzyme Commission numbers, and MetaCyc (Langille et al., 2013; Douglas et al., 2020). The resulting list of predicted metabolic pathways associated with each community was then analyzed via LefSe-1.1.2 as above for enrichment by region or by shrub presence, and discriminant pathways were further defined using the MetaCyc reference database.

Statistics

R version 4.0.2 was used for all statistical analyses. Wilcox Signed Rank tests were used to determine the effect of site and soil sampling location on millet growth.

Tukey's HSD was used to means separation of site and sampling location on millet growth response, relative abundance of taxa, and enzyme activities. Preprocessing of OTU and taxonomy tables was performed using the Phyloseq package. Reads were rarefied to an even depth prior to calculating Shannon's Diversity and species richness. Non-rarefied data were then square root transformed and Non-metric Multidimensional Scaling (NMDS) and Permutational Analysis of Variance tests (PERMANOVA) were performed to determine differences in the compositions of the microbial and fungal communities and potential drivers of these differences. Spearman's correlations were used to determine relationships among OTUs, millet health characteristics, and site descriptors (Figure S1).

Results

Millet Response

At time of sampling, millet had significantly greater fresh biomass in the presence of shrubs at all sites ($P < 0.05$). Millet grown in the presence of shrubs had an average fresh biomass of 463 g^{-1} plant, while millet plants grown outside shrub influence, averaged 115 g^{-1} plant. The shrub effect on millet biomass was highest in the Northern and Central sites. Conversely, there was no significant difference on millet biomass in the absence of the shrub treatment across the gradient sites (Figure 1A).

Soil Chemistry and Enzyme Activities

Total N and C increased north to south along the rainfall gradient in both the presence and absence of the shrub, and NH_4^+-N was highest in the central sites and lowest in the Southern sites (Table 1). There was a consistent shrub effect on total C and N across ($P < 0.05$) (Table 1). There was no significant shrub effect for the Northern and Central sites on soil pH, but there was at the Southern site

Table 1 shows soil chemical properties averaged over 2012 and 2013, where the presence of *G. senegalensis* significantly ($P< 0.05$) increased total C, total N, NH_4^+-N, and zinc but had no significant effect on Ca, Cu, Fe, K, Mg, SO_4-S, PO_4^-- P, or NO_3^-N (Table 1). The Mehlich extractable nutrients (excludes total N and C), NO^-_3-N, and NH_4^+-N varied between years, except for Zn and K which were similar between 2012 and 2013 (data not shown). There was also some variation for the ranking of extractable nutrients between sites that varied between years - the Northern site had the lowest levels in 2013, whereas during 2012 Ca, SO_4, and Cu had the highest levels in the northern region and the lowest in the southern region (data not shown).

All enzyme activities averaged over 2012 and 2013, were lower in the Northern sites compared with the Southern and Central sites but not always significant between sites at $P<0.05$ (Figure 2). The Northern site consistently had a significant shrub effect for the all enzyme activities, whereas the Central site this effect was shown for β-glucosidase and β-glucosaminidase ,except for urease (Figure 2). Figure 2 shows that the most consistent impact ($P<0.05$) of *G. senegalensis* was on β-glucosaminidase (chitinase) and β-glucosidase activities at the Northern and Central sites. For the most part these averaged results were the same between years, except for the northern site in 2012 for acid phosphatase and β-glucosaminidase activities and in 2013 for β-glucosidase activity were significantly ($P<0.05$) affected by the presence of *G. senegalensis* (data not shown).

Alpha diversity and microbial community composition

Deep amplicon sequencing resulted in a per-sample average of 589981 post-QC reads. These produced 8,020 bacterial + archaeal 99% OTUs across 60 samples, 871 of which could be identified to the genus level, and 1,093 fungal OTUs, with 114 identified

to the genus level. Lineage accumulation curves suggest that 99% OTU diversity was saturated at this high per-sample sequencing depth (Figure S2), and for diversity metrics the data were rarefied to a depth of 250,000 and 45,000 reads per sample for bacterial + archaeal and fungal sequences, respectively. No statistically significant differences were observed in species richness or Shannon's Diversity with shrub presence across all sites, although fungal diversity increased with shrub presence in the Southern site and fungal richness increased with shrub presence in the Northern site (Figure S3).

Differentially enriched OTUs

Ten bacterial and four fungal OTUs were found to be significantly enriched in the presence or absence of the shrub. Thirteen OTUs (four fungal and nine bacterial) were significantly ($P < 0.05$) enriched by at least 2 log-fold in either the presence or absence of shrubs (Figure 3). One bacterial OTU and zero fungal OTUs were enriched in the absence of shrubs in at least one site. On average, the enriched OTUs comprised a very small proportion of the total community. The most abundant of these was an uncultured member of the bacterial order Vicinamibacterales (0.0700%) and *Burkholderia-Caballeronia-Paraburkholderia* (0.0003%) was the least abundant overall. In a simplified community composed of only the enriched OTUs, bacterial genus *Enterobacter* comprised a large part of the community (39.9%), and an unknown member of the fungal phylum Ascomycota was the least abundant (0.348%). Although there were differences in the relative abundances or log-fold enrichments of certain OTUs, all enriched OTUs are found at all three sites.

It was also observed that, similar to the pattern observed in both the fungal and bacterial communities, landscape sampling site was responsible for the most variation in

community composition across all sites (R^2 = 0.13), followed by shrub presence (R^2 = 0.06) ($P < 0.05$) (Figure 4). The strongest relationship between shrub presence and community composition was in the South site (R^2= 0.111), with the relationship between shrub presence and community composition in the Northern and Central site trailing behind (R^2 = 0.098 and 0.094, respectively), although the only site with significant enrichment + or - shrub was the South site ($P < 0.05$).

Many of the +shrub-enriched OTUs (three of the four fungal, and eight of the nine bacterial) were significantly and positively correlated with fresh millet biomass in at least one site (Table 2). It was more common for bacterial OTUs to positively correlate with millet fresh biomass in the Southern site (four of nine OTUs) and for fungal OTUs to correlate with millet fresh biomass at the central site (all four OTUs) (Figure 3). One bacterial OTU, *Paucibacter*, was correlated with reduced millet biomass across all sites, and this correlation was the strongest and most negative at the Central and Southern sites (rho = - 0.50 & -0.60, respectively) (Table 2). The strength of the correlations between each differentially enriched OTU and millet fresh biomass varied across samples and sites. There were no significant differences in the average strength of these relationships across the landscape (Table S4).

Beta diversity and drivers of community variation

In the total bacterial and fungal communities, NMDS with Bray Curtis distances resulted in clustering by landscape region first, and then by shrub sampling location in both the bacterial and fungal communities ($P < 0.05$). Therefore, the drivers of the overall bacterial and archaeal community were observed to be landscape sampling site (R^2 = 0.193), followed by shrub presence (R^2 = 0.050) (Figure 5). The drivers of the overall

fungal community followed a similar trend; region and shrub presence accounted for 10.8% and 2.7% of the variation in community composition. Additionally, total C accounted for the most variation in the fungal community ($R^2 = 0.113$), and interaction between total C and shrub presence was also a significant driver at the landscape scale ($R^2 = 0.24$) ($P < 0.05$).

Members of the bacterial + archaeal community significantly clustered by shrub presence within each site (Figure 5). 15.5% of the variation within the community within the Northern site could be explained by proximity to the shrub, and in the Central and Southern sites, shrub presence accounted for 8.6% and 4.6% respectively. Congruent with the clustering of enriched OTUs at the Southern site, the variation observed in the bacterial + archaeal community was significantly driven by total C ($R^2= 0.078$) and the interaction between total C and shrub presence ($R^2 = 0.096$) ($P < 0.05$). Percent total C was also the main driver in differences in fungal community composition across all sites ($R^2 = 0.11$), followed by region ($R^2 = 0.108$), shrub presence ($R2 = 0.027$), and the interaction between total C and shrub presence ($R^2 = 0.024$) ($P < 0.05$, Figure 6).

Predicted function

PICRUSt2 was used to predict metabolic pathways present in the community inferred by phylogeny. The composition of the pathways clustered by rainfall regime, which accounted for 7.4% of their variance (PERMANOVA, $P < 0.05$), and were significant drivers of community structure (Figure 7). Shrub presence did not influence the composition of community metabolic pathways in the dataset overall or at any site.

Despite not influencing the composition of metabolic pathways in the overall community the presence of the shrub enriched 74 specific predicted metabolisms across

regions related to biosynthesis and cell growth (P >0.05, LDA > log (2)). In the Northern site, 38 pathways were enriched +shrub, and 42 pathways were enriched -shrub. Twenty-six pathways enriched in the presence of the shrub at the Northern site were related to biosynthesis or growth, many of which were related to fatty acid biosynthesis. There were 21 related to biosynthesis were enriched in the absence of shrubs. Eight related to the degradation of compounds in the soil and their subsequent assimilation were enriched -shrub, and 14 were enriched +shrub. In the Southern site, 33 pathways were enriched in the presence of shrubs, and 24 pathways were enriched in their absence. In both the presence, 12 enriched pathways were related to biosynthesis of cellular compounds and cellular growth, whereas in the absence of shrubs, 16 pathways were related to biosynthesis (Figure S4, Table S4).

Discussion

Nutrient Dynamics

The effect on extractable macro- and micro-nutrients across the landscape gradient varied over 2012 and 2013. For instance, Ca levels were much higher in 2012 than 2013. Cu, Fe, K, Mg, and SO_4 levels were higher during the 2012 year for at least one of the sampling regions. This could be due to variations in rainfall observed between the two years. For instance, rainfall data collected from two research stations in Senegal showed that 2013 was a drier year, which would reduce microbial activity and in turn mineralization of nutrients from organic sources.

Research in arid and semi-arid regions has documented that woody species such as shrubs accumulate nutrients and organic matter, which is referred to as “islands of fertility” or “resource islands”. These distinct soil ecosystems have higher soil C and N, and improved microclimate and water availability (Schlesinger et al. 1996; Kieft et al.

1998; Van Miegroet et al. 2000). This is largely accomplished by roots exploring soil horizontally and vertically for nutrients and water, which are then redistributed in soil beneath woody species through litter input, root turnover, and root exudates (Gathumbi et al., 2003).

However, the "island of fertility" effect of the shrubs in this study was not reflected in extractable nutrient levels as a majority were not significantly affected in millet root zone soils in the presence of *G. senegalensis*. This can be attributed to tillage homogenization and burning of coppiced residues that occurred in these fields under farmer management (Lufafa et al., 2008; Dossa et al., 2012). In the case of PO_4-P, our results are contrary to Dossa et al., (2008; 2009; 2012) who found a significant shrub effect, likely because those studies were done at the long-term experimental site of Keur Matar, Senegal, where optimized shrub management had coppiced residue incorporated from shrubs at a much higher density (~ 1500 shrubs ha^{-1}) (Dossa et al., 2012) than in farmer's fields (200 - 400 shrubs ha^{-1}) (Lufafa et al., 2008). Further, it should be noted that the nutrients (except for inorganic N forms) in our study were extracted with the Melich 3 extractant, which captures plant available nutrient forms (Melich, 1984). Since the sampling was done during the growing season and from soil in millet root zone, it is likely all the nutrients were taken up by the millet plants, masking the shrub effect.

None-the-less, there was an "island of fertility" effect reflected in extractable zinc, and total N and C which in 2012 were at elevated levels across all regions in soils beneath *G. senegalensis*. Since total N and C likely is a more permanent shift in soil chemistry over extractable nutrients, this outcome supports *G. senegalensis* developing

resource islands in farmers' fields across a landscape gradient that varied in soil type and climate.

The elevated level of total N, and NH_4^+-N in the soils beneath *G. senegalensis* could be due to the stimulation of free-living N fixers. For example, a likely mechanism is that this shrub promotes diazotrophs – supported by observations that this shrub stimulates microbial biomass, diversity and activity (as shown in the current study and by Debenport et al., 2015).

Enzyme Activities

All enzyme activities were lower in the Northern sites than the Southern and Central sites, which can be attributed to lower production and stabilization of these enzymes in the soil matrix. This corresponds to the lower rainfall and sandy soils of the Northern region. Sandy soils generally have low soil organic content and cation exchange capacity, as do our Northern site soils (Table 1). Furthermore, sandy soils have high nutrient leaching rates (Pieri,1992; Sanchez and Logan, 1992). This was the case for the Northern site that had the lowest nutrient levels and total C (Table 1).

Extracellular enzymes are largely of microbial origin, with some enzymes having a significant fraction stabilized on soil colloids while remaining catalytic over long periods (Burns, 1982; Nannipieri et al., 1996; Knight and Dick, 2004). The activity of ß-glucosidase in soils, for example, is largely associated with this stabilized fraction (50 to as much as 75%, Busto and Perez-Mateos, 1995; Knight and Dick, 2004, respectively). A key factor for stabilizing enzymes is clay and organic matter content, and as the clay and organic matter content decrease there is less ability for extracellular enzymes to be protected in soils. Thus, given the sandy and low organic matter soils of the northern

region, it would be expected to have less potential to stabilize enzymes in the soil matrix, allowing for the decreased activities in this site.

In most cases, the presence of *G. senegalensis* in millet fields across the main cropping region of Senegal promoted enzyme activities. Both sampling years the activities of β-glucosidase, acid phosphatase, and β-glucosaminidase were highest in soils within the influence of the shrub and lowest in the millet root zone soils, far from the shrub. This enzyme response corresponded to the higher total C and N levels in soil beneath shrub canopies compared to outside the shrub, as discussed in the previous section. The presence of shrubs provides litter inputs, root exudates, and root turnover which are C and nutrient substrates that stimulate microorganisms to produce hydrolytic enzymes to degrade these compounds. In addition, the ability of *G. senegalensis* to perform hydraulic lift or redistribution could be another factor. Redistribution occurs at night when stomata close, which allows water to move through roots along a water potential gradient, from the wet subsurface to the dry soil surface (Scholz et al., 2002; Kizito et al., 2012). This mechanism contributes to greater microbial biomass and greater production of enzymes, by maintaining some level of moisture in the rhizosphere of *G. senegalensis*, even over the 9-month dry period in Senegal (Diedhiou-Sall et al., 2013; 2021).

There was a consistent shrub effect for β-glucosaminidase activity but not always statistically significant ($P>0.05$) for acid phosphatase (central) and β-glucosidase activity (Central and Northern sites). The overall positive *G. senegalensis* effect on enzyme supports previous findings by Diedhiou-Sall et al., (2013; 2021) but are more nuanced. This is likely due to a couple factors. One is that the previous research was on the

Optimized Shrub Intercropping System (OSS) that was compared to a treatment with no shrubs – where OSS had high shrub density (1200-1500/ha) and coppiced biomass was annually incorporated. In contrast the current study was done in farmers' fields where coppiced biomass was burned and derived soils of organic inputs. Secondly, the previous studies were done on soil samples collected beneath shrubs in the absence of any crop plants – whereas the current study took soil samples through the millet root zone where dense mass of roots could confound or influence microbial enzyme production by root exudates and root turnover.

Urease, however, exhibited a different pattern compared to the other enzymes both sampling seasons - being slightly higher in soil outside the influence *G. senegalensis* with the Central site having the highest activity. This corresponded to higher levels of NH_4 and NO_3 at these same locations which could drive suppression of urease. This is because urease releases ammonia, which is quickly converted to ammonium in soil (Bremner and Mulvaney, 1978). Thus, if NH_4, the end-product of urease is present, microorganisms suppress urease production due to feedback inhibition (Dick et al., 1988). However, a more likely reason is that the presence of shrubs would not contribute to or affect the distribution of urea, the substrate of urease.

Microbial community composition

PERMANOVA analysis showed that the composition of each community was greatly affected by shrub presence, second only to the rainfall gradient effect (Figures 5 and 6). Shannon's diversity analysis was similar in the presence and absence of shrubs for both the fungal and bacterial communities, except for the fungal community at the South site. However, overall species richness of the fungal community tended to decrease

with shrub presence; but was significantly increased with shrub presence at the Northern site only ($P < 0.05$, Figure S3).

Studies in general have shown that plant roots promote high microbial activity and diversity, which in turn drive plant-microbial-soil interactions and their functions (Baudoin et al., 2001; Reinhold-Hurek et al., 2015; Schmidt et al., 2019; Li and Wu, 2018; Jones et al 2019). However, in the current study there was no significant shrub effect on microbial diversity. This stands in contrast to Diedhiou-Sall, et al. (2009; 2021) where diversity was impacted by OSS. There are potentially several reasons for this. First OSS has high shrub density (~1500 ha^{-1}) and all coppiced residues were incorporated. Conversely, the current study was done in farmers' fields where shrub densities are low (<200 to ~ 350 shrubs ha^{-1}) which reduces the potential for organic inputs and most importantly farmers typically burn coppiced shrub residues, thus depriving soils of C inputs to stimulate the microbial community. Furthermore, the soil was sampled from the millet root zone and thus the millet root effects (exudates and root turnover) may have overridden the shrub effect.

However, diversity by itself does not necessarily indicate an improved microbiome for delivering agro-ecosystem services. Rather shifts in sub-populations with beneficial or detrimental properties or functionality are potential mechanisms for improved or inhibited plant growth in the presence of shrubs. Indeed, the following sections discuss potentially positive functional traits and stimulation of beneficial microorganisms due to the presence of *G. senegalensis*.

Differentially Enriched OTUs

While dominant taxonomic groups did not change in relative abundance in the presence of shrubs, some rare OTUs were found to be significantly enriched by shrub presence at all sites. It was determined that twelve bacterial OTUs and four fungal OTUs were enriched by shrub presence (Table 2). Several of these bacterial OTUs were from the Burkholderieaceae family, which was also observed as shrub-enriched by Debenport et al., (2015) at the OSS experimental site. The relative abundance of the genera *RB41*, a member of the order Xanthomondales, was found to be enriched in the presence of shrubs in this study and in rhizosphere soils of maize in other studies (Meier et al., 2020; Schmidt et al., 2019). *Burkholderia-caballeronia-paraburkholderia* is another common rhizosphere genus, and *Massilia* is a genus common to the rooting zones of plants in arid- and semi-arid soils (Ofek et al., 2012; Ren et al., 2018).

Several taxa enriched in the presence of shrubs are known to have plant growth promoting properties. For example, *Enterobacter agglomerans* is capable of PO_4^{3-} solubilization and hydrolysis of organic P for plant growth via acid phosphatase production; and is stimulated by organic matter amendments (Kim et al., 1998) which is consistent with *G. senegalensis* increasing total C. Another group, *Paraburkholderia*, have beneficial properties, including the production of chitinase and other hydrolytic enzymes which promote fungal and plant residue decomposition (Eberl and Vandamme, 2016; Tapia-García et al., 2020). This is supported in that both *Paraburkholderia* and chitinase activity increased in the presence of *G. senegalensis*.

Burkholderia-caballeronia-paraburkholderia also correlated with millet biomass production. This could be due to its suppression of fungal pathogens, as chitinase activity is a pathogenic antagonist and that other members of Burkholderiaceae can reduce fungal

pathogens (Benítez and McSpadden-Gardener, 2008). Furthermore, these organisms promote plant growth by fixing N2 gas and providing N inputs (Estrada de los Santos et al, 2001), and by producing the beneficial plant hormones, gibberellin, and auxin (Poupin et al., 2013).

In addition to the enrichment of beneficial microorganisms by *G. senegalensis*, an OTU of the genus *Paucibacter* was found to be enriched in -shrub plots (Table 2). Some Paucibacter species have been recently found to inhabit the rhizosphere soils of diseased plants (Liao et al., 2021), and others have been found to produce antimicrobials (Mullis et al., 2019), suggesting a relationship between this genus and plant disease. Further, in our study, this genus was negatively correlated with millet fresh biomass. It is potentially an important observation that warrants further investigation, because if *Paucibacter* has species that are deleterious or pathogenic this would provide a previously unrecognized mechanism for low millet yields in degraded soils throughout the Sahel. Historically low productivity has been attributed to soils having low organic matter and poor structure where even with the addition of inorganic fertilizer, there is little yield response (Badiane et al., 2000). However, it may well be that the lack of organic inputs and/or absence of shrubs also promotes pathogenic and/or deleterious microorganisms such as *Paucibacter*. More research is needed to determine the species-level identity of *Paucibacter* and confirm that it has negative effects on millet growth.

Enriched taxa may also colonize unique niches provided by the association between millet and shrubs or to take advantage of other emergent properties of the system. One such taxa may be *Candidatus Udaeobacter*. This group is abundant in soil, but poorly described in literature and may use nutrients released when other microbes are

lysed via antimicrobial compounds produced by other community members (Willms et al., 2020). As described in Diedhiou-Sall et al. (2009), community diversity tended to increase in the presence of shrubs, and *Ca. Udaeobacter* may be highly competitive for limited nutrients in densely populated rhizosphere, while being resistant to multiple antibiotics.

In the low-C, low-rainfall northern site, it could be expected that intercropping with shrubs may have a stronger effect on composition and diversity of predicted function, but this was not the case. However, as discussed above there were shifts in abundance of sub-populations due to the presence of *G. senegalensis* within each region, and significant changes in community composition at the South, high C site. This indicates that *G. senegalensis* affected microbial metabolic processes more in more C-rich, higher rainfall regions compared to drier, low-C regions, as determined via NMDS, similar to the community overall, enriched OTUs clustered by region first and secondly by shrub presence. However, when split by region, only the South site shows significant clustering with shrub presence (Figure 4).The significant clustering may be linked to the increased total C content in the southern site, implying that there may exist a threshold for total soil C, past which it has a significant impact on the microbial community and function. Such a phenomenon has been observed by Hao et al., (2021) and Reischke, et al. (2015), adding a layer of complexity to the relationship between shrubs, the microbial community, and carbon storage in arid soils under climate change. For future research, predicted or potential functions of the microbial community may be of more interest for determining the role of *G. senegalensis* in drought resilience in millet (Langille, 2018).

Finally, there was no significant difference in the average strength of relationship across sites between each differentially enriched OTU and the fresh biomass of millet (Table S4). This indicates that, although *G. senegalensis* enriches for distinct OTUs with the potential to influence the growth of millet, there was no one organism that could be linked to millet growth across landscape sites; the increased millet growth was at least in part an emergent property of the entire microbial community, the assembly of which was driven by intercropping with *G. senegalensis*.

Predicted function of the bacterial community

Previous studies have also shown that shrub presence increases enzyme activities and microbial properties, possibly due to the increase in shrub residues, root exudates, and fine root turn over (Diedhiou et al., 2020, 2021; Diakhate et al., 2016; Debenport et al., 2015; Diedhiou-Sall et al, 2013). Specifically, the availability of energy sources, particularly labile C and other rhizodeposits, impact community composition or capabilities (Hester et al., 2019; Baudoin et al., 2001; Schmidt et al., 2019). A greater diversity of substrates tends to reduce metabolic overlap and higher diversity of metabolic pathways, decoupled from the taxonomic diversity or species richness (Hester et al., 2019), as could be surmised from the current study; soils in the Southern site are richer in C and on average receive more rainfall, increasing the availability of substrates.

Further, although there is no consistently significant pathway enrichment across all sites, it does appear that in +shrub samples at the Northern site, there are a greater number of biosynthesis pathways related to fatty acid synthesis (Table S4). This is notable because there has previously been observed a significant increase in phospholipid fatty acids in +shrub soils, which has been linked to increased microbial activity and

diversity (Diedhiou-Sall et al., 2009). Significantly increased fungal diversity and increased acid phosphatase, β-glucosidase, and β-glucosaminidase were also observed at this site (Figures 3, S3), further suggesting that the shrub promotes the growth of certain microbial clades that are highly active in the more degraded/low soil quality at the northern, more arid site.

Millet Response to G. senegalensis

Millet biomass increased in the presence of shrubs at each site; notably this increase was higher in the northern low soil quality, low rainfall site than the higher soil quality, higher rainfall southern site. This is the first report across a landscape gradient on the impact on millet growth of *G. senegalensis* under farmer management. This highlights the unusual ability of *G. senegalensis* to promote a favorable growth environment for millet, even at low plant densities where farmers use little or no external inputs, and coppiced shrub residue is annually burned.

These growth responses to shrub intercropping are consistent with long-term studies that had optimized shrub intercropping (elevated plant densities) and annual incorporation of coppiced residues. For *G. senegalensis* in long-term experiments as a companion plant, Dossa et al. (2013) and Bright et al. (2021) showed dramatic yield responses (groundnut and millet); even in years with low rainfall in the northern Peanut Basin (same region as our Northern site). Another shrub species found in farmers' fields of the Sahel, *Piliostigma reticulatum,* has also improved crop yields in Burkina Faso (sorghum) (Félix et al., 2018) and in Senegal (groundnut and millet) (Bright et al., 2017). Furthermore, Félix et al. (2018) reported that *P. reticulatum* promoted sorghum yields under low rainfall and naturally low fertility soils, similar to the Northern site in the

current study. This crop growth response can be attributed to the higher quality soil generated by shrubs and from the current study and that of Debenport et al. (2015), a shift in sub-populations that have plant growth promoting properties and suppress deleterious or pathogenic microorganisms.

It is common in West Africa for farmers to have trees in cropped fields which is known as the Parkland system. Parkland management is promoted as a means to increase sustainability of dryland cropping systems (Takimoto *et al*., 2008; Garrity *et al.* 2010; Mbow *et al*., 2014). Although trees provide landscape stability and reduce wind erosion, the tree species typically found in the Sahelian Parkland agroforestry systems, except for *Faidherbia albida* (Garrity *et al.* 2010), do not increase crop yields, largely due to shading (Sinare and Gordon, 2015; Bayala *et al.*, 2012, Kessler and Breman, 1991). The presence of shrubs in the intra-tree space would synergestically improve tree based systems, by increasing crop productivity and remediating degraded soils.

Conclusions

The presence of *G. senegalensis* at low densities typically found in Senegalese farmers' fields increased aboveground millet fresh biomass and enriched certain bacterial and fungal genera; some of which are known to have plant growth promoting properties. It was found that site location and the presence of *G. senegalensis* drives shifts in structure of bacterial and fungal communities and some of the bacterial community's predicted metabolic pathways. These positive shrub effects were most evident in the Northern site of the major cropping region of Senegal, that has low rainfall and low organic matter soils. Total soil C content across all sites, also was a factor for controlling predicted metabolic pathways.

The results showed that when *G. senegalensis* is in farmers' fields that are at low densities and where coppiced residues are annually burned, it still increased soil enzyme activities and shifted microbial communities, that corresponded to enhanced millet productivity. These results are similar to optimized shrub intercropping that has high shrub densities and incorporation of coppiced shrub residues shown in the long-term experiments by Dossa et al. (2012), Diedhiou-Sall et al. (2009), Debenport et al. (2015), and Bright et al., (2021). However, in the current study because these were under farmer management where coppiced shrub residue was burned, the amount of litter inputs was greatly diminished. This suggests that an important factor over litter inputs in driving shrub induced crop response – is the presence of shrub roots that provides organic inputs through root turnover and exudates and water inputs through hydraulic lift.

These mechanisms would not only benefit crops directly but also cause a shift to a microbiome that has plant growth promoting subpopulations. This can be inferred from the positive correlation crop growth due to *G. senegalensis* with the abundance of genera known for having plant growth properties. Furthermore, the presence of this shrub completely suppressed to undetectable levels the genera *Paucibacter* that has deleterious and/or pathogenic properties. Although more research is needed to connect shifts in microbiome with beneficial plant responses due to the presence of *G. senegalensis*; the current results provide support for farmers to conserve and increase *G. senegalensis* density to improve soil quality and crop productivity to reduce food insecurity.

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Tables

Table 2.1. Soil chemical characteristics +/- and along the rainfall gradient

Rainfall Gradient Site	pH		Total Carbon		Total Nitrogen		N-NH4+		N-NO3-		P-PO4	
	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub
			---------- % ----------				---------- mg kg-1 ----------					
North	5.73a†	5.75a	0.131a	0.104b	0.011a	0.008b	8.00a	7.76a	0.482a	0.361a	12.9a	13.7a
Central	5.58a	5.67a	0.241a	0.215a	0.027a	0.024b	9.72a	9.09a	0.282a	0.248a	10.2a	9.78a
South	5.63a	5.73a	0.301a	0.251b	0.023a	0.018b	7.26a	6.25a	0.538a	0.619a	11.0a	9.37b
Mean	5.65a	5.71a	0.224a	0.190b	0.020a	0.017b	8.37a	7.70b	0.434a	0.410a	11.4a	10.9a

Rainfall Gradient Site	Ca		Cu		Fe		K		Mg		S-SO4		Zn	
	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub	+Shrub	-Shrub
	---------- mg kg-1 ----------													
North	1170a	1180a	0.330a	0.310a	27.7a	26.7a	22.6a	22.7a	28.7a	28.6a	2.88a	2.47b	0.884a	0.704b
Central	790a	802a	0.412a	0.432a	28.6a	28.7a	41.1a	42.7a	48.8a	47.7a	3.38a	3.47c	1.87a	1.17a
South	388a	437a	0.217a	0.222a	33.4a	32.6a	24.0a	21.5a	47.7a	43.8a	4.66a	4.70a	0.46a	0.41a
Mean	782a	806a	0.321a	0.322a	29.9a	29.3a	29.2a	28.8a	41.8a	41.2a	3.64a	3.55a	1.07a	0.76b

†Pairs of $^{+}$shrub and $^{-}$shrub values followed by the same letter are not significantly different within site at $P \leq 0.05$.

Table 2.2 Spearman's correlation between discriminant OTUs and millet fresh biomass.

OTU	Lowest Taxonomic Rank Identified	Rainfall Gradient Site:			
		North	Central	South	Overall
OTU1	Ascomycota (unassigned)	0.349	0.460*	-0.290	0.230
OTU2	Fungi (unassigned)	0.332	0.631*	-0.062	0.420*
OTU3	*Microdochium*	† 0.693*	0.6615*	-0.020	0.400*
OTU4	Fungi (unassigned)	0.044	0.7233*	0.252	0.376*
OTU A	*Burkholderia-Caballeronia-Paraburkholderia*	0.700*	0.289	0.044	0.498*
OTU B	*Candidatus Udaeobacter*	0.604*	0.262	-0.088	0.303*
OTU C	*Massilia*	0.451	0.545*	-0.099	0.394*
OTU D	*RB41*	0.601*	0.353	-0.168	0.385*
OTU E	*Candidatus Udaeobacter*	0.537*	0.350	-0.133	0.185
OTU F	*OLB12*	0.048	0.305	-0.191	0.470*
OTU G	Vicinamibacterales (uncultured)	-0.115	-0.189	0.345	0.128
OTU H	*Enterobacter*	0.137	-0.226	-0.096	0.061
OTU I	*Paucibacter*	-0.574*	-0.496*	0.050	-0.194
OTU J	Acidobacterales (uncultured)	0.232	0.550*	0.730*	0.252
OTU K	*Acidibacter*	0.413*	0.413	0.69*	0.547*
OTU L	*Lysobacter*	0.506*	0.512*	0.503	0.503*
OTU M	*Haliangium*	0.357	0.576*	0.521*	0.319*

† Values followed by * are significantly correlated with millet fresh biomass at $P \leq 0.017$.

Figure legends

Figure 2.1 A) Fresh millet biomass (g plant-1), at time of sampling, for 2012 & 2013. Pairs of +shrub and -shrub values within a site followed by the same letter are not significantly different at wilcox $P \leq 0.05$. Brackets indicate a significant difference of fresh millet biomass between sites in the presence of shrubs at * $P<0.05$ or ** $P<0.01$ (ANOVA). B) Percent total soil C at time of sampling, averaged for 2012 and 2013. Pairs of +shrub and -shrub values within a site followed by the same letter are not significantly different wit at wilcox $P \leq 0.05$. Brackets indicate a significant difference ($P < 0.001$, ANOVA) in total C between sites in both +shrub and -shrub samples ***.

Figure 2.2 Extracellular enzyme activities for the 2012 and 2013 sampling seasons. Pairs of +shrub and -shrub values followed by the same letter are not significantly different within site at $P \leq 0.05$ (Welch's T test).

Figure 2.3 The effect of presence or absence of *G. senegalenis* on log fold OTU enrichment of 16S or ITS soil communities as determined via LefSE. Differentially enriched OTUs were identified to the lowest possible taxonomy via SILVA NGS 138.1, and all are at least 2 log-fold enriched in either the presence or absence of shrubs across all sites.

Figure 2.4 Non-Metric Multidimensional Scaling of a simplified microbial community generated from the differentially enriched OTUs determined via LefSE, shown across the

community and within each site. P and R2 values included on the plots refer to the influence of the presence or absence of shrub on the composition of the microbial community at each site ($P < 0.017$ with Bonferroni's correction, PERMANOVA).

Figure 2.5 Non-Metric Multidimensional Scaling of Bacterial communities at each site. Unless otherwise indicated, p and R2 values included on the plots refer to the influence of the presence or absence of shrub on the composition of the microbial community at each site ($P < 0.017$ with Bonferroni's correction, PERMANOVA)

Figure 2.6 Non-Metric Multidimensional Scaling of Fungal communities at each site. Unless otherwise indicated, P and R2 values included on the plots refer to the influence of the presence or absence of shrub on the composition of the microbial community at each site ($P < 0.017$ with Bonferroni's correction, PERMANOVA)

Figure 2.7 Non-Metric Multidimensional Scaling of microbial metabolic pathways at each site. Unless otherwise indicated, P and R2 values included on the plots refer to the influence of the presence or absence of shrub on the composition of the microbial community at each site ($P < 0.017$ with Bonferroni's correction, PERMANOVA)

Figures

Figure 2.1. Millet fresh biomass and % Total C at time of sampling, for 2012 & 2013.

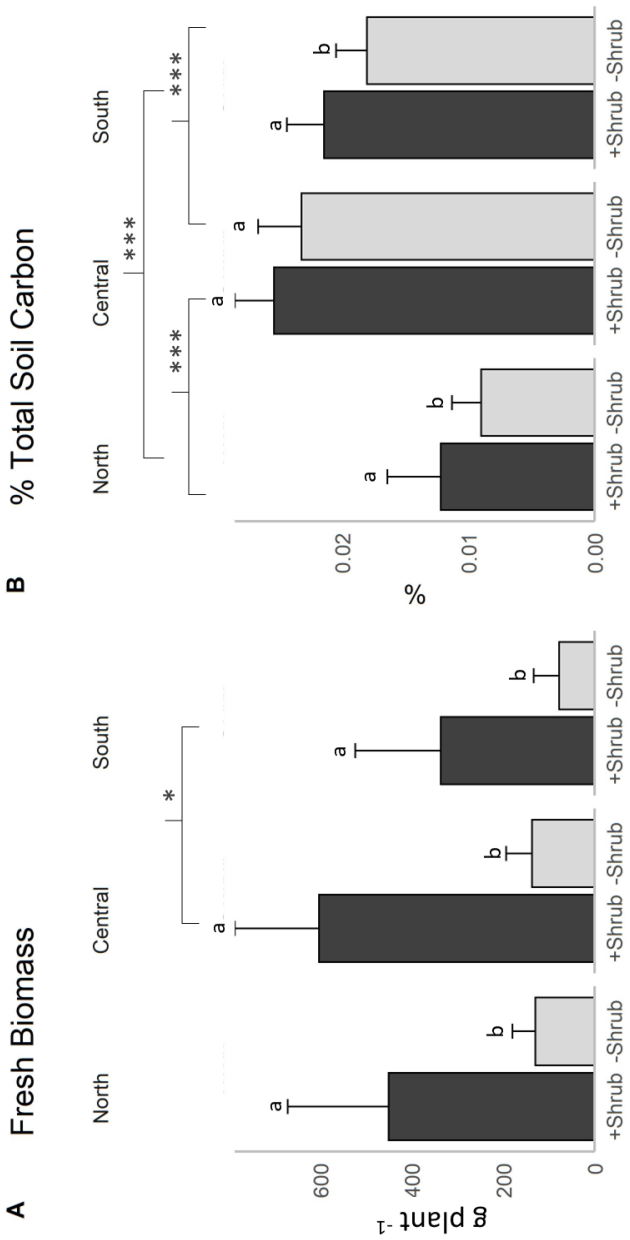


Figure 2.2. Extracellular enzyme activities for the 2012 and 2013 sampling seasons

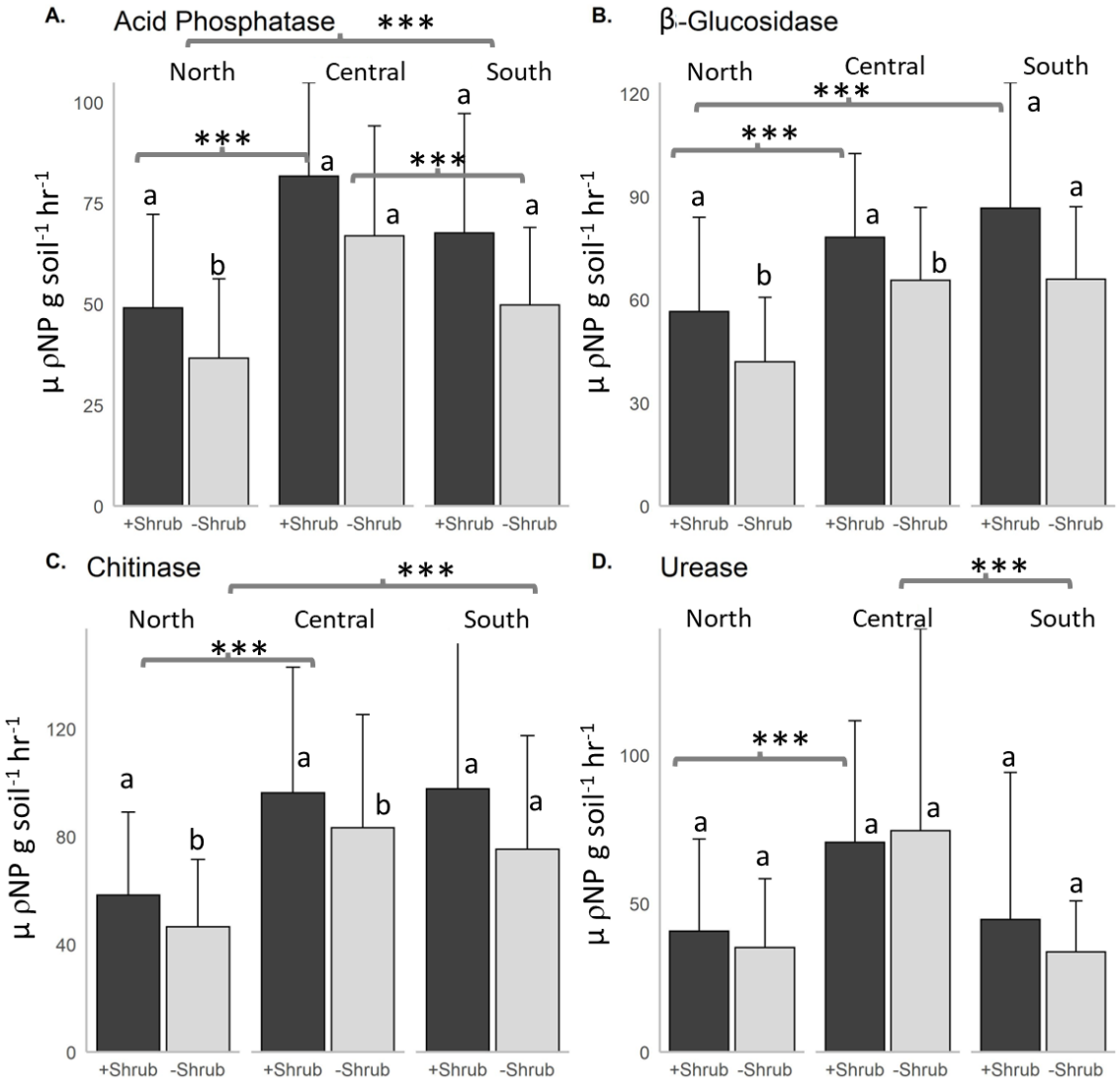
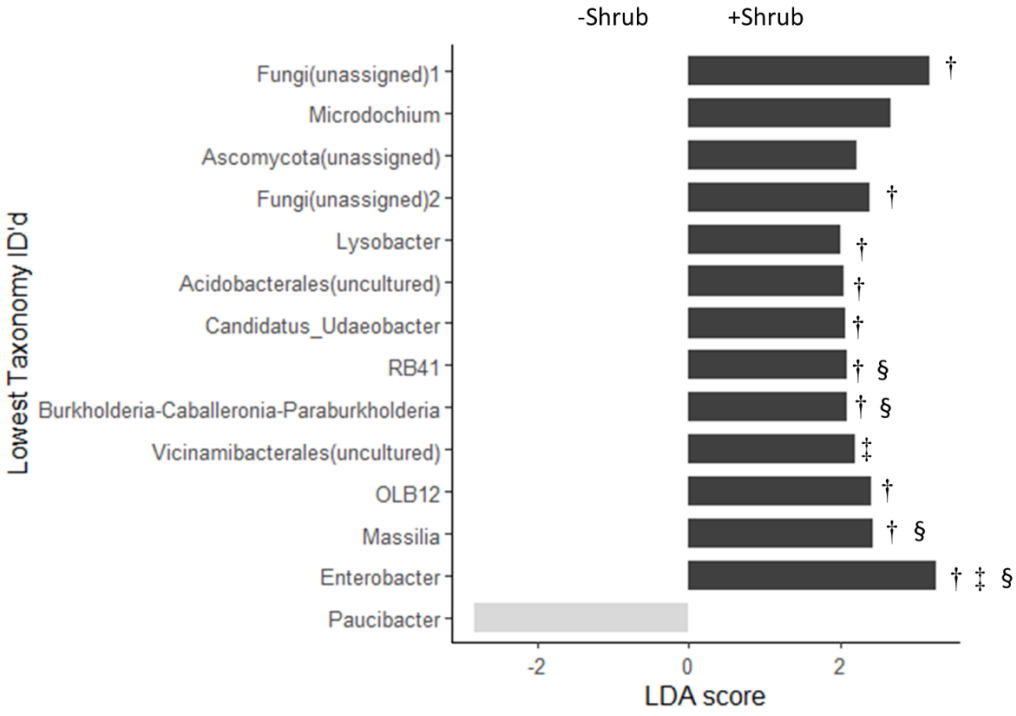


Figure 2.3. OTU enrichment +/- shrub



† Microbial Genus that was significantly and positively correlated with millet biomass.
‡ Microbial Genus that was significantly and positively correlated with total soil C (%).
§ Microbial Genus that contains known species with plant growth promoting properties.

Figure 2.4. NMDS of enriched OTUs

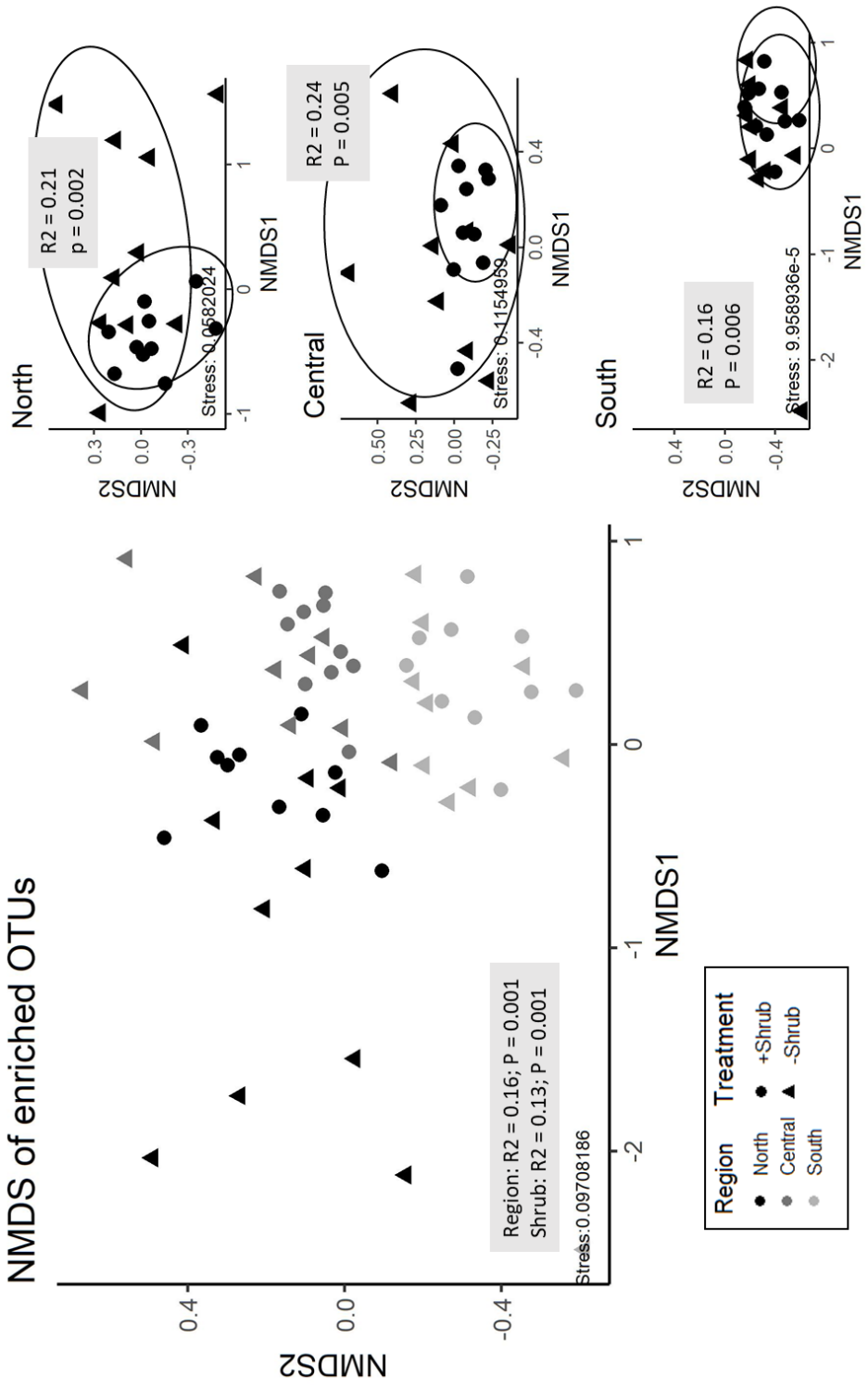


Figure 2.5. NMDS of 16S OTUs

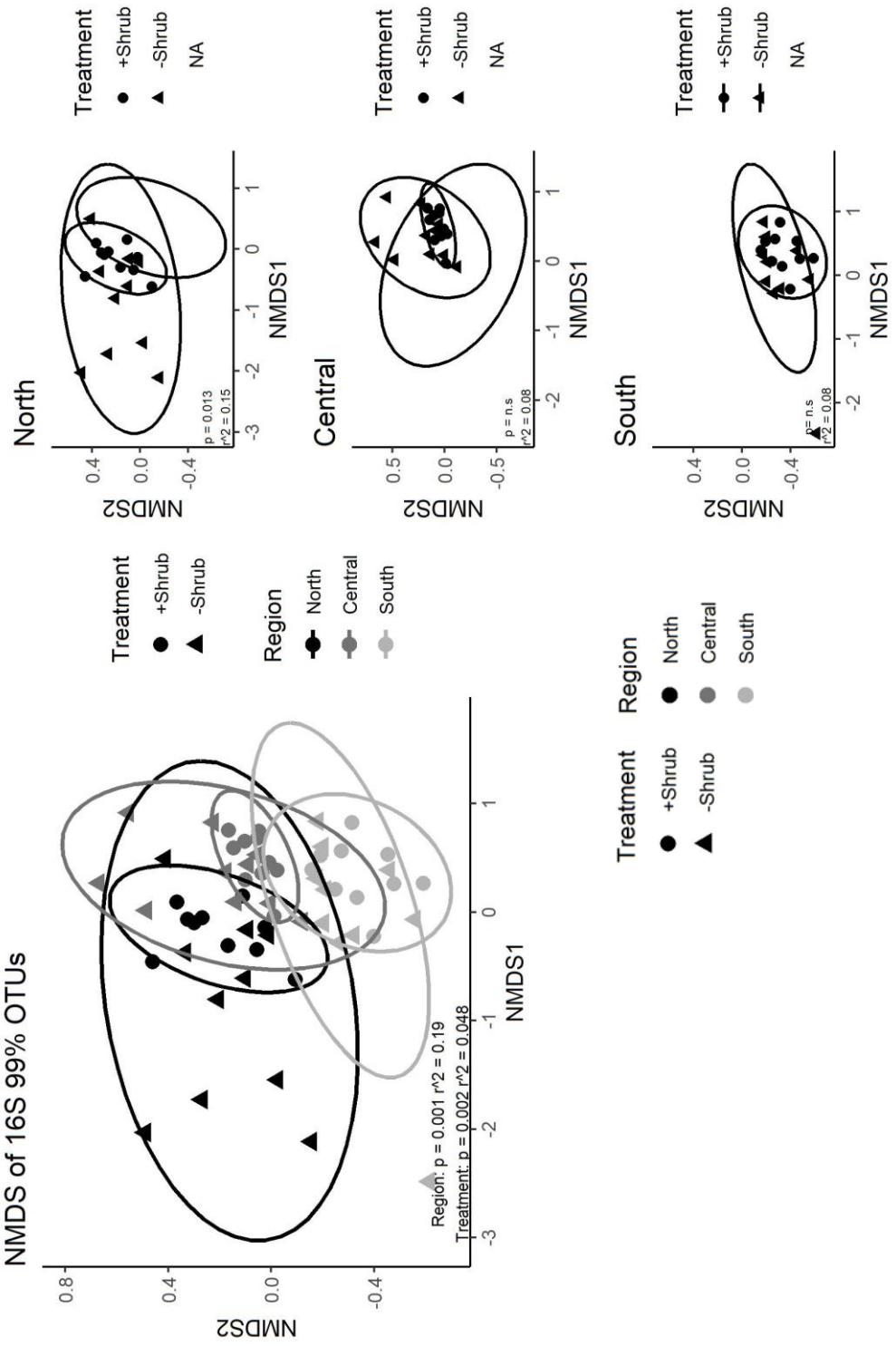


Figure 2.6. NMDS of ITS2 OTUs

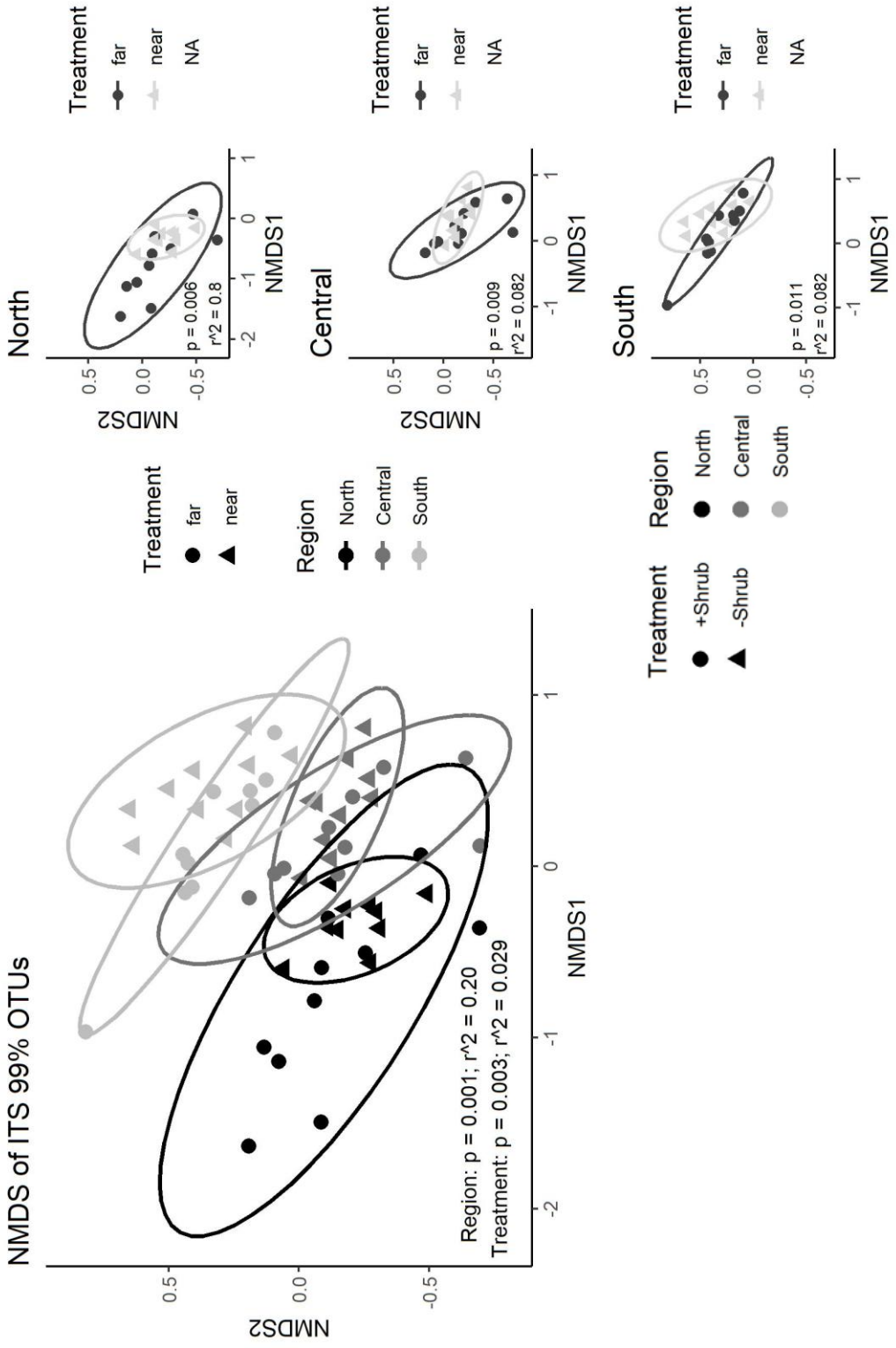
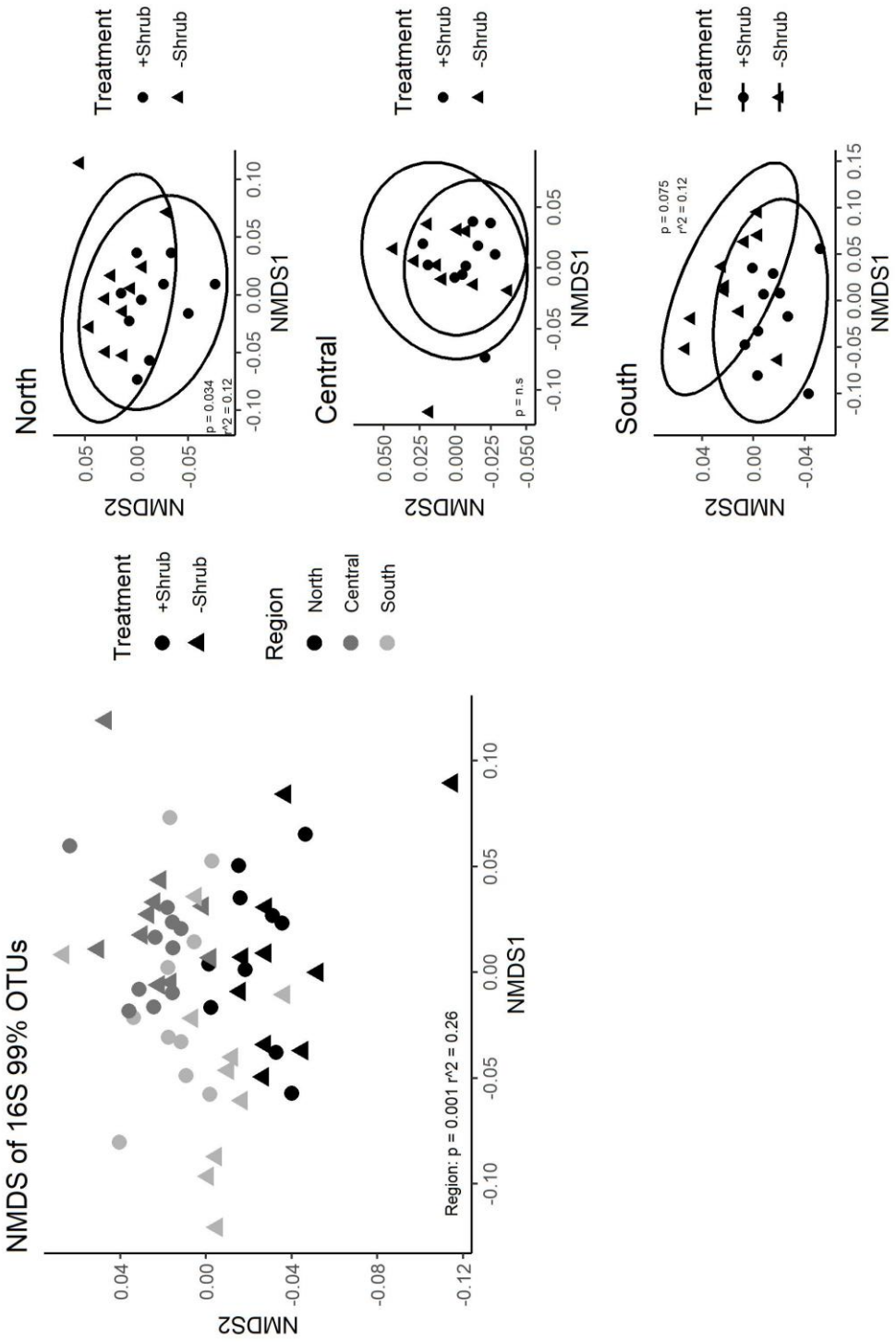


Figure 2.7. NMDS of metabolic pathways



Supplemental tables

Table S2.1 Illumina forward and reverse primers + individual adapters for multiplexing

Primer Name	Primer Sequence
V3_F	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctCCTACGGGAGGCAGCAG
ITS3	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctGCATCGATGAAGAACGCAGC
V3_Fa	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctACCACTCCTACGGGAGGCAGCAG
V3_Fb	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctTTGTGACCTACGGGAGGCAGCAG
ITS3_a	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctACCACTGCATCGATGAAGAACGCAGC
ITS3_b	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctTTGTGAGCATCGATGAAGAACGCAGC
V3_R1	caagcagaagacggcatacgagatCGTGATgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R2	caagcagaagacggcatacgagatACATCGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R3	caagcagaagacggcatacgagatGCCTAAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R4	caagcagaagacggcatacgagatTGGTCAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R5	caagcagaagacggcatacgagatCACTGTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R6	caagcagaagacggcatacgagatATTGGCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R7	caagcagaagacggcatacgagatGATCTGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R8	caagcagaagacggcatacgagatTCAAGTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R9	caagcagaagacggcatacgagatCTGATCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R10	caagcagaagacggcatacgagatAAGCTAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R11	caagcagaagacggcatacgagatGTAGCCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R12	caagcagaagacggcatacgagatTACAAGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R13	caagcagaagacggcatacgagatCGTACTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R14	caagcagaagacggcatacgagatGACTGAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R15	caagcagaagacggcatacgagatGCTCAAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R16	caagcagaagacggcatacgagatTCGCTTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R17	caagcagaagacggcatacgagatTGAGGAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R18	caagcagaagacggcatacgagatACAACCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R19	caagcagaagacggcatacgagatACCTCAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R20	caagcagaagacggcatacgagatACGGTAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R21	caagcagaagacggcatacgagatAGTTGGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R22	caagcagaagacggcatacgagatCTCTCTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R23	caagcagaagacggcatacgagatCAAGTGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R24	caagcagaagacggcatacgagatCCTTGAgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R25	caagcagaagacggcatacgagatACCACTgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R26	caagcagaagacggcatacgagatAGTGTCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R27	caagcagaagacggcatacgagatAGAAGGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG

V3_R28	caagcagaagacggcatacgagatTTATCCgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R29	caagcagaagacggcatacgagatTTAAGGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
V3_R30	caagcagaagacggcatacgagatTTCTTGgtgactggagttcagacgtgtgctcttccgatctATTACCGCGGCTGCTGG
ITS4_1	caagcagaagacggcatacgagatCGTGATgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_2	caagcagaagacggcatacgagatACATCGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_3	caagcagaagacggcatacgagatGCCTAAgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_4	caagcagaagacggcatacgagatTGGTCAgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_5	caagcagaagacggcatacgagatCACTGTgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_6	caagcagaagacggcatacgagatATTGGCgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_7	caagcagaagacggcatacgagatGATCTGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_8	caagcagaagacggcatacgagatTCAAGTgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
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ITS4_23	caagcagaagacggcatacgagatCAAGTGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_24	caagcagaagacggcatacgagatCCTTGAgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_25	caagcagaagacggcatacgagatACCACTgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_26	caagcagaagacggcatacgagatAGTGTCgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_27	caagcagaagacggcatacgagatAGAAGGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_28	caagcagaagacggcatacgagatTTATCCgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_29	caagcagaagacggcatacgagatTTAAGGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC
ITS4_30	caagcagaagacggcatacgagatTTCTTGgtgactggagttcagacgtgtgctcttccgatctTCCTCCGCTTATTGATATGC

Table S2.2. Supplement Taxonomy of enriched OTUs and their abundances within the total community and the reduced community of enriched OTUs

Kingdom	Phylum	Class	Order	Family	Genus	Name in main text	Relative abundance (total community)	Relative abundance (reduced community)
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	*Burkholderia-Caballeronia-Paraburkholderia*	*Burkholderia-Caballeronia-Paraburkholderia*	0.00003	0.02959
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Oxalobacteraceae	*Massilia*	*Massilia*	0.00013	0.02768
Bacteria	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	*RB41*	*RB41*	0.00338	0.03323
Bacteria	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	*Candidatus Udaeobacter*	*Candidatus Udaeobacter*	0.00003	0.00411
Bacteria	Bacteroidota	Bacteroidia	Cytophagales	Microscillaceae	*OLB12*	*OLB12*	0.00063	0.04961
Bacteria	Acidobacteriota	Vicinamibacteria	Vicinamibacterales	uncultured		Vicinamibacterales (uncultured)	0.00748	0.03354
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	*Enterobacter*	*Enterobacter*	0.00225	0.39991
Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	*Paucibacter* **previously Candidatus Koribacter*	*Paucibacter*	0.00078	0.09001
Bacteria	Acidobacteriota	Acidobacteriae	Acidobacteriales	uncultured		Acidobacteriales (uncultured)	0.00097	0.02294
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Lysobacter*	*Lysobacter*	0.00095	0.01846
Fungi	Ascomycota	Sordariomycetes	Xylariales	Microdochiaceae	*Microdochium*	*Microdochium*	0.00083	0.08772
Fungi						Fungi unknown 1	0.00148	0.18114
Fungi	Ascomycota					Ascomycota unknown	0.00018	0.00348
Fungi						Fungi unknown 2	0.00016	0.01858

Table S2.3. Supplement Spearman's correlation and regression R2 between enriched OTUs and millet fresh biomass and total C

	Millet Fresh Biomass		Total C	
Lowest Taxonomy Identified	p value	R^2	p value	R^2
Ascomycota (unassigned)	0.239	0.008	0.907	-0.018
Fungi (unassigned) 1	0.015	0.088	0.657	-0.015
Microdochium	0.630	-0.014	0.939	-0.018
Fungi (unassigned) 2	0.004	0.131	0.342	-0.0012
Burkholderia-Caballeronia-Paraburkholderia	0.343	-0.002	0.347	-0.002
Massilia	0.020	0.079	0.741	-0.016
RB41	0.045	0.055	0.619	-0.01
Candidatus Udaeobacter	0.035	0.063	0.356	-0.002
OLB12	0.073	0.041	0.445	-0.007
Vicinamibacterales (uncultured)	0.736	-0.016	0.000	0.189
Enterobacter	0.022	0.077	0.0855	0.036
Paucibacter	0.035	0.062	0.078	0.0300
Acidobacterales (uncultured)	0.051	0.051	0.084	0.037
Lysobacter	0.011	0.097	0.129	0.083

Table S2.4. Supplement Summary of enriched pathways defined by MetaCyc

Pathway	Site	Enriched	LDA	Parent Class 4	Detailed class description
BIOTIN_BIOSYNTHESIS_PWY	N	Near	2.3915	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Biotin Biosynthesis
PWY_5989	N	Near	2.6427	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Stearate Biosynthesis
PWY_6282	N	Near	2.6317	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis → Palmitoleate Biosynthesis
PWYG_321	N	Near	2.6234	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis
PWY_7664	N	Near	2.6084	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis → Oleate Biosynthesis
PWY0_862	N	Near	2.6044	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis → (5Z)-dodecenoate Biosynthesis
FASYN_INITIAL_PWY	N	Near	2.5673	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Fatty Acid Biosynthesis Initiation
PWY_6519	N	Near	2.4737	Biosynthesis	Biosynthesis → Other Biosynthesis → 8-Amino-7-oxononanoate Biosynthesis
PWY0_1586	N	Near	2.3964	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis
PWY_5855	N	Near	2.383	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Ubiquinol Biosynthesis
PWY_5856	N	Near	2.383	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone

					Biosynthesis → Ubiquinol Biosynthesis
PWY_5857	N	Near	2.383	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Ubiquinol Biosynthesis
PWY_6708	N	Near	2.383	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Ubiquinol Biosynthesis
UBISYN_PWY	N	Near	2.3797	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Ubiquinol Biosynthesis
PWY_5973	N	Near	2.3508	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis
PWY_7663	N	Near	2.3422	Biosynthesis	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Unsaturated Fatty Acid Biosynthesis
TYRFUMCAT_PWY	N	Near	2.2943	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-tyrosine Degradation
PWY_6507	N	Near	2.2223	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation
PWY_6467	N	Near	2.2037	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis → Kdo Transfer to Lipid IVA
PWY_6269	N	Near	2.2016	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Cobamide Biosynthesis → Cobinamide Salvage → Adenosylcobalamin Salvage from Cobinamide
PWY_5509	N	Near	2.1972	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Cobamide

					Biosynthesis → Cobamide de novo Biosynthesis → Adenosylcobamide Biosynthesis
THISYN_PWY	N	Near	2.1932	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Thiamine Biosynthesis
GLUCOSE1PMETAB_PWY	N	Near	2.1697	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation
COBALSYN_PWY	N	Near	2.1553	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Cobamide Biosynthesis → Cobinamide Salvage → Adenosylcobalamin Salvage from Cobinamide
SO4ASSIM_PWY	N	Near	2.1531	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Inorganic Nutrient Metabolism → Sulfur Compound Metabolism → Assimilatory Sulfate Reduction
LEU_DEG2_PWY	N	Near	2.1424	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-leucine Degradation
PWY_5384	N	Near	2.1362	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → Sucrose Degradation
PWY_6897	N	Near	2.1198	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Thiamine Biosynthesis → thiamine Diphosphate Salvage
TCA_GLYOX_BYPASS	N	Near	2.1183	Superpathways	Superpathways
PWY_1269	N	Near	2.0911	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → CMP-sugar Biosynthesis → CMP-3-deoxy-D-manno-octulosonate Biosynthesis
P105_PWY	N	Near	2.0725	Precursor metabolites	Precursor metabolites ; TCA cycle
TCA	N	Near	2.0385	Precursor metabolites	Generation of Precursor Metabolites and Energy
GLYOXYLATE_BYPASS	N	Near	2.0357	Precursor metabolites	Generation of Precursor Metabolites and Energy
TRPSYN_PWY	N	Near	2.0309	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic

					Amino Acid Biosynthesis → L-tryptophan Biosynthesis
SULFATE_CYS_PWY	N	Near	2.0274	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Inorganic Nutrient Metabolism → Sulfur Compound MetabolismSuperpathways
HEME_BIOSYNTHESIS_II	N	Near	2.0212	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis
PWY_5189	N	Near	2.0176	Biosynthesis	Biosynthesis → Tetrapyrrole Biosynthesis
METHYLGALLATE_DEGRADATION_PWY	N	Near	2.0138	Degredation/Ultilization/Assimilation	Degredation/Ultilization/Assimilation
P161_PWY	N	Far	2.678	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate
PWY_5100	N	Far	2.4255	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate → Pyruvate Fermentation to Acetate
PWY0_1297	N	Far	2.4195	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation
HEXITOLDEGSUPER_PWY	N	Far	2.3795	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Alcohol Degradation
PWY_6609	N	Far	2.3488	Biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide Salvage → Adenine and Adenosine Salvage
GLYCOGENSYNTH_PWY	N	Far	2.335	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Glycan Biosynthesis → Polysaccharide Biosynthesis → Glycogen and Starch Biosynthesis
PWY0_1298	N	Far	2.3159	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Pyrimidine Nucleotide Degradation
GLYCOCAT_PWY	N	Far	2.2882	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Polysaccharide Degradation → Glycan Degradation
ASPASN_PWY	N	Far	2.2494	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis
ARGORNPROST_PWY	N	Far	2.2414	Degredation/Ultilization/Assimilation	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic

					Amino Acid Biosynthesis → L-arginine Biosynthesis
DENOVOPURINE2_PWY	N	Far	2.2372	Biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis
PWY_6471	N	Far	2.2299	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Peptidoglycan Biosynthesis
PRPP_PWY	N	Far	2.219	Other	Superpathways
PWY_6901	N	Far	2.1968	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation
NONOXIPENT_PWY	N	Far	2.1961	Precursor metabolites	Generation of Precursor Metabolites and Energy → Pentose Phosphate Pathways
DTDPRHAMSYN_PWY	N	Far	2.1871	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → dTDP-sugar Biosynthesis
P124_PWY	N	Far	2.1869	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation
PWY_6317	N	Far	2.1826	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → Galactose Degradation
PWY_6737	N	Far	2.1823	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Polysaccharide Degradation → Starch Degradation
ANAGLYCOLYSIS_PWY	N	Far	2.1735	Precursor metabolites	Generation of Precursor Metabolites and Energy → Glycolysis
PWY_6588	N	Far	2.1626	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate
PWY_6608	N	Far	2.1582	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation → Guanosine Nucleotide Degradation
PWY_5121	N	Far	2.1534	Biosynthesis	Biosynthesis → Polyprenyl Biosynthesis → Geranylgeranyl Diphosphate Biosynthesis

P122_PWY	N	Far	2.137	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Ethanol
PWY_6876	N	Far	2.1345	Precursor metabolites	Generation of Precursor Metabolites and Energy
PWY_5838	N	Far	2.1326	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_7187	N	Far	2.1299	Biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → 2'-Deoxyribonucleotide Biosynthesis → Pyrimidine Deoxyribonucleotide De Novo Biosynthesis
PWY_5840	N	Far	2.1279	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_5897	N	Far	2.1242	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_5898	N	Far	2.1242	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_5899	N	Far	2.1242	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
CALVIN_PWY	N	Far	2.116	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis
PWY0_1296	N	Far	2.1079	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation

PWY_7003	N	Far	2.1006	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols
PWY_5861	N	Far	2.0758	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Demethylmenaquinol Biosynthesis → Demethylmenaquinol-8 Biosynthesis
TRNA_CHARGING_PWY	N	Far	2.0572	Biosynthesis	Biosynthesis → Aminoacyl-tRNA Charging
PWY_6386	N	Far	2.0391	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → UDP-N-Acetylmuramoyl-Pentapeptide Biosynthesis
PWY_6353	N	Far	2.034	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation
PENTOSE_P_PWY	N	Far	2.0307	Precursor metabolites	Generation of Precursor Metabolites and Energy → Pentose Phosphate Pathways
PWY_5845	N	Far	2.0298	Biosynthesis	
PWY_7208	N	Far	2.0278	Biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide Salvage
PWY_6387	N	Far	2.006	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → UDP-N-Acetylmuramoyl-Pentapeptide Biosynthesis
GLYOXYLATE_BYPASS	C	Near	2.0739	Precursor metabolites	Generation of Precursor Metabolites and Energy
PWY_1269	C	Near	2.2256	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → CMP-sugar Biosynthesis → CMP-3-deoxy-D-manno-octulosonate Biosynthesis
PWY_6629	C	Near	2.2355	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-tryptophan Biosynthesis
TCA_GLYOX_BYPASS	C	Near	2.1246	Superpathways	Superpathways
MET_SAM_PWY	C	Far	2.169	Biosynthesis	Superpathways

PWY_5347	C	Far	2.1549	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-methionine Biosynthesis → L-methionine De Novo Biosynthesis
ALL_CHORISMATE_PWY	S	Near	2.2841	Superpathways	Superpathways
CENTFERM_PWY	S	Near	2.3097	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate
ENTBACSYN_PWY	S	Near	2.3816	Biosynthesis	Biosynthesis → Secondary Metabolite Biosynthesis → Siderophore and Metallophore Biosynthesis
GALACTARDEG_PWY	S	Near	2.0235	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Sugar Acid Degradation → D-Galactarate Degradation
GLUCARDEG_PWY	S	Near	2.0409	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Sugar Acid Degradation → D-Glucarate Degradation
GLUCARGALACTSUPER_PWY	S	Near	2.0235	Superpathways	Superpathways
HOMOSER_METSYN_PWY	S	Near	2.1192	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-methionine Biosynthesis → L-methionine De Novo Biosynthesis
KDO_NAGLIPASYN_PWY	S	Near	2.1951	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis
MET_SAM_PWY	S	Near	2.0272	Biosynthesis	Superpathways
P461_PWY	S	Near	2.3516	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Fermentation to Acetate
P562_PWY	S	Near	2.1805	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Alcohol Degradation
PWY_1861	S	Near	2.5306	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → C1 Compound Utilization and Assimilation → Formaldehyde Assimilation
PWY_2941	S	Near	2.5317	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-lysine Biosynthesis
PWY_4361	S	Near	2.1974	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → S-

					methyl-5-thio-alpha-D-ribose 1-phosphate Degradation (human)
PWY_4984	S	Near	2.2734	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Inorganic Nutrient Metabolism → Nitrogen Compound Metabolism
PWY_5005	S	Near	2.2596	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Biotin Biosynthesis
PWY_5347	S	Near	2.0544	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-methionine Biosynthesis → L-methionine De Novo Biosynthesis
PWY_5850	S	Near	2.2115	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_5860	S	Near	2.1154	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Demethylmenaquinol Biosynthesis → Demethylmenaquinol-6 Biosynthesis
PWY_5896	S	Near	2.2115	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis
PWY_6507	S	Near	2.3137	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation
PWY_6590	S	Near	2.3591	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate
PWY_6891	S	Near	2.3585	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Thiamine Biosynthesis → Thiazole Biosynthesis
PWY_6895	S	Near	2.6348	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme

					Cofactor Biosynthesis → Thiamine Biosynthesis
PWY_7237	S	Near	2.5359	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Secondary Metabolite Degradation → Sugar Derivative Degradation → Sugar Alcohol Degradation
PWY_7242	S	Near	2.2049	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carboxylate Degradation → Sugar Acid Degradation
PWY_7527	S	Near	2.2787	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-methionine Biosynthesis → L-methionine Salvage
PWY0_1296	S	Near	2.232	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Purine Nucleotide Degradation
PWY0_845	S	Near	2.2383	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Vitamin B6 Biosynthesis
PYRIDOXSYN_PWY	S	Near	2.2997	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Vitamin B6 Biosynthesis
RHAMCAT_PWY	S	Near	2.1472	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → L-rhamnose Degradation
RUMP_PWY	S	Near	2.4324	Precursor metabolites	Degradation/Utilization/Assimilation → C1 Compound Utilization and Assimilation → Formaldehyde Oxidation
TEICHOICACID_PWY	S	Near	2.1506	Biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Cell Wall Biosynthesis → Teichoic Acid Biosynthesis
COLANSYN_PWY	S	Far	2.339	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis
HEME_BIOSYNTHESIS_II	S	Far	2.1163	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis
HSERMETANA_PWY	S	Far	2.2214	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-methionine Biosynthesis → L-

					methionine De Novo Biosynthesis
ILEUSYN_PWY	S	Far	2.1295	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation
NADSYN_PWY	S	Far	2.0791	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → NAD Metabolism → NAD Biosynthesis
NONOXIPENT_PWY	S	Far	2.2923	Precursor metabolites	Generation of Precursor Metabolites and Energy → Pentose Phosphate Pathways
P122_PWY	S	Far	2.3648	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate → Pyruvate Fermentation to Ethanol
P124_PWY	S	Far	2.3896	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation
PROTOCATECHUATE_ORTHO_CLEAVAGE_PWY	S	Far	2.5415	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Protocatechuate Degradation
PWY_3781	S	Far	2.4102	Precursor metabolites	Generation of Precursor Metabolites and Energy → Electron Transfer Chains
PWY_5101	S	Far	2.1099	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis
PWY_5415	S	Far	2.0579	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Catechol Degradation
PWY_5419	S	Far	2.0071	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Catechol Degradation
PWY_5420	S	Far	2.0551	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Catechol Degradation
PWY_5430	S	Far	2.0172	Degredation/Ultilization/Assimilation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Benzoate Degradation
PWY_5505	S	Far	2.1651	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-glutamate Biosynthesis
PWY_5659	S	Far	2.1793	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar

					Nucleotide Biosynthesis → GDP-sugar Biosynthesis
PWY_5913	S	Far	2.2176	Precursor metabolites	Generation of Precursor Metabolites and Energy → TCA cycle
PWY_6545	S	Far	2.2615	Biosynthesis	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → 2'-Deoxyribonucleotide Biosynthesis → Pyrimidine Deoxyribonucleotide De Novo Biosynthesis
PWY_7111	S	Far	2.4214	Precursor metabolites	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation of Pyruvate
PWY_7323	S	Far	2.2675	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → GDP-sugar Biosynthesis
PWY_7332	S	Far	2.185	Biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Sugar Biosynthesis → Sugar Nucleotide Biosynthesis → UDP-sugar Biosynthesis
PYRIDNUCSAL_PWY	S	Far	2.0685	Biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → NAD Metabolism → NAD Biosynthesis
VALSYN_PWY	S	Far	2.1295	Biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-valine Biosynthesis

Supplemental figure legends

Figure S2.1. Flowchart of bioinformatics methods, data analyses, and related questions

Figure S2.2. Rarefaction curves for the 16S and ITS datasets. Vertical line represents level of rarefaction to an even depth for alpha diversity analyses

Figure S2.3. Shannon's diversity and observed richness for 16S and ITS communities. Datasets were rarefied before analysis. Pairs of $^{+}$Near and $^{-}$Near values followed by the same letter are not significantly different within site at $P \leq 0.05$.

Figure S2.4. Enriched microbial metabolic pathways defined by MetaCyc and displayed by proximity to shrub and geographic region. Results displayed here are counts of broadly classified pathways (Parent Class 4). For more detailed information on the distribution and identity of these enriched pathways, see Table S4.

Supplemental Figures

Figure S2.1 Flowchart of bioinformatics methods and data analyses

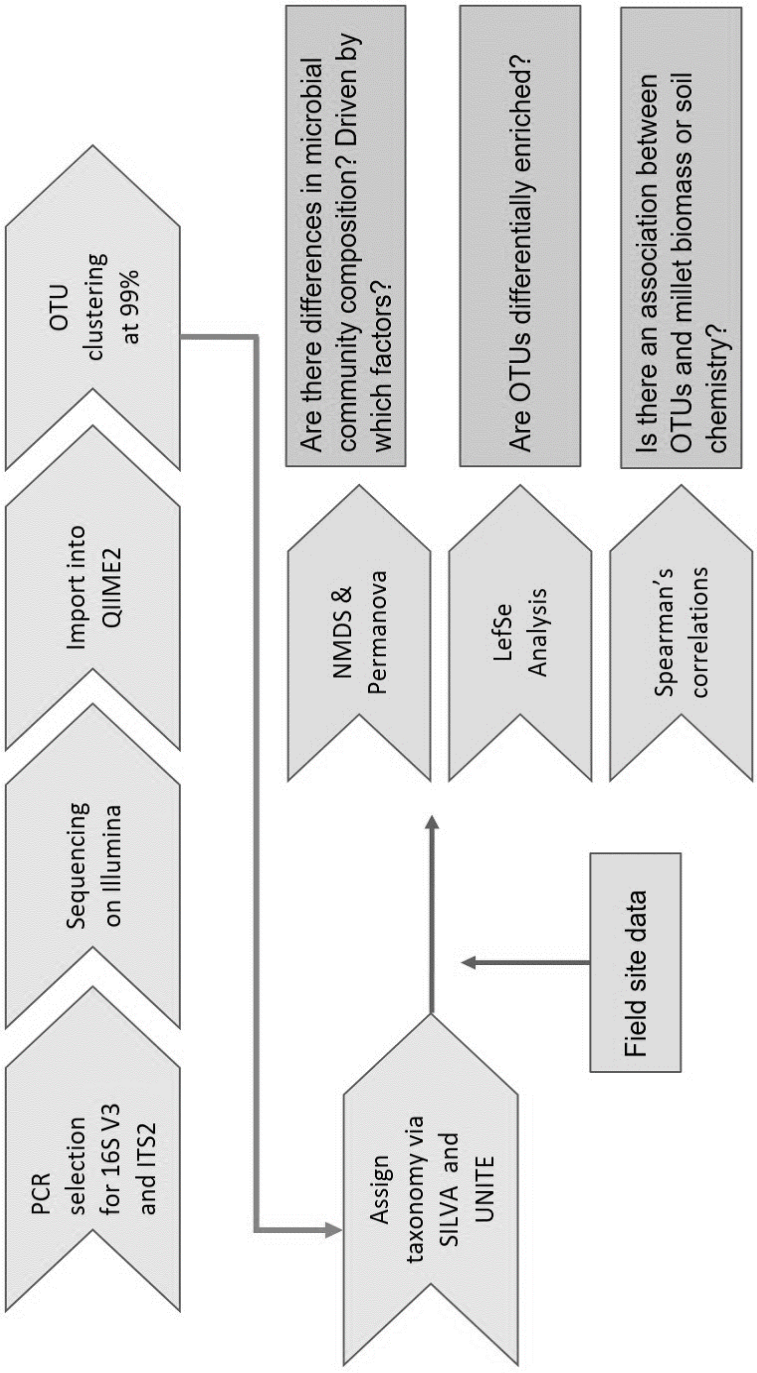


Figure S2.2. Rarefaction curves for the 16S and ITS datasets

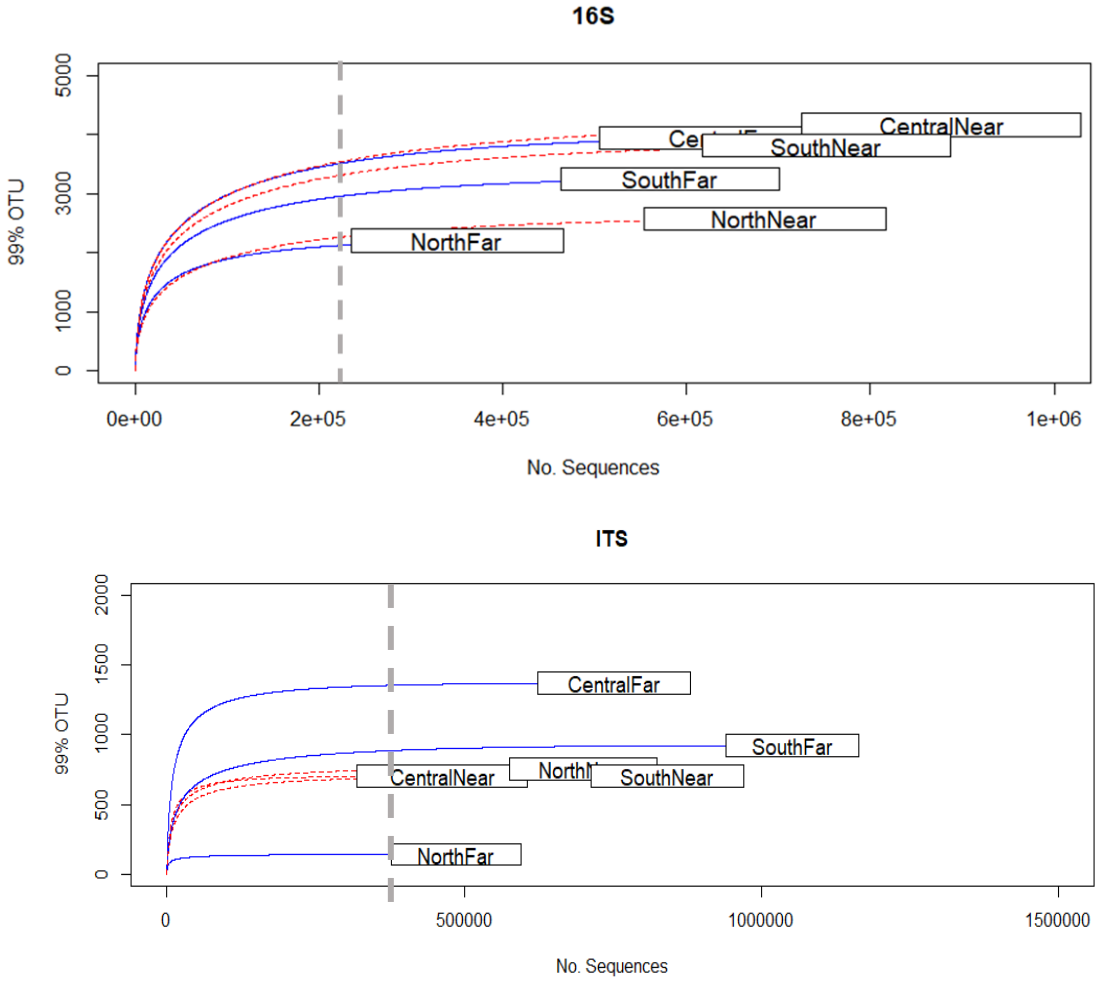


Figure S2.3 Shannon's diversity and observed richness for 16S and ITS communities.

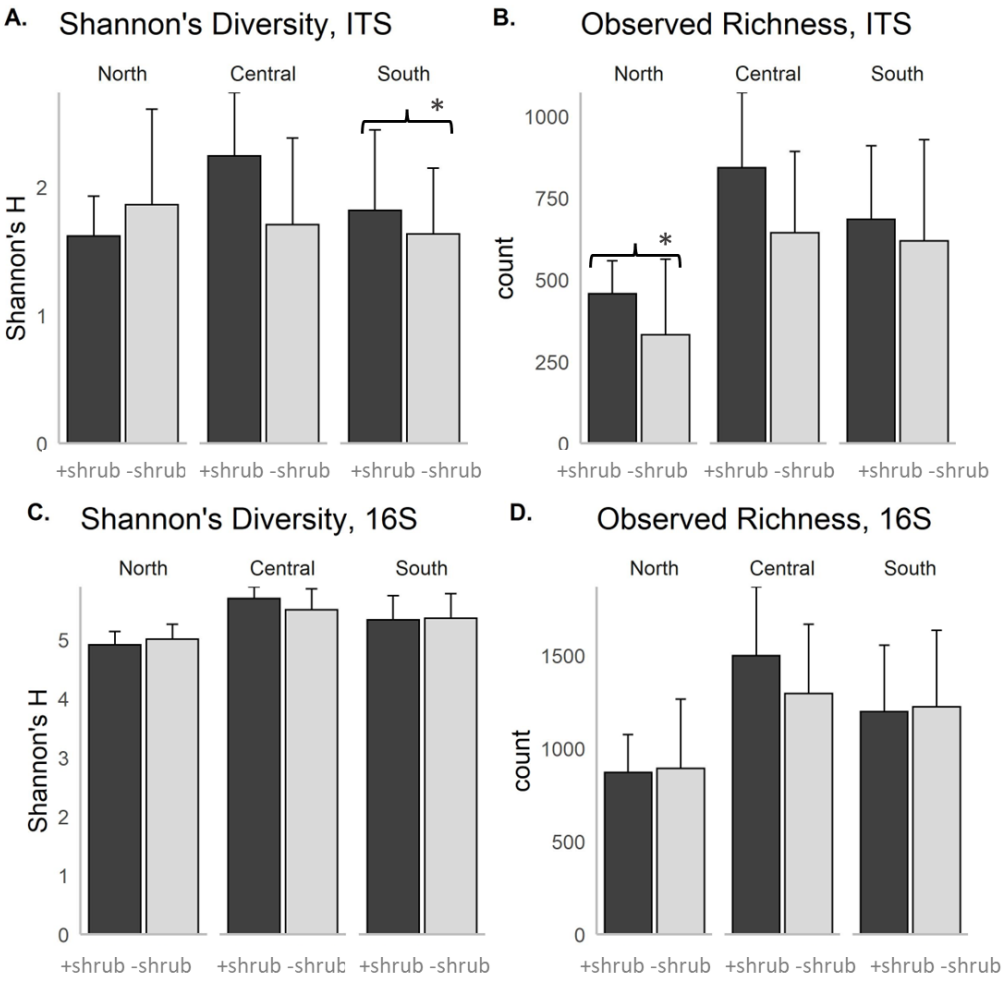
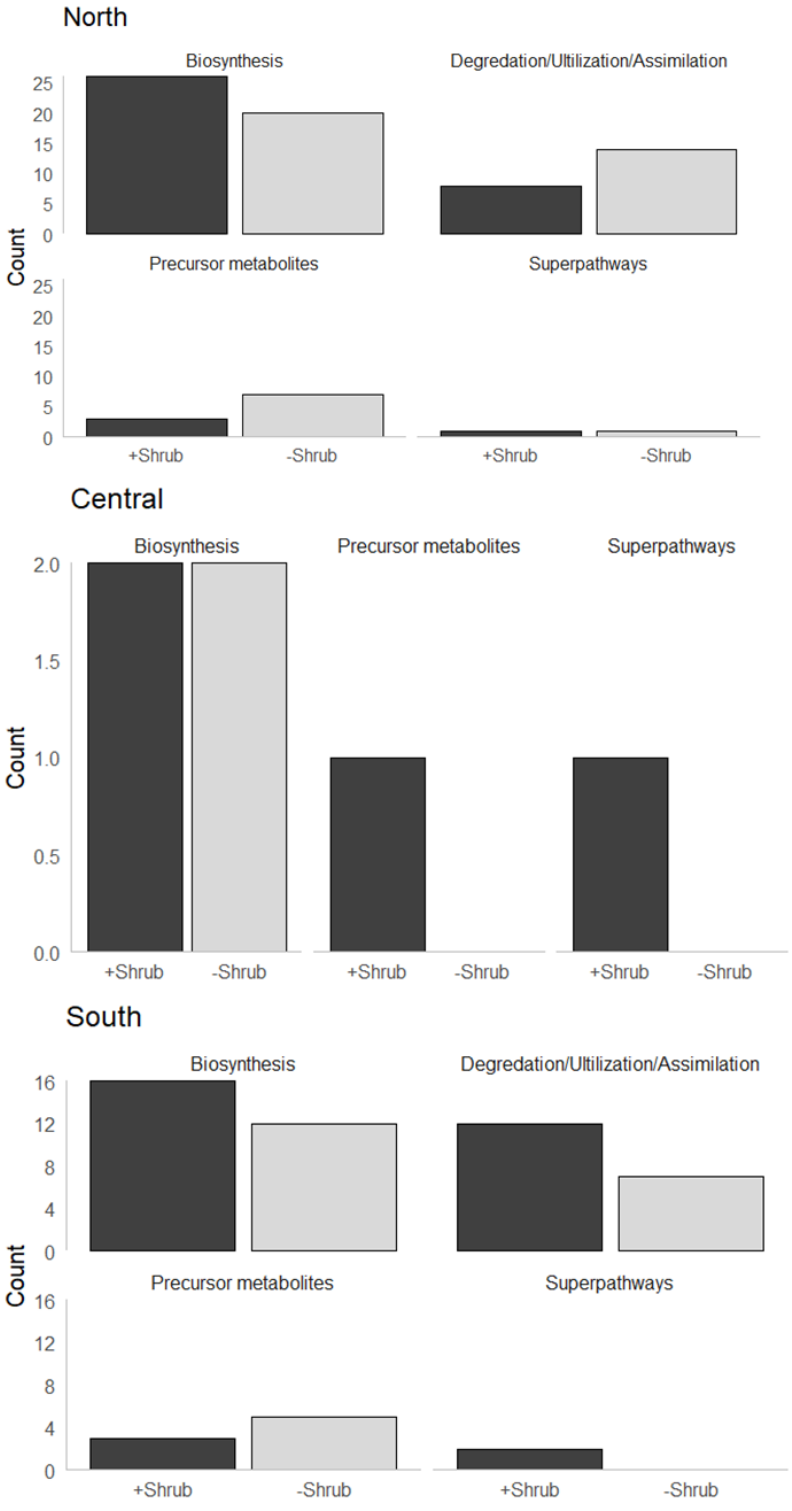


Figure S2.4. Summary of enriched metabolic pathways by site and proximity to shrub



Chapter 3. Soil, plant, & microbial Dynamics of the Optimized Shrub Intercropping System during Early Season Drought: Part III

In prep for submission to *Plant Soil*
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Abstract

Background & Aims: The Sahel of West Africa is a vulnerable eco-region where a growing population has increased agricultural intensity, degrading soils, and climate-change induced-drought threatens food security. Subsistence farmers grow pearl millet (*Pennisetum glaucum*) without fertilizers or irrigation. Hence, local, biologically-based systems are needed to remediate degraded soils and buffer water stress. The agroforestry approach of Optimized Shrub-intercropping System (OSS) uses *Gueira senegalensis* as a companion plant and is a solution because it dramatically increases millet yields and drought resistance. Hydraulic lift (HL) and improved soil quality may contribute to crop drought resilience. However, HL provides little water, and beneficial microorganisms may also contribute to crop drought resistance. To test this hypothesis, a growth chamber simulated-drought experiment was conducted in the absence of shrubs (eliminating HL) by comparing soils from +/-OSS experiments. The effect of *G. senegalensis* residue amendments ("OM") were examined to determine their importance in conferring drought resistance.

Methods: The microbial response was determined via amplicon sequencing of the 16S rRNA gene (V3-V4 region) and the ITS2 over a 30-day period after millet planting, included during and after a simulated drought. Millet height was measured pre-and post-drought and at harvest, and biomass was measured at harvest.

Results: Drought, OM, and OSS affected microbial composition. For prokaryotes, the largest drought impact occurred in -OM treatments, and +OSS/-OM enriched PGPR lineages under drought. The fungal community behaved differently, shifting significantly +OSS/+OM treatments under drought.

Conclusions: This experiment isolated the effect of the microbiome in conferring drought resistance in millet. +OSS soil and OM inputs shifted microbiota, potentially increasing PGPRs. These results are part of a growing body of work aimed at understanding microbiome roles in increasing ecological resilience and combating food insecurity.

Key words: Sahel; Optimized Shrub-Intercropping System (OSS); hydraulic lift; soil microbiome; imposed drought; growth chamber

Introduction

Long-term experiments have shown that OSS with *G. senegalensis* or *P. reticulatum* results in crops being less impacted by low rainfall and in-season drought than when shrubs are absent (Dossa et al., 2012,2013; Bright et al. 2017, 2021). This can be attributed to the improved soil quality and that shrubs also perform hydraulic lift which is deep tap roots moving water from high water potential in the subsoil to low water potential of the surface soil. This occurs at night when photosynthesis stops and stomata close, disabling evapotranspiration and resulting in water leaking from surface roots of shrubs to surrounding surface soil (Kizito et al., 2006; 2012). Isotopic tracking confirmed that this hydraulically-lifted water was transferred from *G. senegalensis* to adjacent millet plants during a simulated in-season drought experiment under field conditions (Bogie et al., 2018), However, the amount of water produced by hydraulic lift

is relatively small (Kizito et al., 2012; Bogie et al., 2018). Thus, other mechanisms are expected to play a significant role in promoting millet drought resilience.

Since microbial communities inside and outside the influence of *G. senegalensis* shrubs are significantly different (Diedhiou et al 2009, Diedhiou-Sall et al., 2013, Debenport et al., 2015). Given this and that OSS reduces water stress in crops, it was hypothesized that shrub intercropping promotes a community of beneficial microorganisms that confer drought resilience and promote the growth of millet (Debenport et al., 2015; Mason et al., 2022). However, it would be necessary to eliminate hydraulic lift as a factor during an investigation of the role of microorganisms in mitigating drought stress due to OSS. Therefore, the objective was to investigate microbiome shifts in response to early-season drought on soils that had been under long-term OSS or non-OSS management with or without shrub residue soil amendments.

Methods

Experimental Design and Soil Sampling

Soils were collected in September 2019 from the long-term experimental station of Keur Matar Arame (Harpole et al., 2016) near Thies in the northern Peanut Basin of Senegal, Sahelian climatic zone (Le Houerou, 1980) of West Africa (14º45'N, 16º51'W). Air temperatures range from 20.0 to 33ºC and the mean annual precipitation of 450 mm mainly comes between July and September. The soil is a loamy sand with <5% clay and 95% sand, loose consistency, and has a 5.5 pH (1:2 soil:water). The soil is classified as a Rubric Arenosol in FAO taxonomy (Michéli et al., 2006) and as a Typic Torripsamment in USDA Soil Taxonomy (Lufafa, 2005).

A full description of the field experiment that was sampled, is described in Charles et al (2024a). In brief, the experiment was initiated in 2004 with a randomized

complete block split-plot design with the presence (1,521 plants ha^{-1}) or absence of shrubs as the main plot (46 x 10 m) and fertilizer rate (0 to 1.5 recommended NPK rate) as the subplot (10 x 6m) with four replicates (Bright et al., 2021). In the +shrub treatment coppiced biomass was chopped and incorporated into soil annually (~3 Mg ha^{-1}). All treatments have been under a millet-peanut (*Arachis hypogaea* L.) crop rotation. The 0 to 15 cm depth was sampled in the zero fertilizer plots as per the practice of most subsistence farmers in the Sahel. Soils were express-shipped to the United States, to the Ohio State University (OSU) and immediately frozen at -20 ℃.

The experimental design of the simulated drought experiment was a 2 X 2 X 2 factorial with three replicates and the following treatments: 2 soils (long-term +OSS or -OSS); 2 soil amendments (no residue (-OM) or plus *G. senegalensis* residue (+OM) at equivalent field rate of 4 Mg ha^{-1} for OSS (Lufafa et al,. 2008); and a drought treatment (imposed drought or watered control).

The mesocosms receiving the drought treatment were not watered for 10 days after the millet reached the five-leaf stage to mimic an early season drought, common to Senegal. The remaining plants were watered to maintain 3.75% gravimetric water content (2/3^{rds} field capacity). After 10 days, the drought treatment had the soil moisture returned to 3.75% gravimetric water content, which was maintained until experiment ended. Soil samples were collected with a 1 cm core at four times or phases during the experiment: 1) at the time of planting (P0), 2) at the five-leaf stage (at the start of the drought, PI), 3) at the end of the 10-day drought (PII) , and 4) at the end of the experiment (30 days after planting) (PIII). Millet height was measured at PI, PII, and PIII (before the destructive

sampling). After ~30 days, above and below ground millet biomass was measured. Further experimental details are in Charles et al. (2023a, b).

Soil DNA extraction & Sequencing

At all timepoints, soil samples for DNA extraction were flash frozen with liquid nitrogen and stored at -80 ºC. Soil microbial (fungal and bacteria and archaeal) DNA was extracted from soil samples using the Zymo RNA/DNA co-extraction kit following manufacturer's instructions with minor modifications. Briefly, nucleic acids were extracted from 0.25 g field moist soil, and cells were lysed via FastPrep (Savant Bio 101 FastPrep FP120 Cell disruption system). The extraction proceeded following the manufacturer's instructions. DNA concentrations were obtained via QuBit.

Sample preparation and sequencing were-performed at Argonne National Lab in on Illumina MiSeq 250x250 PE in Spring of 2022. Briefly, DNA samples for all four sampling times (n= 96) were prepared for 16S rRNA gene V4 region using the updated primers 515F (Parada; AATGATACGGCGACCACCGAGATCTACACGCT XXXXXXXXXXXX TATGGTAATT GT GTGYCAGCMGCCGCGGTAA) and 806R (Apprill; CAAGCAGAAGACGGCATACGAGAT AGTCAGCCAG CC GGACTACNVGGGTWTCTAAT) (Caporaso et al., 2018) (Table S1). The same sample set (n= 96) was also prepared for amplicon sequencing of the ITS2 region using primers ITS1f (AATGATACGGCGACCACCGAGATCTACAC GG CTTGGTCATTTAGAGGAAGTAA) and ITS2 (EMP.ITS.Skabir, CAAGCAGAAGACGGCATACGAGAT NNNNNNNNNN CG GCTGCGTTCTTCATCGATGC). PCR mixes included 13.0 µL PCR-grade water, 10 uL 2X PCR master mix, 0.5 µL, each forward and reverse primers, and 1 µL template DNA (Smith et al., 2018). To selectively amplify the 16S rRNA V4 region, samples were incubated at 94 °C for 3 min followed by 35 cycles with the following protocol:

denaturing at 94 °C for 45 s, annealing at 50 °C for 60 s, and elongating at 72 °C for 90 s, followed by 10 min final elongation at 72 °C. To selectively amplify the ITS2 region, samples were incubated at 94 °C for 1 min, followed by 35 denaturation cycles each of at 94 °C for 30 s, annealing at 52 °C for 30 s, and elongating at 68 °C for 30 s, followed by 10 min final elongation at 68 °C per the Earth Microbiome Project protocol. (Copyright Earth Microbiome Project 2022; https://earthmicrobiome.org/protocols-and-standards/).

Data processing & Statistics

Raw reads from the prokaryotic dataset were trimmed to 150 base pairs in QIIME1.9 (Caparoso et al., 2010). The fungal dataset underwent limited truncation (forward reads truncated to 248 base pairs with no other trimming or truncation). Both sets of reads were demultiplexed via QIIME1.9 (Caparoso et al., 2010) before dereplicating and de novo clustering at 99% identity on through VSEARCH on the QIIME2 platform (Rognes et al., 2016; Boylen et al., 2019; Chiarello, et al., 2022). Raw data is stored on NCBI under BioProject PRJNA930014. OTUs with fewer than three reads assigned to them were removed, and taxonomy was assigned via the SiLVa138 non-redundant database and the UNITE 99% clustering analysis for bacteria and archaeal and fungal datasets respectively (Mason et al., 2023). All OTUs assigned as eukaryotic were removed from the bacteria and archaeal dataset after taxonomic assignment.

Data were then exported for statistical analyses in Phyloseq (R v4.0.3) (McMurdie & Holmes, 2013; R Core Team, 2022). Bacteria and archaeal OTUs were transformed for relative abundance and three samples were removed due to very low sequence numbers (less than 16,000 reads). Fungal OTUs transformed for relative

abundance, and no samples were removed. PERMANOVA was used to determine statistical differences in community composition in response to the treatment factors: for soil management treatment (+/- OSS), drought (+/-), organic matter amendment (+/- OM), and phase. Principle Coordinates Analysis (PCoA) was used to visualize these differences. Enriched OTUs were determined using the linear discriminant analysis effect size package (LEfSe; Segata et al., 2011) with the main class set as the soil management system and organic matter treatments and the subclass as phase. The internal Wilcoxon signed-rank test, incorporated into the second step of the lefse analysis was conducted on OTUs within the same subclass, and the LDA clusters were identified "one against all". Alpha diversity metrics were calculated on rarefied data; OTUs in the fungal dataset were first rarefied to a depth of 10,000 reads per sample, and OTUs in the prokaryotic dataset were rarefied to a depth of 20,000 reads per sample (Figure S1). Statistical differences in alpha diversity were measured via a linear mixed effects model in R with soil type, organic matter amendment, and imposed drought as the fixed effects and replicate as the random effect.

Results

Soil Microbial Community Composition

Amplicon sequencing resulted in 46,370 post-QC prokaryotic OTUs (Figure S1), representing members of 36 prokaryotic phyla. Alpha diversity (richness, evenness, and Shannon's diversity) of the prokaryotic communities differed significantly by soil management treatment, OM treatment, and sampling time (Figure S4). Proteobacteria was the most abundant phylum in these communities, where there was a synergistic of soil management with the OM treatment. Proteobacteria abundance was ~20 % greater

for +OM over -OM with the +OSS/+OM treatment being near-double that of -OSS/-OM treatment in the treatments (Table S2, Fig. S2). The next three most abundant phyla did not show clear treatment effects and collectively accounted for roughly 40% of the communities (~20% Firmicutes, and ~10% each Chloroflexi and Actinobacteria).

The variation in the prokaryotic community (Fig. 1A) was most accounted for by soil management (+/-OSS; accounting for ~22% of variation, PERMANOVA, $p = 0.001$), organic matter amendment treatment (~11% of variation, $p=0.001$), sampling time (~5% of variation, $p = 0.017$), and the interaction between soil management and organic matter amendment (~4% of variation, $p =0.001$). Only significant results are given here; all PERMANOVA permutations and results are reported in Table S3. In the overall experiment (i.e., all time points collectively), 31 OTUs were significantly enriched (LEfSe, $p<0.05$, LDA>2) in -OSS/-OM, 19 were enriched -OSS/+OM, 11 were enriched +OSS/-OM and 16 were enriched +OM/+OSS (Figure 1B). Generally, there was little difference in the observed richess, diversity, or evennness at any of the timepoints or under any treatment except that prokaryotic richness under -OSS/-OM was significantly higher than the other treatments at this time point (Figure S5).

Sequencing of the ITS2 region resulted in 101,007 post-QC fungal OTUs (Fig. S2). There were no significant alpha diversity differences (in observed richness, or evenness, or Shannon's diversity) by treatment or sampling time in the ITS dataset (Fig. S6). Across all treatments, the phylum Ascomycota dominated (averaging ~60% overall), comprising 55% of the taxa in the -OSS/-OM treatments to 80% of all taxa in the +OSS/-OM treatments -OSS/+OM 42%, +OSS/+OM 66%. This was followed by Basidomycota (average: 24.2%) and "unidentified" (average: 9.77%) (Table S2, Figure

S4). Similar to the patterns observed in the prokaryotic community, variation in the fungal community was most accounted for by soil management (~12% variation, PERMANOVA, P = 0.001), organic matter amendment treatment (~4% variation, P = 0.001), sampling time (~4% variation, P = 0.017), and the interaction between the soil management and OM amendment (~3% variation, P = 0.001). The interaction between sampling time and OM amendment contributed to ~3% of the variation in the community, but this interaction was not significant (p = 0.062), nor was sampling time. Thirteen OTUs were found to be significantly enriched in +OSS samples across all four phases; nine OTUs were enriched in the +OSS/ -OM treatments, and four were enriched in the +OSS/ +OM treatment. Eighteen OTUs were found to be enriched in the -OSS samples; 13 in -OSS/ -OM and five in -OSS/ +OM (Figure 3). Generally, there was little difference in the observed richness, diversity, or evenness at any of the timepoints, except for planting. At the time of planting, evenness and diversity were significantly higher under -OSS and -OM treatments (compared with +OSS and +OM, respectively), and specifically highest under the -OSS/-OM treatment (Figure S5, $p < 0.05$).

Effects of OSS and OM across all time points

At all phases, soil management and organic matter amendment drove most of the variation in both the prokaryotic and fungal communities (Figure 1A & 2A, tableS3, $p < 0.05$). In the prokaryotic communities, in the +OSS soils, OM amendment again drove significant change in composition (accounting for ~26% of variance, PERMANOVA, p = 0.001), and the interaction of OM and drought was included as a factor in the regression, the effect of the imposed drought became significant at P = 0.042 ($R^2 = 0.06669$). In the -OSS, the driver of prokaryotic community change was again the OM amendment

(accounting for ~22% of the variance, p = 0.001). In the fungal communities, +OSS samples again varied most by the OM amendment treatment but with less than a third as much variance explained (~7%, p = 0.001), followed by the interaction between OM amendment and watering (~3% variance explained, p = 0.004). -OSS samples only varied significantly with OM amendment (~7% variance explained, p = 0.001) (Figure 1, 2, Table S3).

Effect of Drought

Planting to the start of drought (P0 - PI)

The prokaryotic community varied significantly by soil management (+/-OSS) (~31% variation, PERMANOVA p = 0.001), organic amendment (+/- OM) (~17% variation, p = 0.001), and the interaction between the two treatments (~4% variation, p = 0.008). The community also shifted significantly during the pre-drought time period, accounting for ~7% of the variation (p = 0.001). The fungal community significantly varied by soil management (~12% variance explained, p = 0.001) and OM (~6% variance explained, p = 0.002) and the interaction between the two terms (~4% variation explained, p = 0.011). In the prokaryotic community under +OSS/+OM treatment, sampling time accounted for ~35% of the variation in the community (p = 0.001). Under the +OSS/-OM treatment, sampling time accounted for ~27% of the community variation (p = 0.002). Sampling time accounted for ~15% of the community variation in -OSS datasets in both OM treatments, with and without OM (p = 0.031 and p = 0.004). In the fungal community under the +OSS/+OM treatments, sampling time accounted for ~13% of the variation with OM (p = 0.007). The community did not significantly shift by

sampling time in any of the other treatments, despite accounting for ~10% of the variation in each treatment (Table S3).

Dry down period (during drought, PI - PII)

For the drought period when soils were in the dry down phase, soil management had the greatest impact on the variance (~31% variance explained, PERMANOVA p = 0.001), followed by the organic matter amendment treatment (~17% variance explained, p = 0.001), and sampling time (~7% of variance explained, p = 0.001). Similarly, in the fungal community, soil management explained most of the variation (~12%, p = 0.001), the organic matter amendment treatment (R^2 = 0.047, p = 0.001), and the interaction between the two treatments (R^2 = 0.032, p = 0.002). In +OSS/+OM samples, the bacteria and archaeal community experienced no change in community composition over the course of the drought. In the +OSS/-OM treatments however, the drought treatment significantly impacted the community (R^2 = 0.116, p = 0.043). The fungal community was significantly impacted by the imposed drought in the +OSS/+OM samples (R^2 =0.148, p = 0.037), but not in the +OSS/-OM samples.

During the drought treatment the prokaryotic community was enriched for four OTUs in the +OSS/+OM treatment; eight OTUs in the -OSS/-OM treatment (five of which belong to the phylum Actinobacteria); five OTUs in the +OSS/-OM treatment; and three OTUs in the -OSS/+OM treatment. In the fungal community, the drought treatment enriched one OTU of the genus *Talaromyces* in the +OSS/-OM treatment. No other fungal OTUs were enriched by the drought treatment (Figure 3).

Rewetting Phase at harvest (PII - PIII)

Both the prokaryotic and fungal communities changed significantly during the rewetting period, although this change was not related to time. In the prokaryotic community, soil management was responsible for most of the variation in the community (~28% variance explained, PERMANOVA P = 0.001) , followed by the OM amendment treatment (~17% variance explained, p = 0.001), and the interaction between the two treatments (~6% variance explained, p = 0.001). Similarly, soil management had the greatest effect on fungal community composition (~13% of variance explained, p = 0.001), followed by OM amendment treatment (~7% of variance explained, p = 0.001), and the interaction between the two treatments (~4% of variance explained, p = 0.001). During the water recovery period, the previously imposed drought appeared to have no significant effect on either community nor did sampling time.

When the data were analyzed with more granularity, patterns emerged. Under the +OSS/+OM treatment, the prokaryotic was not affected by the drought treatment (p = 0.177). However, for the drought treatment the +OSS/-OM (~19% variance explained, p = 0.005) and the -OSS/-OM (~14% of variance explained, p = 0.012) treatments accounted for the most variation. No change was observed in the prokaryotic community under the -OSS/+OM treatment. The fungal community under the +OSS/+OM treatment was impacted by the drought treatment (~14% of variance explained, p = 0.007), but the +OSS/-OM communities were unaffected. Under the -OSS/-OM treatments, the interaction between sampling time and rewetting phase after the drought had a significant impact on the fungal community composition (~11% of variance explained, p = 0.019), although neither factor was significant on its own (Table S3).

During the recovery phase following the drought there was enrichment of four prokaryotic OTUs in the +OSS/-OM treatment; three OTUs in the -OSS/+OM treatment; and five OTUs in the -OSS/-OM treatment. No bacteria and archaeal OTUs were enriched in the +OSS/+OM treatment. The imposed drought enriched for one fungal OTU in the +OSS/+OM treatment; five in the +OSS/-OM treatment; one in the -OSS/+OM treatment; and four OTUs in the -OSS/-OM treatments. The watering treatment enriched six prokaryotic OTUs in the +OSS/-OM treatments; and four OTUs in the -OSS/-OM treatment. No bacteria and archaeal OTUs were enriched in the +OSS/+OM treatment. The drought treatment enriched for three fungal OTUs in the +OSS/+OM treatment; two OTUs in the +OSS/-OM treatment; and one OTU in the -OSS/-OM treatment (Figure 3).

Community shift with time

Planting to harvest (P0 – P3)

The change in community composition was observed through the course of the experiment via PERMANOVA and PCoA. From the start of the experiment to the harvest, there were no significant effects of the drought treatment the on the composition of the fungal and prokaryotic communities' treatment. The prokaryotic communities differed by soil management (~24% variation explained, $p = 0.001$), OM amendment (14% variation explained, $p = 0.001$), and the interaction between the two (~6% variation explained, $p = 0.002$). The community also shifted significantly during the course of the experiment (~6% of community variation explained by sampling time, $p = 0.001$) and by the interaction between organic matter and sampling time (~3% variation explained, $p = 0.017$). Prokaryotic richness, evenness, Shannon's diversity increased significantly

between planting and harvest (Figure S4). The fungal community followed a similar trend; the community shifted due to soil management (~13% variance explained, p = 0.001), organic matter (~6% variance explained, p = 0.001), and the interaction between the two (~3% variation explained, p = 0.007). The fungal community also changed over the course of the experiment (~3% community variation explained by sampling time, p = 0.002) and the interaction between organic matter and sampling time (~3% variance explained, p = 0.007). It should be noted that the drought treatment had little effect on the overall community composition of either prokaryotes or fungi.

Prokaryotic community, time of sampling also drove ~45% of the variation under the +OSS/+OM treatment (p = 0.004); under the +OSS/-OM treatment, time of sampling accounted for 27% of the community variation (p = 0.003); under the -OSS/+OM treatment time of sampling accounted for ~20% of the community variation (p = 0.013); and under the -OSS/-OM treatment, time of sampling drove about ~15% of the community variation (p = 0.002). For the fungal community, time of sampling drove about 15% of the community composition under the +OSS/+OM treatment (p = 0.008). Under the -OSS/+OM treatment, time of sampling drove about 11% of the community variation (p = 0.059), and under the -OSS/-OM treatment, time of sampling also accounted for about 11% of the community variation (p = 0.042).

Discussion

In this study it was shown that the soil microbial community significantly shifted due an early-season drought, and that there was a differential shift due to soil management and organic matter amendment. Overall, soil management (+/-OSS) was the most responsible for the microbial community variation across timepoints, and that this

was closely followed by the organic matter amendment treatment. The result that the greatest shift in microbial (both prokaryotic and fungal) community composition was due to soil from OSS over the traditional management system that lacked shrubs is consistent with field experiments and an incubation study (Diedhiou-Sall et al., 2009, Debenport et al., 2015, Diakhate et al., 2016, Mason et al., 2023). Similarly, the G. *senegalensis* soil amendments have been shown to influence microbial communities (Diedhoiu-Sall et al., 2009; Diakhate et al., 2016; Griffith & Philipott, 2013). Sampling time (before or after drought) had a significant effect on both the composition of the fungal and bacteria and archaeal communities to differing degrees with soil management and organic matter amendment.

Effect of Organic Matter

Generally, organic matter amendments strongly affected community response, which highlights the role of organic matter in maintenance of soil function through water retention, microbial community abundance and diversity, and soil physical stability, especially in arid soils (Félix et al., 2018; Hernandez et al., 2015). Throughout the experiment, the prokaryotic and fungal communities appeared to show opposite responses to the organic matter amendments. From the start to the end of the drought, the prokaryotic community was only impacted in the +OSS/-OM treatments (i.e. there was no change in community composition in the +OSS/+OM, -OSS/-OM, and -OSS/+OM treatments). It seems plausible that the presence of organic matter may have decreased the communities' sensitivities to environmental change, in this case, drought (Veach & Zeglin, 2020). The increased water holding capacity and nutrient availability of +OM amended soils may have reduced the effects of the drought, allowing for better survival

of the prokaryotic community in the drying soil, as evidenced by the reduced response in community composition in +OM amendment treatment in both +OSS and -OSS soils. It has previously been reported that the -OSS soils have significantly less total C and POM (Bright et al, 2027; 2021; Charles et al 2024b). The OM treatment shifted the bacterial and archaeal community in -OSS soil to be more similar to +OSS soil through the drought period, despite the decreased C content of -OSS soil. bacteria and archaeal diversity and evenness were also significantly reduced in +OM samples in the drying soil, implying the enrichment of a few lineages with +OM while not altering the overall community structure.

Conversely, the fungal community was most significantly impacted by the imposed drought in the +OSS/+OM samples compared with the other treatments, although the +OSS/-OM and -OSS/-OM samples experienced marginal change ($P < 0.1$). It was found that +OM amendments increased the amount of fungal PLFAs (compared with samples that did not receive the amendment) in the drying soil (Charles et al, 2024b), potentially contributing to this shift. Fungi also tend to be more drought-resistant than bacteria and archaea, so it is possible that resistance, coupled with the increased cellulose with +OM amendments and the increased total C inherent to the +OSS soils allowed for fungal proliferation in the drying soil (Treseder et al., 2018)

An increase in soil microbial biomass with the incorporation of Guiera residues has been previously reported (Diedhiou et al., 2009), and likely contributed to the significant changes observed in soil microbial community composition in the current study during the recovery phase. The prokaryotic community in the +OSS/+OM and -OSS/+OM samples experienced no change, while the composition of the bacteria and

archaeal community in the +OSS/-OM & -OSS/-OM samples shifted significantly in response to the history of the imposed drought. Here, the OM amendment may have also contributed to the stability and resiliency of the community. +OM samples changed very little from the start of the drought through the harvest, while -OM samples experienced greater change in community composition possibly because of reduced water holding capacity and nutrient availability. The fungal community responded differently in this phase as well. There was no difference between the samples that went through the drought and those that did not in +OSS/-OM, -OSS/+OM, and -OSS/-OM samples; only the +OSS/+OM samples were significantly affected by the history of imposed drought during this phase. Charles et al. (2024b), also reported that +OM amendments accounted for the largest proportion of variance in soil microbial phospholipid fatty acids (PLFAs) across all sampling time points and increased all abundances of nearly all measured clades during the re-wetting phase.

Under the -OSS/-OM treatments, the interaction between sampling time during the course of the experiment and watering appeared to have a significant impact on the fungal community composition, indicating that the amount of time that passed between the start of the drought and the harvest may have played a significant role in how the fungal community responded to the drought. This shift through time was observed in a previous incubation study using Guiera shrub residues and soils from the same region (Diedhiou-Sall et al., 2009) and was linked to the amount of time the microbes were allowed to decompose organic matter. Diedhiou-Sall et al., (2009) also reported that this shift differs through time inside and outside the influence of the shrub *G. senegalensis.* Similar results are observed in the current study where soil type, organic matter, and

phase interact to influence the fungal and bacteria and archaeal communities. Results of both studies contribute to our knowledge of whole-ecosystem function under changing environmental parameters.

Legacy Effect of Soil Management

Previous environmental conditions including human interventions of agricultural production confers a phenomenon termed the 'legacy effect' on soils (Leizaga et al 2020). For the current simulated drought experiment this legacy effect from long-term cropping with +OSS or -OSS was investigated as one factor in the microbial response and recovery to drought compared to a short-term effect of the organic shrub-residue amendment. Prior to establishment of the OSS field experiment in 2004, this site had been under a peanut–millet rotation for >50 years (likely with some fallowing). The treatments imposed (Dossa et al., 2012) were to remove shrubs from the -OSS plots whereas the density of *G. senegalensis* shrubs for +OSS plots were increased to 1200-1500 shrubs ha $^{-1}$ by planting seedlings. *G. senegalensis* residues were incorporated into the +OSS plots yearly, whereas -OSS plots received no external amendments and only millet biomass. These treatments have resulted in a divergent legacy effect on the soils as evidenced by +OSS over -OSS having significantly greater: soil microbial activity/diversity (Diedhiou et al., 2009, 2021; Diedhiou-Sall et al., 2013; Debenport et al., 2015; Mason et al., 2022), nutrient availability, C content and ultimately millet and peanut yield//aboveground biomass production (Dossa et al 2012, Bright et al., 2021). Micro-climatic conditions have also shifted with -OSS soils being warmer and drier throughout the rainy season (Bogie et al 2018; Kizito et al 2006). All of these factors, the legacy effect, would be expected to play a role in the structure and function of the soil

microbial communities and their responses to drought. Indeed, soil microbial communities were significantly different in +/- OSS soils at each phase of the experiment (Figures 1 - 3).

This legacy affect was manifest in the microbial responses to drought; notably, the communities in the -OSS samples appeared to be less impacted by the imposed drought during soil drying than the microbial communities in the +OSS samples, and this could be due to the history of dryness and low nutrient availability in the -OSS soils (Dossa et al., 2012, Bright et al., 2021; Bogie et al 2018; Kizito et al 2006). This soil legacy effect of drought on the microbial response is consistent with other studies (ex: Griffiths & Philippot, 2013; Veach & Zeglin, 2020; Leizeaga et al., 2020; Gebauer et al., 2022).

Drought and a history of low nutrient availability selects for oligotrophs (Barnard et al., 2013; Treseder et al., 2011). During soil drying, members of the phylum Actinobacteria were found to be significantly enriched in -OSS/-OM samples. Actinobacteria are known to have resilience low-water and -nutrient conditions, as gram-positive sporulators and more resistant abiotic stress (Mohammadipanah and Wink, 2016; Naylor & Coleman-Derr 2017; Treseder et al., 2011, Barnard et al 2013). Other gram-positive phyla enriched under drought conditions include members of the phylum Firmicutes (all class Bacilli) and Proteobacteria, enrichment of which have been seen in other studies (Zhao et al., 2020). Through PLFA, Charles et al., (2023) also found that the -OSS soils tended to be enriched in fungi, another group that is typically more resilient to abiotic stress (Barnard et al., 2013). This enrichment of these oligotrophs during soil drying is not surprising, as nutrients become less available as water film thickness

decreases (Barnard et al., 2013). However, their enrichment in the -OSS soil (low nutrient concentrations to begin with) further supports the hypothesis that there is a legacy effect of drought and low nutrient concentrations in -OSS soils that selects for oligotrophs.

Debenport et al. (2015) and Mason et al. (2023) provided evidence that +OSS promotes plant growth promoting rhizobacteria (PGPRs)). This is supported by the current simulated drought experiment where the genera *Tumebacillus* and *Bacillus* were significantly enriched in +OSS/-OM samples after the drought period ended. Studies have shown that members of these *Bacilli* ameliorate drought stress in crops (Vardharajula et al., 2011; Gowtham et al., 2020; Moreno-Galván et al., 2020; Murali et al., 2021;). Notably, Murali et al. (2021), reported drought resilience induction in pearl millet by *Bacillus amyloliquefaciens* producting ACC deaminase production which degrades ethylene. Ethylene is produced by plants under stress and causes plant senescence and death; thus by reducing ethylene ACC deaminase better enables plants to withstand drought stress (Vurukonda et al., 2016). An OTU assigned to the bacterial genus *Massilia* was also found in +OSS soils. This lineage has been previously shown to be enriched in the presence of *G. senegalensis* shrubs and correlated with increased millet biomass and has been found to have PGPR properties (Mason et al 2023).

Charles et al., (2023b) observed that millet biomass, height, and drought resilience were generally diminished in -OSS soils compared with +OSS soils. This failure to thrive may be due to the lack of disease suppression in the -OSS soils, (Schlatter et al., 2017) or, potentially, due to the promotion of a deleterious community. Certain management practices, such as continuous cropping with one species, may promote a deleterious or suppressive microbial community (Turco et al., 1990). The -

OSS plots have been continuously cropped with a millet-groundnut rotation for nearly two decades with very little organic matter inputs (Dossa et al., 2012), so it is possible that the continually low yields resulting from the -OSS plots may be partially attributed to a deleterious community. Also, an increase in general fungal biomass was observed in -OSS samples, particularly during the re-wetting period, where the abundance of fungi increased from 36.6% under +OM treatment and 30.6% under -OM treatments (Charles et al., 2023a). Since fungi are associated with over 80% of crop diseases, the results of the current study and Charles et al. (2024) of dominance in fungi in -OSS soils that was not found in +OSS soils, maybe an indicator that +OSS has some level of disease suppression (Tian et al., 2020; Almeida et al., 2019).

Conclusions

Ecological resilience and resistance of a community are linked to myriad biotic and abiotic factors including substrate availability, vegetation, and climate (Griffiths and Philipott, 2013). Here, these factors are the history OSS management, OM additions, the imposed drought, and time, and each of these impacted the structure of the microbial community. The specific soil microbial community response to drought depended on soil management and the organic matter amendment treatments – lack of organic matter inputs (-OM) or on soil from the long-term treatment (-OSS) resulted in a much greater shift in the microbial community. Whereas the organic matter rich treatments (+OM and +OSS) maintained diversity and a more stable community that was associated with better response of millet to drought reported by Charles et al. (2024a).

A major finding is that both long-term management with OSS and the soil amendment with *G. senegalensis* residues increased the diversity and stability of the

microbial community. This shift included the stimulation of microorganisms that assist plants through drought – and most importantly these microbial outcomes coincided with better growth of millet in this same experiment as reported by Charles et al. (2024a). Secondly, it is notable that adding *G. senegalensis* residue (+OM) by itself on the -OSS soil, caused a positive shift in the community that also corresponded to improved millet growth as reported by Charle et al. (2024a). This has very practical implications because it shows that just adding *G. senegalensis* residue by itself and not burning coppiced biomass, as is currently done with farmers, can jump start a microbial response to promote drought resistance. Thus, one does not have to wait years for OSS to start providing beneficial impacts on crop growth and resistance to drought.

The differing bacteria and archaeal and fungal responses to soil drying and rewetting with organic matter additions is an important finding because of the high proportion of potential fungal pathogens, and further sheds light on the interactions between soil management, crop outcome, and the soil microbial community in this system. The objective of this study was to remove hydraulic lift as a potential mechanism for crop drought resistance noted in field studies that have shrubs present, i.e. to isolate the effects of a higher quality soil that develops under OSS. The data supports this hypothesis with evidence that drought resistance is related to the microbial community and therefore, not solely due to hydraulic lift.

Although climate change is certain, the specific effects for a given region are difficult to predict for precipitation, flooding events, and temperature change (Trisos,2022). This follows for soils with Evans et al., (2022) indicating no consensus on how soil microorganisms will respond to climate change with variations in rainfall (soil

moisture) and temperature. None-the-less, in the Sahel of West Africa, the effects of climate change are predicted to be particularly devastating, with millions of people expected to experience food shortages (New York times, 2022). Understanding the relationship between the changing climate and the soil microbial community in this region is of the utmost importance for policy makers and researchers. The result of the current study provides evidence that OSS shifts the microbial community members toward organisms that reduce drought stress and indeed this response corresponds to better growth of millet during the drought for the same experiment reported by Charles et al. (2024a). Furthermore, the outcomes support the promotion of shrub intercropping for subsistence farmers as a low-cost, local, and highly effective means of increasing crop productivity, remediating degraded soils, and sequestering C in the Sahel.

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Author contributions

L.Mason: project design, sample collection, data analyses, growth chamber mesocosm design, main author for text

Christine Charles: sample collection for growth chamber mesocosm experiment

Ibrahima Diedhiou: Program director at ENSA, management of OSS fields

R.P.Dick: Direct mentorship of L.M.Mason,project design, lab space, long term project management

V.I.Rich: Direct mentorship of L.M.Mason, project design

Figure legends

Figure 3.1. Prokaryotic community composition and enriched 16S rRNA OTUs across all timepoints a) PCoA of OTUs in each phase. Ellipse represents 95% confidence interval. In all phases, OTUs cluster significantly by soil management (+/- OSS), OM amendment (+/-OM), and the interaction between the two ($p < 0.05$). Ellipses highlight OM treatment clusters. b) The 77 prokaryotic OTUs enriched in any of the four treatments (+OSS/+OM, +OSS/-OM, -OSS/+OM, or -OSS/-OM) at any of the four phases (planting, pre-drought, post-drought or harvest) . Enrichment was defined as $\log(LDA) > 2$; $P < 0.05$, in LefSe analyses (see Methods).

Figure 3.2. Fungal community composition and enriched ITS OTUs across all timepoints a) PCoA of Fungal Community at each phase. Ellipse represents 95% confidence interval. Within each phase, OTUs cluster significantly by soil management (+/- OSS), organic matter amendment treatment, and the interaction between the two ($P < 0.05$). Ellipses indicate significant clustering by organic matter amendment. b) The 27 fungal OTUs enriched in any of the four treatments (+OSS/+OM, +OSS/-OM, -OSS/+OM, or -OSS/-OM) at any of the four phases (planting, pre-drought, post-drought or harvest). Enrichment was defined as $\log(LDA) > 2$; $P < 0.05$, in LefSe analyses (see Methods)

Figure 3.3. Prokaryotic (via 16S rRNA amplicons) and fungal (via ITS amplicons) OTUs enriched by drought or by watering (comparing droughted vs. watered control samples at

the end-of-drought time point), in any of the four treatments (+OSS/+OM, +OSS/-OM, -OSS/+OM, or -OSS/-OM). Enrichment was defined as log(LDA) > 2 ; P < 0.05, in LefSe analyses (see Methods). c) prokaryotic (via 16S rRNA amplicons) and d) fungal (via ITS amplicons) OTUs at the harvest time point in either droughted or watered control samples. Lefse was used to find 22 significantly enriched OTUs with the imposed drought or the watered control in the one of the following treatments during the dry-down phase: +OSS & organic matter amendment treatment (+OSS/+OM), +OSS/-OM, -OSS/+OM, or -OSS/-OM (log(LDA) > 2 ; P <0.05). Enrichment was defined as log(LDA) > 2 ; P < 0.05, in LefSe analyses (see Methods)

Figures

Figure 3.1. Prokaryotic community composition and enriched 16S rRNA OTUs across all timepoints

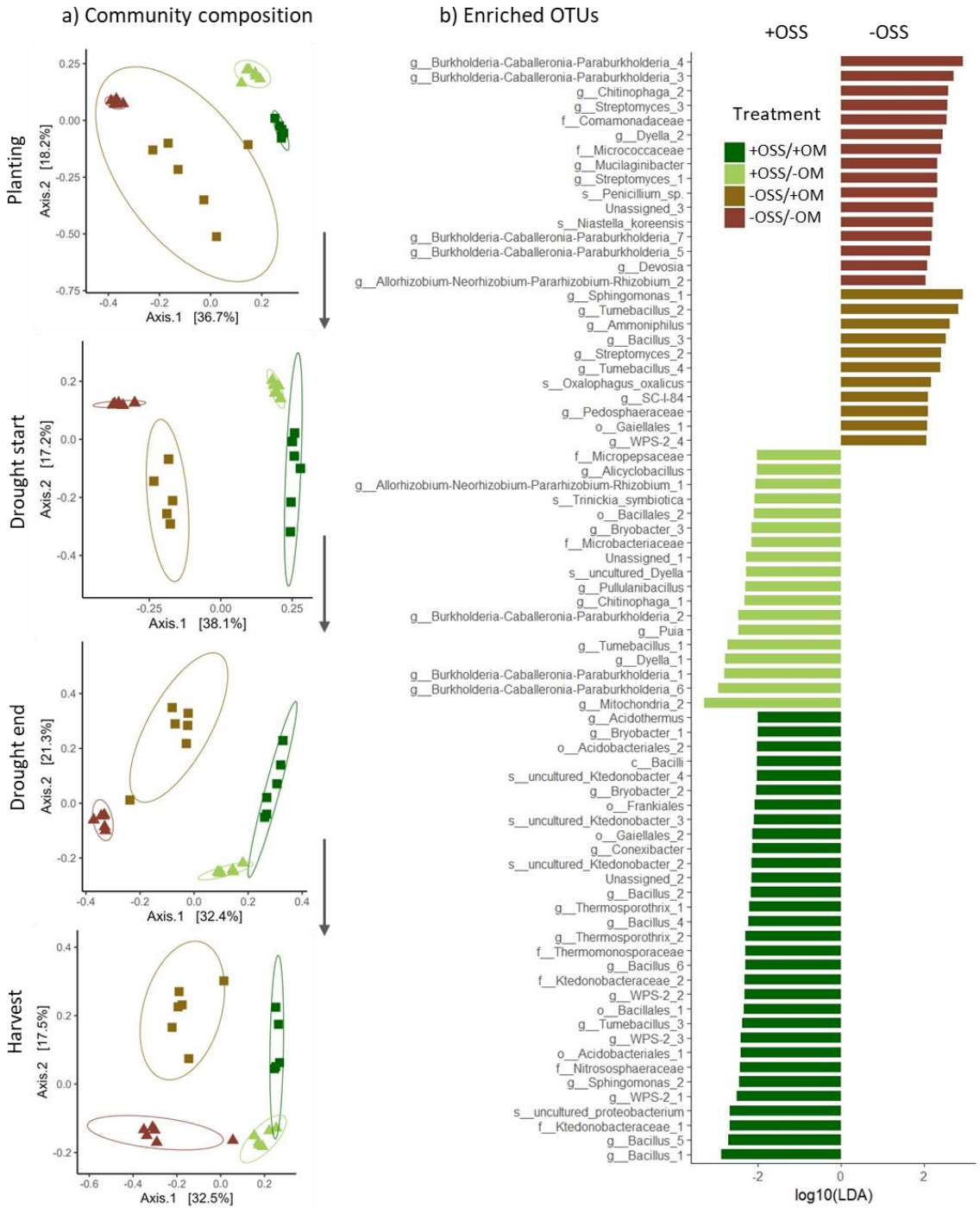


Figure 3.2. Fungal community composition and enriched ITS2 OTUs across all timepoints

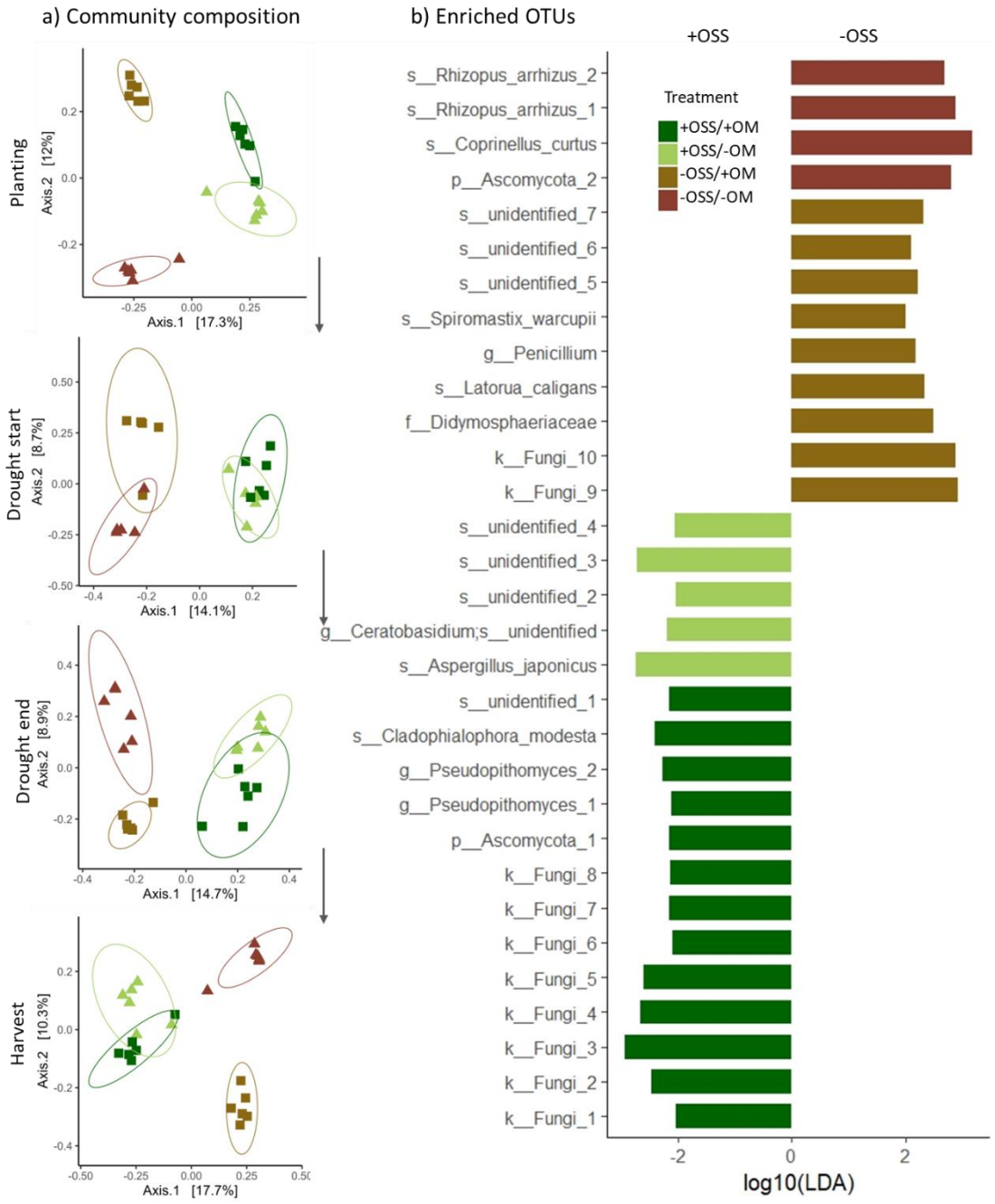
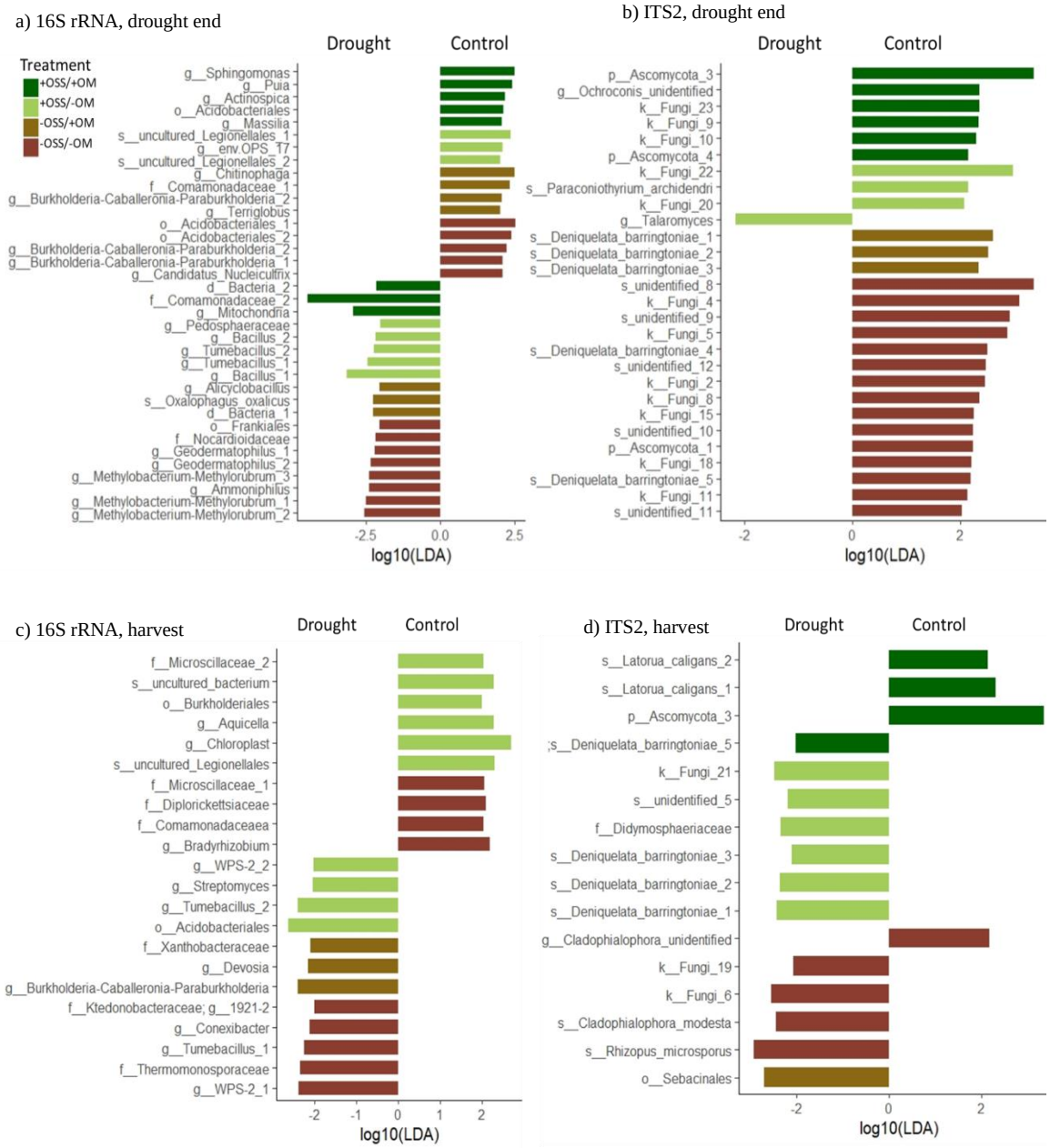


Figure 3.3. Enrichment of 16S rRNA and ITS2 OTUs under drought and control conditions



Supplemental Tables

Table S3.1. Amplification primer sets

ITS			
5' Illumina Adapter	Forward Primer Linker	ITS1-F Forward Primer	
AATGATACGGCGACCACCGAGATCTACAC	GG	CTTGGTCATTTAGAGGAAGTAA	
Primer For PCR	AATGATACGGCGACCACCGAGATCTAC ACGGCTTGGTCATTTAGAGGAAGTAA		
Read 1 Sequencing Primer	TTGGTCATTTAGAGGAAGTAAAAGTCGT AACAAGGTTTCC		
Read2 Sequencing Primer	CGTTCTTCATCGATGCVAGARCCAAGAG ATC		
Index Sequence Primer	TCTCGCATCGATGAAGAACGCAGCCG		
16S			
RC of 3' Illumina Adapter	Reverse Primer Pad	Reverse Primer Linker	806R Reverse Primer (Appril)
CAAGCAGAAGACGGCATACGAGAT	AGTCAGCCAG	CC	GGACTACNVGGGTWTCTAAT
	Reverse Primer Pad	Reverse Primer Linker	806R Reverse Primer (Appril)
	AGTCAGCCAG	CC	GGACTACNVGGGTWTCTAAT
	Forward Primer Pad	Forward Primer Linker	515F Forward Primer (Parada)
	TATGGTAATT	GT	GTGYCAGCMGCCGCGGTAA
Primer For PCR	CAAGCAGAAGACGGCATACGAGATAGT CAGCCAGCCGGACTACNVGGGTWTCTA AT		
Read 2 Sequencing Primer	AGTCAGCCAGCCGGACTACNVGGGTWT CTAAT		
Read 1 Sequencing Primer	TATGGTAATTGTGTGYCAGCMGCCGCG GTAA		
Index Sequence Primer	AATGATACGGCGACCACCGAGATCTAC ACGCT		

Table S3.2. Prokaryotic and Fungal phyla abundances at each phase

Domain	Phylum	-OSS/-OM	-OSS/+OM	+OSS/-OM	+OSS/+OM	Average
Bacteria	Proteobacteria	0.189527	0.338790	0.292134	0.374896	0.298837
Bacteria	Firmicutes	0.249726	0.201580	0.228674	0.162802	0.210695
Bacteria	Chloroflexi	0.160693	0.100077	0.058300	0.090097	0.102292
Bacteria	Actinobacteriota	0.121167	0.088849	0.106427	0.090609	0.101763
Bacteria	Acidobacteriota	0.100895	0.087731	0.087156	0.058016	0.083450
Bacteria	Bacteroidota	0.023354	0.074232	0.046688	0.097948	0.060555
Archaea	Verrucomicrobiota	0.011973	0.017082	0.037188	0.033133	0.024844
Bacteria	Myxococcota	0.018704	0.015243	0.026283	0.022803	0.020758
Bacteria	Planctomycetota	0.024308	0.017389	0.017163	0.011607	0.017617
Bacteria	Cyanobacteria	0.011456	0.009778	0.029426	0.009755	0.015104
Bacteria	WPS-2	0.029408	0.013291	0.010708	0.005043	0.014612
Bacteria	Bdellovibrionota	0.011864	0.011309	0.014250	0.013753	0.012794
Archaea	Crenarchaeota	0.017598	0.005945	0.015557	0.008082	0.011795
Bacteria	Gemmatimonadota	0.011199	0.005626	0.013733	0.008228	0.009697
Bacteria	Armatimonadota	0.005231	0.004898	0.004950	0.004286	0.004841
Bacteria	Patescibacteria	0.003158	0.003446	0.004563	0.003393	0.003640
Bacteria	RCP2-54	0.002406	0.001447	0.000553	0.000286	0.001173
Bacteria	Thermoplasmatota	0.003363	0.001151	0.000087	0.000065	0.001167
Bacteria	Dependentiae	0.000962	0.000587	0.001344	0.001153	0.001012
Bacteria	Elusimicrobiota	0.000828	0.000554	0.001381	0.000702	0.000866
Archaea	Nitrospirota	0.001117	0.000451	0.000788	0.000958	0.000828
Bacteria	Abditibacteriota	0.000128	0.000276	0.000428	0.000675	0.000377
Bacteria	Fibrobacterota	0.000159	0.000018	0.000624	0.000677	0.000370
Bacteria	Deinococcota	0.000347	0.000064	0.000359	0.000196	0.000242
Bacteria	Sumerlaeota	0.000205	0.000047	0.000377	0.000262	0.000223
Bacteria	SAR324_clade Marine_group_B	0.000037	0.000038	0.000267	0.000252	0.000148
Bacteria	Nanoarchaeota	0.000009	0.000010	0.000245	0.000182	0.000112
Bacteria	Desulfobacterota	0.000017	0.000014	0.000079	0.000059	0.000042
Bacteria	GAL15	0.000106	0.000037	0.000019	0.000000	0.000040
Bacteria	Methylomirabilota	0.000010	0.000019	0.000084	0.000031	0.000036
Bacteria	FCPU426	0.000014	0.000005	0.000076	0.000006	0.000025
Bacteria	Entotheonellaeota	0.000005	0.000015	0.000048	0.000024	0.000023
Bacteria	Dadabacteria	0.000022	0.000001	0.000026	0.000012	0.000015
Bacteria	Fusobacteriota	0.000000	0.000001	0.000006	0.000004	0.000003
Bacteria	Latescibacterota	0.000000	0.000000	0.000007	0.000003	0.000002
Bacteria	MBNT15	0.000004	0.000000	0.000004	0.000001	0.000002

Fungi	Ascomycota	0.555352	0.419597	0.807749	0.656391	0.609772
Fungi	Basidiomycota	0.269957	0.456425	0.022359	0.219725	0.242116
Fungi	unidentified	0.129635	0.108012	0.112819	0.040353	0.097705
Fungi	Mucoromycota	0.040344	0.015367	0.043213	0.081834	0.045189
Fungi	Cercozoa	0.000790	0.000354	0.009105	0.001411	0.002915
Fungi	Mortierellomycota	0.000189	0.000002	0.004562	0.000098	0.001213
Fungi	Glomeromycota	0.003224	0.000047	0.000007	0.000002	0.000820
Fungi	Chytridiomycota	0.000379	0.000117	0.000179	0.000185	0.000215
Fungi	Entorrhizomycota	0.000043	0.000072	0.000000	0.000000	0.000029
Fungi	Calcarisporiellomycota	0.000088	0.000008	0.000007	0.000000	0.000026

Table S3.3. PERMANOVA results

	Treatment	Prokaryotic community					Fungal community		
All phases		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.26081	0.001	***			0.11708	0.001	***
	OM amendment	0.13983	0.001	***			0.04419	0.001	***
	Drought	0.0083	0.125				0.01056	0.121	
	Phase	0.05182	0.002	**			0.03533	0.011	*
	Management* OM amendment	0.04867	0.001	***			0.02579	0.001	***
	OM amendment* drought	0.00696	0.206				0.01329	0.028	*
	OM amendment* phase	0.03063	0.016	*			0.03165	0.043	*
Planting (P0)		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.3037	0.001	***			0.16345	0.001	***
	OM amendment	0.19072	0.001	***			0.09941	0.001	***
	Management* OM amendment	0.07385	0.013	*			0.05794	0.026	*
Drought Start		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.366	0.001	***			0.13395	0.001	***
	OM amendment	0.15545	0.001	***			0.05435	0.048	*
	Management* OM amendment	0.07428	0.017	*			0.04796	0.092	.
Drought End		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.29322	0.001	***			0.13882	0.001	***

	OM amendment	0.20385	0.001	***			0.08101	0.003	**
	Drought	0.03523	0.118				0.04224	0.164	
	Management* OM amendment	0.08181	0.003	**			0.05481	0.033	*
	Management* drought	0.01943	0.481				0.03908	0.273	
	OM amendment* drought	0.01856	0.509				0.04105	0.196	
Harvest		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.16566	0.001	***			0.28428	0.001	***
	OM amendment	0.08086	0.004	**			0.1626	0.001	***
	Drought	0.03827	0.282				0.02974	0.292	
	Management* OM amendment	0.05795	0.031	*			0.06378	0.027	*
	Management* drought	0.03338	0.504				0.03413	0.215	
	OM amendment* drought	0.03915	0.23				0.03563	0.177	
P0 - P1 (planting to drought Start)		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.12505	0.001	***			0.12375	0.001	***
	OM amendment	0.05857	0.001	***			0.05051	0.001	***
	Phase	0.0293	0.015	*			0.02896	0.013	*
	Management*OM amendment	0.03848	0.002	**			0.03246	0.007	**
	OM amendment* Phase	0.02689	0.037	*			0.02695	0.027	*
	Management* Phase	0.02237	0.097	.			0.02171	0.107	
P1 - P2 (drought start to end)		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.31235	0.001	***			0.11952	0.001	***
	OM amendment	0.16676	0.001	***			0.05827	0.001	***
	Drought	0.01175	0.31				0.02322	0.084	.
	Phase	0.0676	0.001	***			0.01958	0.277	

	Management: OM amendment	0.01254	0.287				0.04091	0.001	***
	OM amendment* drought	0.01107	0.35				0.02388	0.067	.
	OM amendment *phase	0.02491	0.06				0.0162	0.722	
P2 - P3 (Drought end to harvest)		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.2754	0.001	***			0.13468	0.001	***
	OM amendment	0.1738	0.001	***			0.06684	0.001	***
	Drought	0.01998	0.097	.			0.02102	0.118	
	Phase	0.01116	0.383				0.01608	0.568	
	Management* OM amendment	0.06431	0.001	***			0.04149	0.002	**
	OM amendment* drought	0.01668	0.156				0.02203	0.108	
	OM amendment* phase	0.00918	0.54				0.01638	0.52	
P0 -P3 (planting to harvest)		R^2	Pr(>F)				R^2	Pr(>F)	
	Management	0.13701	0.001	***			0.24086	0.001	***
	OM amendment	0.06318	0.001	***			0.13716	0.001	***
	Drought	0.01746	0.36				0.01195	0.394	
	Phase	0.03446	0.007	**			0.06237	0.001	***
	Management* OM amendment	0.03782	0.004	**			0.04558	0.002	**
	OM amendment* drought	0.01902	0.227				0.01267	0.337	
	OM amendment* Phase	0.03104	0.007	**			0.03003	0.017	*

Supplemental Figures

Figure S3.1. Sampling curves for 16S rRNA and ITS2 OTUs

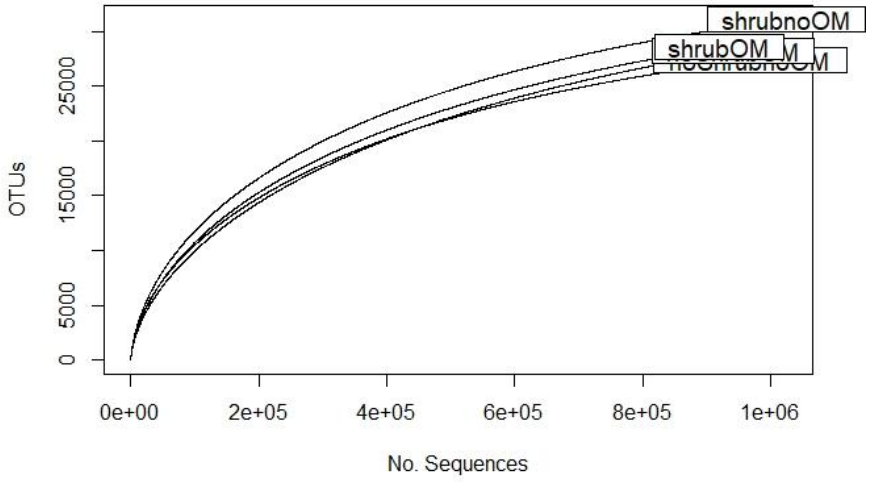
Figure S3.2 Prokaryotic phyla at each phase

Figure S3.3. Fungal phyla at each phase

Figure S3.4. Alpha diversity metrics a) 16S rRNA observed richness, b) 16S rRNA Shannon's H, c) 16S rRNA Pielou's J evenness, e) 16S rRNA observed richness, e) 16S rRNA Shannon's H, f) 16S rRNA Pielou's J evenness. All metrics were calculated using rarefied data. * indicates significant differences between treatments at $p < 0.05$

Figure S3.1 Sampling curves for 16S rRNA and ITS2 OTUs

A. 16S rarefaction



B. ITS rarefaction

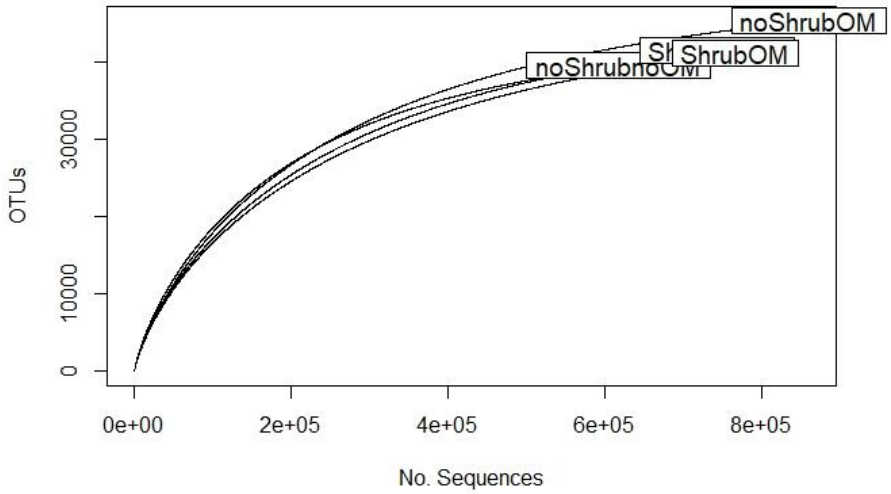


Figure S3.2 Prokaryotic phyla at each phase

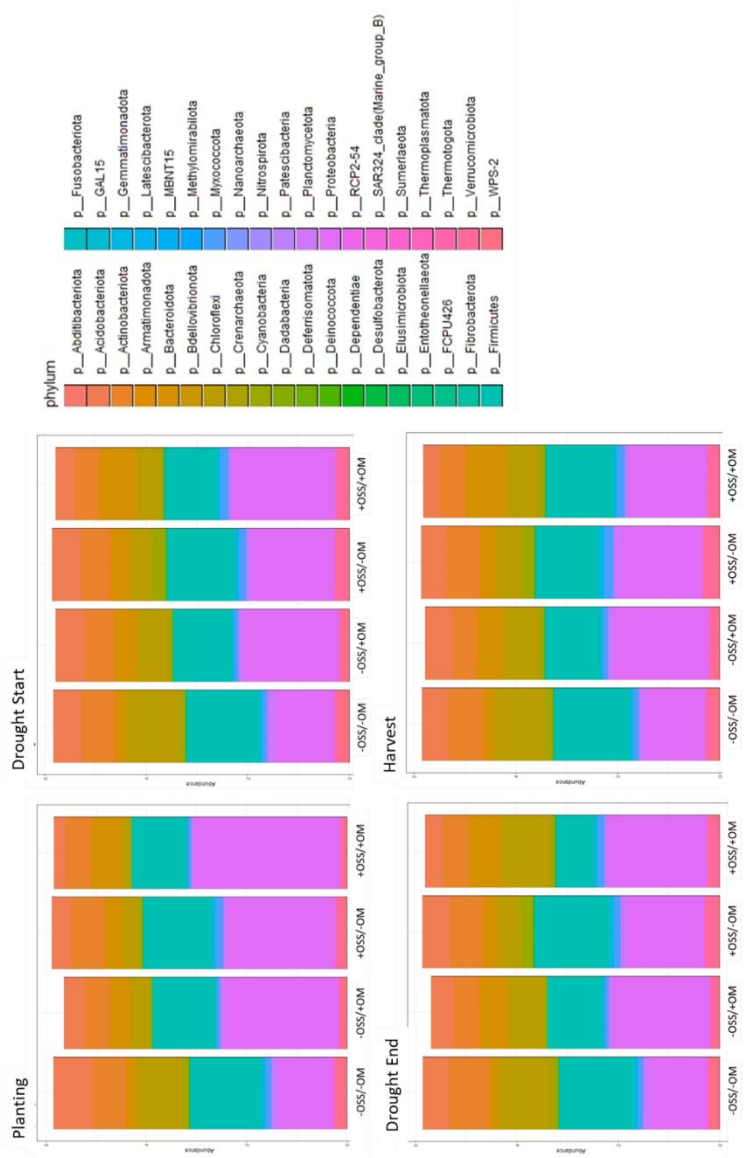


Figure S3.3 Fungal phyla at each phase

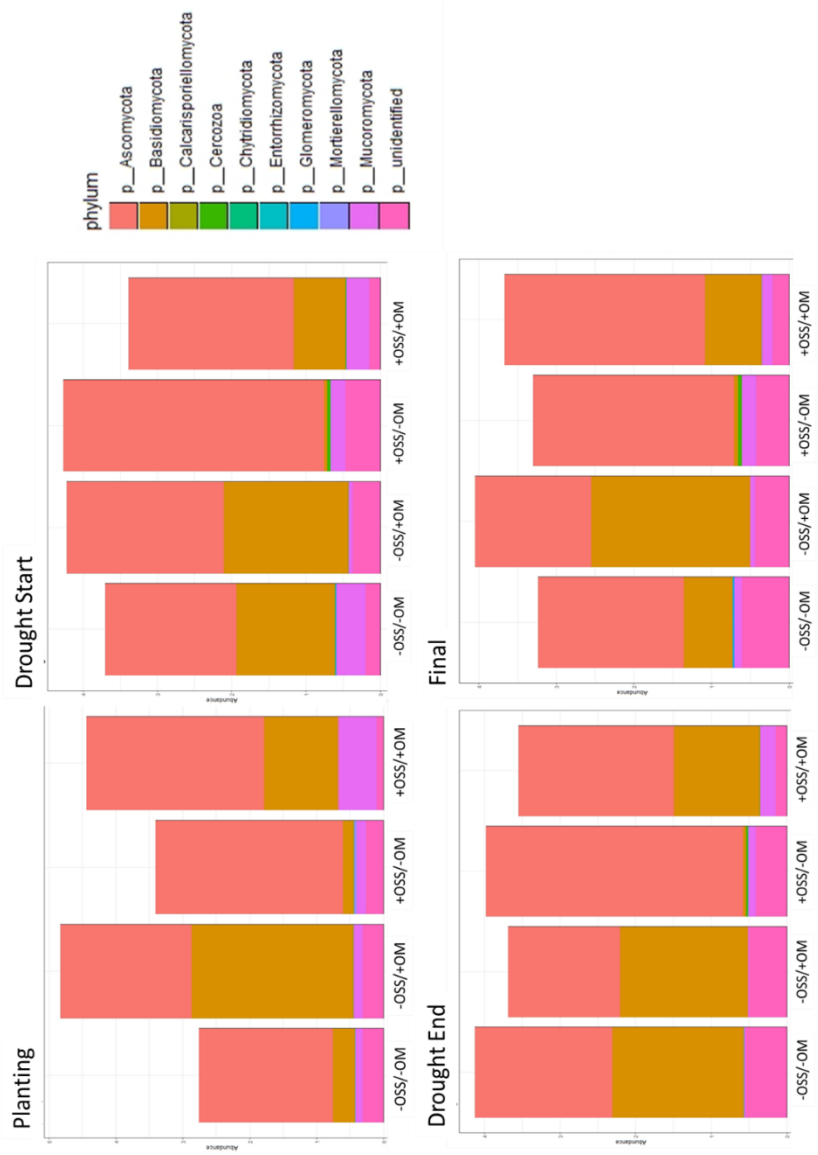
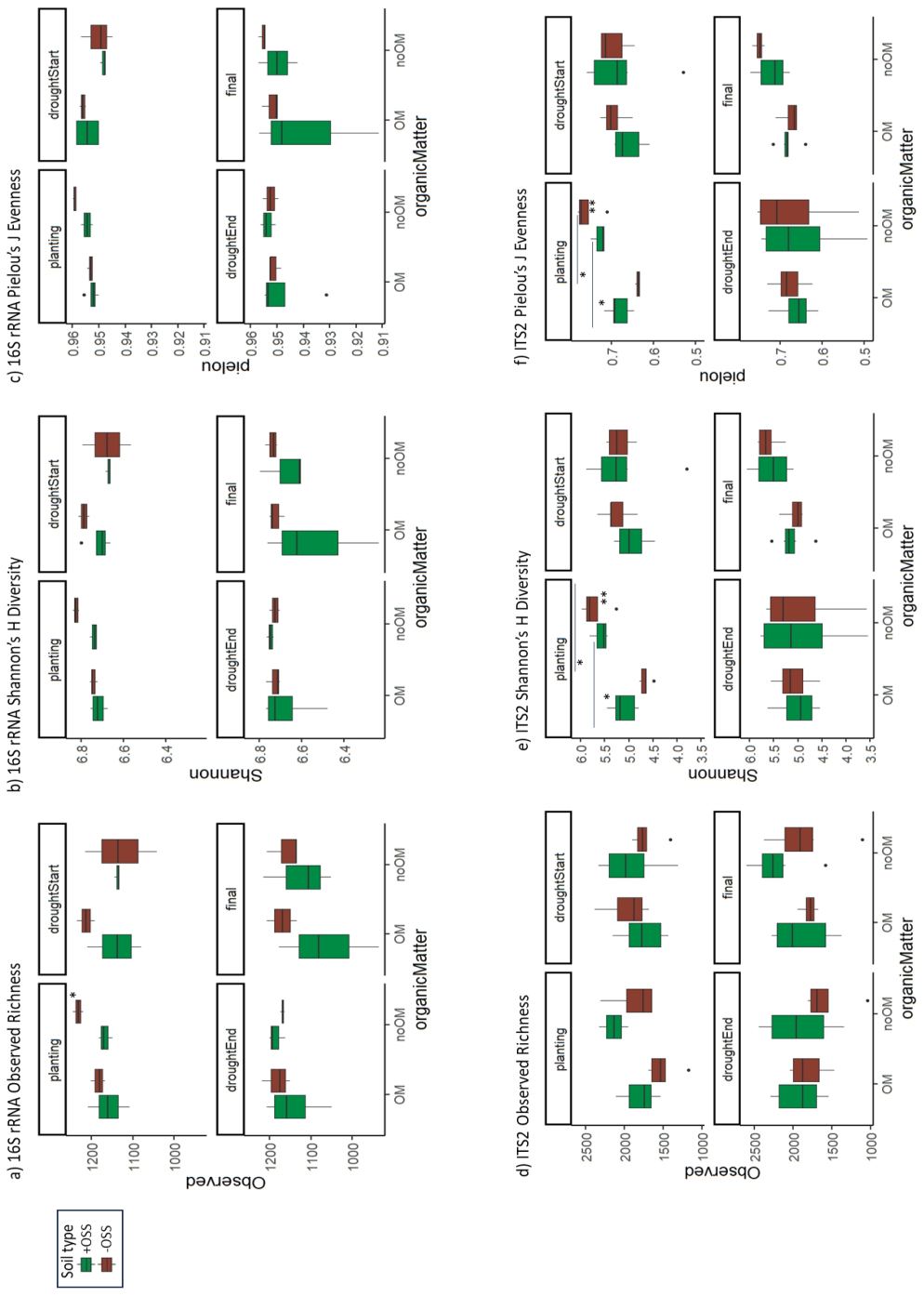


Figure S3.4 Alpha diversity metrics



Chapter 4. Microbial Mechanisms of Millet Drought Stress Mitigation in an Optimized Intercropping Shrub System

In prep for submission to the *International for the Society of Microbial Ecology Journal*

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Abstract

In the Sahel region of West Africa, subsistence farmers grow pearl millet with few external inputs and under a rapidly changing climate. Further, soil degradation and climate change-induced drought threaten this growing population's food security, necessitating local and sustainable means of maintaining yields under climate change. Intercropping the indigenous woody shrub *Guiera senegalensis* improves millet yield under drought through various proposed physical and chemical mechanisms. However, these mechanisms are insufficient to explain the magnitude of intercropping's impact on millet yields, especially under drought. In the well-characterized Optimized Shrub-intercropping System (OSS), millet rhizosphere and bulk soil microbiomes are significantly altered by shrub presence and contain putative plant growth promoting rhizobacteria (PGPRs). Therefore, we hypothesized that this microbial community confers drought resilience and promotes growth of nearby millet plants, and that the metagenomes would contain genes related to these functions. We profiled the microbial community in the OSS, as well as a Simulated Drought experiment, clarifying mechanisms by which intercropping, organic matter incorporation, and an imposed drought affect the structure and function of the microbial community. Results showed that metagenomes and protein cluster profiles were significantly different +/- shrub in both studies, and that organic matter amendment played a significant role in determining

community structure and function. Two-hundred and sixty-three high and medium quality metagenome assembled genomes (MAGs) were also recovered, many containing genes related to PGPR functions. These data represent the first genome-resolved results from the well-characterized OSS site and add to a growing body of metagenomic information obtained from dry land agricultural systems in Sub-Saharan Africa, which have been chronically understudied. This work therefore fills a crucial knowledge gap on the role of microbes in sustainable dry-land agriculture.

Introduction

The Sahel is a semi-arid region where millet is a staple crop and is produced by subsistence farmers, largely without externally-purchased inputs of fertilizer, or irrigation (World Food Programme, 2023). However, the UN reports that this area is a "climate change hotspot" where change is expected to happen 50% faster than other parts of the world (IPCC 2017, ISS Africa 2016). The Palmer drought-severity index predicts patterns of extreme drying across West Africa brought on by global warming in the coming century. The resulting erratic rainfall and drought are expected to decrease production and further exacerbate the high food insecurity in this region. Further, the United Nations estimates a nearly 600% increase in population size by the year 2100, potentially forcing this country to rely substantially on international aid to meet its food needs population by the year 2100, potentially forcing this country to rely on international aid (UN, Department of Economic and Social Affairs, 2016). Therefore, local and biologically-based systems are needed to promote crop resilience to drought (Poppy et al., 2014).

One potential resource that has been identified to address these challenges for the Sahel is the shrub *Guiera senegalensis*. This species can coexist with crops in Senegal (Lufafa et al.,2008) and throughout the Sahel. The absence of mechanized agriculture has allowed this indigenous species to live in cropped fields of the Sahel. However, shrub densities are low, and the shrubs are typically coppiced before the growing season, and burned, depriving soils of much needed organic inputs (Diedhiou-Sall et al., 2013). This largely unmanaged agroforestry system (except to burn coppiced biomass) is the basis of the Optimized Shrub-intercropping System (OSS) which increases current shrub densities of <200 to ~350 shrubs ha^{-1} (Lufafa et al., 2008) to 1200 to 1500 shrub ha^{-1}. Then instead of burning the coppiced shrub residues, they are incorporated into soils (~3 Mg ha^{-1} dry wt.) (Dossa et al., 2012). OSS dramatically increases yields, buffers against drought (Kizito et al., 2006; Bogie et al., 2018; Bright et al., 2021), and promotes microbial diversity (Diedhiou-Sall et al., 2013; Debenport et al., 2015; Mason et al., 2023).

Shrubs perform hydraulic lift, which is the movement of water along a water potential gradient of higher water potential in the sub-soil (above the water table) to dry surface soil by plant root systems up through tap roots that are released in surface roots (Kizito et al., 2006). Recently, Bogie et al. (2018) used isotopically labeled water to confirm that hydraulically lifted water was transferred from *G. senegalensis* to adjacent millet plants during a simulated in-season drought under field conditions. However, the volume of water transferred to inter-cropped millet is relatively low (Kizito et al., 2006) which means there is extremely efficient transfer of water and suggesting a second mechanism of drought resilience conferred by shrubs. Previous research has shown that the shrub supports a microbial community that assists millet through drought by direct

and indirect mechanisms (Debenport et al., 2015; Bogie et al 2018; Mason et al., 2023, Mason et al., 2024a, Charles et al., 2024b). These include osmolyte production, antioxidant production, phytohormone manipulation, exopolysaccharide production, and changes to the availability of certain nutrients.

The objective was to determine: 1) genes and organisms related to plant drought resilience and growth promotion; and 2) if the effects of the OSS can be recapitulated in a growth chamber Simulated Drought experiment, decoupled from the presence of the living shrub, under an imposed early-season drought. These objective were investigated via metagenomic and metatranscriptomic analyses in the long-term field experimental site, the OSS, and a Simulated Drought Simulated Drought experiment with soils from the OSS.

Methods

OSS Field Sites and Soil Sampling

The long-term experimental Optimized Shrub Intercropping site is located in the northern region of the Peanut Basin (14°45' N, 16°51' W), Keur Matar, Senegal. Air temperatures range from 20.0 to 33ºC and the mean annual precipitation of 450 mm mainly comes between July and September (Kizito et al., 2006; Bright et al., 2021). The soil is a loamy sand with <5% clay and 95% sand, loose consistency, and has a 5.5 pH (1:2 soil:water). The soil is classified as a Rubric Arenosol in FAO taxonomy (Michéli et al., 2006) and as a Typic Torripsamment in USDA Soil Taxonomy (Lufafa, 2005).

The main experimental +/- OSS plots were established in 2003, by manually removing existing shrubs from "-OSS" plots and maintaining 9 to 11 shrubs per "+OSS" plots for a stand density of 1,500 to 1,833 shrubs ha^{-1} (Lufafa et al., 2008). The site

includes variation in fertilizer additions (Lufafa et al., 2008); in this study, 0x and1X NPK-fertilizer (22kg N, 15kg P, and 15kg K ha^{-1}, applied yearly) plots were used. Field sites are maintained by our partner lab at the École Nationale Supérieure d'Agriculture (ENSA, Thiès, Senegal). For this manuscript, +/-OSS will refer to the soil management type in the field and "field study" will be used to describe results from the samples collected from the +/-OSS plots in the 2019 and 2020 sampling season.

In the growing and dry seasons (September 2019, and March 2020), samples were collected from 16 plots +OSS 0-NPK, +OSS 1X NPK, -OSS 0X NPK, and -OSS 1X NPK. In both seasons, samples were collected from the bulk soil, either impacted by shrub or not (+/- shrub), and in the growing season samples were also collected from the millet rhizosphere and endososphere. Bulk soil was collected to a depth of 15cm +/-OSS plots in triplicate using a 5cm-diameter core. Cores were placed in gallon Ziplock bags and homogenized by hand through the bag. Two millet plants were randomly selected per plot. Two roots were removed from each plant with sterilized scissors, and rhizosphere soil from all four roots was gently scraped from the roots into a Whirl-Pak bag. These same roots were placed in a 50mL falcon tube with 15 mL sterile phosphate buffered saline + 1% Triton-X, and the whole millet plant was placed in a labeled gallon Ziplock bag. The aboveground fresh biomass was weighed, and then averaged per plot. Sampling resulted in 48 samples from the growing season and 16 from the dry season. All samples for this project were transported on ice from field to lab and stored at -20°C prior to extraction.

Roots were separated and surface sterilized for endosphere DNA extraction per McPhearson et al (2018). Briefly, roots and any remaining rhizosphere soil were

separated by vortexing at the lowest setting for 2 minutes. Roots were moved with sterile forceps to a new tube, and soil was pelleted and added to the field-collected rhizosphere soil. Roots were washed with each a 10% bleach solution and a 70% ethanol solution before being cut into ~5 mm pieces with sterile scissors and distributed to the Qiagen PowerBead tube for DNA extraction. For the growing season samples, sample preparation and DNA extraction was performed at the Centre d'Etudes Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS, Thiès, Senegal). Dry season samples (March 2020) were transported directly to the Ohio State University for DNA extraction due to complications arising from the COVID-19 pandemic.

Simulated Drought Simulated Drought experimental design and sampling

Soils for the Simulated Drought experiment were collected from 0-15 cm depth in the +/-OSS, 0 fertilizer field sites in October 2019, shipped overnight, and stored at -20℃ until use. For the purposes of this manuscript +/-OSS soils in this Simulated Drought experiment will refer to soils with a history of +/-OSS management from the field site. Also, the phase "Simulated Drought experiment" will be used when referring to methods and results from the from the Simulated Drought experiment.

Mesocosms were constructed from PVC pipes 10cm in diameter, cut into 40 cm sections and capped on one end. The design did not include drainage holes for ease of maintaining gravimetric water content. The experimental design comprised: 2 soils (+/- shrub presence in the field), by 2 soil amendments (+/- OM, see below), and 2 simulated precipitation levels (+/- drought) (Figure 1). Each mesocosm received 2.7 kg soil (dry weight). For OM treatments, *G. senegalensis* plant stem and leaf were collected in the

field and air dried and returned to Ohio at air temperature under USDA plant import permitting. Each Simulated Drought mesocosm received 1.27 g of a mixture of *G. senegalensis* stems and leaves in a 60%/40% mixture weight/weight. This amount is equivalent to the field rate of 4 Mg ha^{-1}, which is consistent with shrub biomass additions that occur at the experimental field site (Lufafa et al. 2008, Diedhiou et al., 2009). Residues were mixed into the top 15 cm of mesocosm soil per on-site practices. Mesocosms were allowed to incubate at a constant "daytime" temperature of 31 and "nighttime" temperature of 28 with a 12-hour diurnal cycle for 10 days before planting. These conditions are similar to those in the field and were maintained throughout the experiment.

The Simulated Drought experiment spanned four phases (Figure 1). In phase 0, the mesocosms rested for 10 days at 31℃ before planting, which commenced phase I. Millet seedlings grew to the 5-leaf stage under optimal soil moisture (field capacity, determined to be 3.75% gravimetric water content); this phase lasted ~12 days. Soil moisture was measured gravimetrically, daily. Watering to field capacity was maintained for the entire experiment in control mesocosms, as described in Charles et al., 2024a. In phase II, in the drought treatment replicates water was withheld for 10 days to mimic the effects of an early season drought (Bidinger & Mahalakshmi, 1987), while the non-drought replicates were maintained at field capacity soil moisture. In phase III, soil in the drought replicates was rewetted to field capacity, and that moisture level was maintained in all replicates for a 10-day recovery period.

Planting (Phase 0, after 10-day incubation), Pre-drought (Phase I) and drought (phase II) samples for microbial community analyses were collected at ~ 12 days after

emergence and ~22 days after emergence using a small soil corer (Figure 1). Samples for soil chemistry were collected at PI and PIII using the same core. Phase III material was collected at the end of phase III via destruction sampling of the mesocosms. Microbial and plant samples were flash frozen and stored at -80℃ until further processing, and samples for soil chemistry were transported on ice and stored at -20℃.

Nucleic Acid Extraction

For the field samples, DNA was extracted from bulk soil and rhizosphere via the PowerSoil Pro kit (Qiagen), according to the manufacturer's instructions. Endophyte DNA was extracted from millet roots via the Plant Mini DNA extraction kit (Qiagen) according to manufacturer's instructions, with minor modifications. using a bead beater 2x for 1 min each to rupture the plant cells. DNA extractions were performed in-country for all rainy season samples (September 2019). Extraction success was confirmed via gel electrophoresis. DNA was precipitated with ethanol and transported to the US where it was reconstituted and quantified via Qubit.

For the Simulated Drought experiment, samples from phases I and II were targeted for paired metagenomic and -transcriptomic characterization. RNA and DNA were co-extracted from 0.25 g soil, using the Zymo RNA/DNA co-extraction kit, following manufacturer's instructions with one minor modification; cells were lysed using a Powerlyzer for 45 seconds on setting 4. DNA and RNA were QC'd via Qubit, and RNA was checked for quality via Agilent Bioanalyzer Tapestation. The average RIN score was 7.3.

Library Preparation and Sequencing

Field study metagenomic libraries were prepared and sequenced at the Department of Energy's Joint Genome Institute. Briefly, 0.2 ng of genomic DNA was sheared to 300 bp using the Covaris LE220-Plus and size selected with SPRI using TotalPure NGS beads (Omega Bio-tek). The fragments were treated with end-repair, A-tailing, and ligation of Illumina compatible adapters (IDT, Inc) using the KAPA-HyperPrep creation kit (KAPA Biosystems), and 5 cycles of PCR was used to enrich for the final library. The prepared libraries were quantified using KAPA Biosystems' next-generation sequencing library qPCR kit and run on a Roche LightCycler 480 real-time PCR instrument. Sequencing was performed on the Illumina NovaSeq sequencer using NovaSeq XP V1.5 reagent kits, S4 flowcell, following a 2x151 indexed run recipe. 1.3 TB of data was produced for these 64 samples.

Simulated Drought experiment metagenomic libraries were prepared at Ohio State University, using the Illumina Nextera XT DNA Library Prep kit (San Diego, CA, USA) per manufacturer's instructions, with minor modifications. DNA was fragmented and indexing was performed at 95℃ for 30 seconds. Amplification was performed with 15 - 25 cycles (based on input mass, see below) of 95℃ for 20 seconds, 55°C for 30 seconds, and 72℃ for 30 seconds, followed by the final elongation step at 72℃ for 5 min, then a 10℃ hold. Samples with a starting mass of greater than 0.8ng were amplified using 15 cycles; 0.5 - 0.8 ng were amplified using 18 cycles; 0.2 - 0.5 ng were amplified using 20 cycles; N/A - 0.2 were amplified using 25 cycles. AmPureXP beads (1.8x volume) were used to select for fragments between 300-500 bp. Library concentration was assessed via Qubit, and quality and peak sizes were assessed via Agilent BioAnalyzer TapeStation.

Samples with a large proportion of DNA greater than 1kb underwent a right-hand bead selection following the SPRI select protocol with minor modifications (Beckman Coulter B24965AA). Simulated Drought experiment metagenomes were sequenced at the Columbia Genomics core on the Illumina NovaSeqS4 platform. Two samples failed sequencing, and sequencing was repeated via NextSeq2000 at the Applied Microbiome Science Laboratory at the Ohio State University. Simulated Drought metatranscriptomic library preparation and sequencing were performed by the Columbia Genomics Core using RNA RIBOZERO 40M PE100 kit on the Illumina NovaSeq4 platform.

Upstream meta'omic read processing

Metagenomes from the field study were trimmed via BBDuk in BBTools (Bushnell, n.d.), and raw metagenomic and metatranscriptomic reads from the Simulated Drought experiment trimmed in Trimmomatic (v.0.3.6, Bolger et al., 2014) (ILLUMINACLIP: TruSeq3-PE.fa: 2:30:10:2:True SLIDINGWINDOW:4:15 LEADING:3 TRAILING:3 MINLEN:36). FastQC (v0.11.8, Andrews, S. 2010) was used to assess read quality before and after trimming.

Metagenomic Assembly

All metagenomic samples were assembled using Megahit (v1.2.9) with default settings (Li et al., 2015). For field study assemblies, unmapped reads were indexed via Bowtie2 v2.5.2 (Langmead et al., 2012) and assembled via Megahit (v1.2.9), and these assemblies were combined with the original samples and deduplicated as needed via DeDupe (BBtools, Bushnell, n.d.). Trimmed metatranscriptomic reads were assembled in MetaSpades (v3.14.1), and Kraken (v2.1.2, Wood et al., 2019) was used to verify that very little eukaryotic DNA was present in the assemblies. Quality of all assemblies was assessed using QUAST (v0.4.5, Mikheenko et al., 2015). Abundance of trimmed reads

mapped to assemblies was determined using CoverM (v0.6.1, Woodcroft, 2022) with --min-covered-fraction 10 and the trimmed mean method as a means to further assess assembly quality. Functional annotations of all ORFs were performed in DRAM (Schaffer et al., 2020), and all proteins from both studies were clustered using the *mcl* Markov Cluster Algorithm (van Dongen, 2008) to produce ~1.6M protein clusters. Read coverage of protein clusters was assessed via CoverM0.6.1 with the above settings, and these values were used to determine differential enrichment of protein clusters via LefSE (Segata et al., 2011), using treatment as class and replicate as subclass.

Recovery of Metagenome Assembled Genomes

Binning and refinement of field study metagenomic assemblies was performed in MetaWRAP (Uritskiy et al., 2018) using Maxbin2 (v2.12.1) and Metabat2 (v2.2.7) with a minimum contig length of 500 bp. Bins were also obtained from the field study metagenomes via the Joint Genome Institute standard metagenome analysis pipeline, using the MetaSPAdes assembler (v3.13.0, Nurk et al., 2017) and MetaBat (v0.32.4) with a 3,000 bp minimum contig cutoff and parameter '-superspecific' for maximum specificity. Quality of all bins was evaluated in CheckM (v1.1.6, Parks et al., 2014) , and bins that were > 70% complete and < 10% contaminated were retained as MAGs (MIMAG, Bowers et al., 2017) and subsequently dereplicated to 95% ANI (min covered fraction: 10%) in dRep (v2.4.2) (Olm et al., 2017).

1,180 medium (>70% complete, <10% contaminated, n= 819)and high quality (>90% complete, <5% contaminated, n= 361) MAGs were recovered from OSS assemblies (n=989 using in-house scripts, see Methods, and n=166 from the Joint Genome Institute pipeline), Simulated Drought assemblies (n=25). These 1180 were then

dereplicated at 95% ANI to a total 263 MAGs via DRep (Olm et al 2017). 8% of JGI derived MAG and 100% of MAGs derived from the chamber experiment formed their own clusters; i.e. these MAGs were not a subset of the field-derived MAGs. taxonomy was assigned to this set of dereplicated medium- and high-quality MAGs (n = 263) via the GTDB-tk v2.3.0 (Chaumeil PA, et al. 2022), and functional annotation of ORFs was performed in DRAM (Schaffer et al., 2020).

MAG read coverage in transcripts per million of trimmed metagenomic and metatranscriptomic reads from both studies was obtained via CoverM v0.6.1 with --min-read-aligned-percent 75 --min-read-percent-identity 95 (Woodcroft, 2022). Coverage values were used to assess differential enrichment of MAG by treatment in LefSE (Segata et al., 2011) with treatment as class and replicate as subclass. The proportion of the total community recovered in the medium and high quality MAG set was determined using singleM appraise (Woodcroft, 2022) with the flags --imperfect --sequence_identity 0.89 to determine genus-level recovery estimates at --imperfect --sequence_identity 0.95 to determine roughly species level recovery estimates (Singleton et al., 2023).

Taxonomic Profiling

Taxonomic identity of raw metagenomes and metatranscriptomes defined via SingleM v0.13.2-pipe. These data were used to confirm enrichment of individual lineages (Table S1). Genome-resolved signals were then compared to lineages observed in the broader community, with the goal of improving taxonomic granularity and relating genome and lineage enrichment. To this end, taxonomic identity of enriched MAGs was confirmed via clustering with single copy marker gene derived lineages in VSEARCH (v2.6.0) (Rognes et al., 2016) at 95% ANI. Enriched MAGs taxonomically defined as

members of the same genus or family were also clustered via FASTANI at 95% (EDGAR 3.2.)

Data Availability

Raw metagenomes and metatranscriptomes are publicly available at the National Center for Biotechnology Information under PRJNA930014 (Simulated Drought experiment) and PRJNA928765 (field study) and functional annotations and metadata are available at https://zenodo.org/uploads/8384851

Statistics

Statistical analyses were performed in the Phyloseq package in R 4.0.3 (McMurdie & Holmes, 2013; R Core Team, 2022). Permanova (Adonis package) was used to determine statistical differences in community composition with original soil type (+/- shrub), drought, organic matter additions, and phase, using block or replicate as the random effect. Ordination analysis was done with Principal Component Analysis (PCoA) to plot multivariate data to show spatial separation of treatments. Heatmaps were made using the R package Pheatmap in R 4.0.3. Differences in soil and plant chemistry, plant biomass , and PC category by treatment were evaluated via a Wilcoxon signed rank test and linear mixed effects models in R v4.0.3. Spearman's correlations were performed to assess relationships between the abundance of individual MAGs and soil and plant outcomes.

Results

Microbial Datasets

The number of distinct OTUs recovered from each of the 59 ribosomal proteins in the Simulated Drought experiment was 192 - 22,300 (median = 1607, out of 9,596,170 - 82,405,472 raw reads). Assuming that 10% of those reads were errors and also singletons

(per Woodcroft & Singleton et al., 2018), the number of distinct lineages was estimated as the number of lineages detected minus 10%. After 10% of the median richness was 14,420 distinct lineages , but the large proportion of singletons that remained out of the total (73%) suggests that low abundance populations were not well sampled. In the field study, 974 – 188,155 distinct OTUs were recovered in each of the 59 ribosomal proteins (median = 90,133, out of 12,095,607 - 244,773,536 reads). Here, 9,013 singletons were removed from the total OTU count for each of the ribosomal proteins and used to estimate the actual richness (median = 80,526). A large proportion of singletons remained out of the total (41%), suggesting that here, too, singleM underestimates the abundance of rare lineages.

Metagenomic assemblies from the field study and metatranscriptomic assemblies from the Simulated Drought experiment were annotated in DRAM and clustered via a Markov clustering algorithm into 1,582,254 protein clusters (PCs), about 10% of which were uncharacterized. 752 PCs were identified as PGPR- and drought resilience-related (Table S2). However, although the current methods of annotation are robust, they may not be sufficient; the databases used by DRAM are not specifically for PGPR genes, so many PGPRs may be missed. In addition, many PGPR target genes could have multiple functions in the cell, and, although care was taken to choose target genes with only PGPR related function, it is possible that those selected could serve multiple purposes.

1,180 medium quality (>70% complete, <10% contaminated, n= 819) and high quality (>90% complete, <5% contaminated, n= 361) MAGs were recovered from field study assemblies (n=166 from the Joint Genome Institute pipeline, and n=989 using in-house scripts, see Methods) and Simulated Drought assemblies (n=25).

These 1,180 were dereplicated at 95% ANI via DRep to 263 MAG clusters (Olm et al 2017). For 207 of these clusters, the representative bin was derived from OSS in-house scripts (152 contained only OSS in-house, 4 clustered with GC, 51 clustered with JGI-script), for 43 clusters the representative bin was from OSS JGI-scripts (5 only JGI, 38 clustered with OSS), and for 13 clusters the representative bin was derived from the Simulated Drought experiment (11 were Simulated Drought only, 2 clustered with OSS). In terms of the full composition of these clusters, the in-house-pipeline-derived MAGs comprised ~84% (989 out of 1180) of the recovered MAGs, were present in 94% (247 out of 263 contain / are only OSS in-house) of the clusters, were cluster representatives for 78% (207/263) of the clusters, and 58% (152/263) of the MAG clusters were exclusive to the in-house-pipeline-derived MAGs. 46% of JGI pipeline-derived MAGs (77 out of 166) clustered exclusively with other JGI pipeline-derived MAGs, in just 5 clusters; the remaining 54% (89 out of 166) s clustered with those from the in-house pipeline. 44% (11 out of 25) of the growth-chamber-derived MAGs formed their own clusters.

The 263 dereplicated MAGs represented an average of ~30% of the field site microorganisms at the genus level (47% of bacteria and 16% of archaea), and an average of 17% at the species level (25% of bacteria and 13% of archaea). In the Simulated Drought, these 263 MAGs represented an average of 27% (41% of bacteria and 14% of archaea)and 14% (18% of bacteria and 10% of archaea) of the microorganisms at the genus and species levels, respectively.

73 MAGs were selected for further analysis on a basis of having a high degree of enrichment in the field study rhizosphere samples (either +/- shrub), or a high degree of

enrichment under treatment in the greenhouse study, or activity in the metatranscriptome. 48 of these had been previously included in PGPR literature. 16 of these 73 were enriched under the same +/-OSS treatment in both the field and greenhouse experiments. For the portion enriched across either study, 15 MAGs with enriched conspecific lineages were found that were enriched under the same +/-OSS treatment. All of the 73 selected MAGs possessed at least one of the genes from the PGPR and drought resilience related genes included in table S2.

Field study:

Plant and Soil

At time of sampling, millet was significantly larger and had greater fresh biomass in the presence of shrub than not. Soil percent total C and N were significantly higher in +OSS plots ($p < 0.05$) (Table S3).

Microbial ecology

Lineages differed between sample types (millet rhizosphere, dry season soil, or rainy season soil, fertilizer application and +/-OSS (Figure 2). Within each sample type (rhizosphere soil, rainy season bulk soil, and dry season bulk soil), +/-OSS accounts for a significant proportion of variance in the microbial community. The dry season bulk soil communities were significantly different from the rainy season bulk soil communities. Here, the past use of fertilizer was also a significant driver of variance in community composition (Figure 2, Table S3).

PCs vary significantly +/-OSS, fertilizer application, and sample type (Figure2, Table S3). No known PGPR target PCs (Table S2) were enriched by treatment, but

several categories of these genes were significantly increased +OSS compared with -OSS. In the rainy season bulk soil, there was an increase in genes related to osmolyte and antioxidant production as well as the total target PCs. In millet rhizosphere samples, there was an increase in PCs related to antioxidant, osmolyte, and phytohormone production (but not exopolysaccharide), PCs related to increasing the nutrients available to the host, and total target PCs. In the dry season bulk soil, PCs related to antioxidant, osmolyte, and phytohormone production, and total target PCs were enriched +OSS. Fertilization also increased the number of PCs related to exopolysaccharide, osmolyte, and phytohormone production and total target PCs.

MAG composition was significantly influenced by sample type, +/-OSS, and fertilizer application (Figure 2, Table S3). Although no MAGs were enriched +/-OSS *across* sample types, in the rhizosphere 20 MAGs were enriched +OSS and five MAGs were enriched -OSS (table S1).

Growth Chamber Simulated Drought Experiment

Plant and soil

+/- OSS field soils were used in a Simulated Drought experiment to test the effects of an imposed drought on millet and soil health outcomes +/-OSS and +/-OM. Soil percent total C and N and extracellular enzyme activities were significantly higher in +OSS samples ($p<0.001$) at the time of sampling. Post drought, watered plants were taller than droughted plants and +OM millet were taller than -OM of either treatment at $p < 0.05$. Millet biomass (above- and belowground) in soils with +OM contained more than a 50% greater amount of Ca, K, Mg, and P than -OM. At harvest, +OSS plants had significantly greater total biomass and aboveground biomass and total (Charles et al.,

2024b). Millet plants had greater chlorophyll A in +OSS at post-drought, and a higher ratio of chlorophyll A to chlorophyll B, indicating increased stress under -OSS treatments (Croft et al., 2017; Agathokleous et al., 2020).

Microbial ecology of total community

Pre-and post-drought the lineage composition significantly differed with respect to history of intercropping and the organic matter amendment treatment ($p < 0.05$, Figure 4, table S3).

PCs in the total community were impacted by intercropping, organic matter amendment, and drought. The abundance and composition of all protein clusters (n= ~1.6M) in the total community also differed with history of intercropping and organic matter amendment pre-drought. Both the drought and control communities' PC abundances differed by the history of shrub, and the imposed drought treatment had some effect on composition ($p< 0.05$) (Figure 4, Table S3).

In the subset of target PCs related to PGPR and drought resilience (n=752, genes listed in table S2), OM and a history of shrubs drove variation in total gene content at the pre-drought. The drought also impacted PC composition at $p < 0.1$, and both droughted and control communities were significantly different by OM and history of shrubs. At the start of the drought, the total amount of PGPR PCs, and those related to antioxidant production was significantly higher in +OSS/+OM ($p<0.05$) and those related to exopolysaccharide production at ($p < 0.1$) (Figure S7, Table S3)). PCs related to osmolyte and phytohormone production were significantly increased under +OSS/+OM and +OSS/-OM treatments compared with -OSS +/-OM. At the end of the drought, in the

watered control, phytohormone and osmolyte PCs in +OSS/-OM were significantly increased compared with other treatments. Notably, the presence of genes related to beta-1,4-glucosidase production (E.C:3.2.1.21) positively correlated with beta-1,4-glucosidase activity in communities that had experienced the drought (Table S4).

OSS drove most of the MAG variation pre-drought, followed by OM, and the interaction between the treatments (Figure 4, Table S3). Post-drought, both drought and control communities differed by OM and +/-OSS. Up to 67% of genera and 48% of species in the Simulated Drought were found in the MAGs dataset per sample.

Ecology of the active community

Pre-drought, active lineages differed with respect to +/-OSS, and post-drought the composition of watered control communities differed by organic matter amendment (Figure 4).

PCs (n = ~1.6M) did not differ with treatment before or after drought. However, target PGPR-related PCs were significantly different pre-drought by OM and history of shrubs (Figure 4, Table s3). Post-drought, watered control and droughted PC compositions were significantly different from each other, with the effect of drought impacting the community at a significance level of $p < 0.1$. +/-OSS drove composition in the watered control, and +/-OM drove composition in the droughted communities (Figure S7, TableS3). The sum of active PGPR genes and PCs related to osmolyte, phytohormone, and antioxidant production were significantly higher in the +OSS/-OM treatment pre-drought than they were in other treatments. Post-drought, no categories of PGPR PCs were significantly increased between treatments.

The active community MAGs did not vary by treatment although we suspect that this is in part due to the small number of active MAGs in this dataset (n=10) (Figure 4, Figure S5).

Discussion

Comparing the Simulated Drought and Field Investigations

OSS significantly altered the microbial communities at lineage, gene and genome resolutions (Figures 1, 4, S7), in both field and Simulated Drought. In the field, intercropping occurs as both the presence of shrub and the addition of its OM before the start of the growing season (Lufafa et al., 2008) and drove an enrichment of lineages and MAGs from the family Gaillaceae, including 5 lineages and 2 MAGS from genus Palsa_739, *Bradyrhizobium*, *Solirubrobacter*, *Streptomyces* and Sphingomonodaceae and an increase in the genes encoding antioxidants, osmolytes, phytohormones and genes relate to changing nutrient status in the soil (Figure 2). While the composition of the bulk soil and millet rhizosphere communities were quite different, both exhibited a significant shift in the presence of shrub (Figures 2, S1) although the lineages enriched in each sample type are distinct (Figure2, table S5)

16 MAGs out of the 73 target MAGs were enriched under +OSS (either +/-OM) in the Simulated Drought experiment and field study. Several MAGs are enriched in both the +OSS plots in the field and the -OSS mesocosms in the Simulated Drought experiment. All genomes enriched in either +/- OSS or +/- OM had the functional potential to ameliorate host drought stress and senescence through phytohormone manipulation, osmolyte, antioxidant, and exopolysaccharide production, and by

influencing host nutrient availability (Figures 2 - 4, Figure S4). Other researchers (Larkin and Martiny 2017; Louca et al., 2016, 2017) have reported a high degree of functional overlap across diverse phylogenies and variability in functional traits even among closely related lineages. The dispersal of such functional traits across the tree of life is also a product of the environment. It is highly likely that, given the climate of the Sahel, many microorganisms are well adapted to low water low nutrient soils, and these microorganisms respond similarly to drought regardless of shrub presence (Louca et al., 2016, 2017). It is possible that the organisms were dormant in the field and are activated by the OM due to either increased water holding capacity provided by the OM amendment It should also be noted that the genomes recovered from each study comprised a limited proportion of the total lineages captured by this study, and that the lineages captured by this study likely do not represent the total community diversity. This may explain the distinct differences observed in the PCs +/-OSS and +/-OM in both studies and is reflected in the plant and soil outcome (Figure 4, Figure S7). As the MAGs comprised a limited portion of the total community, it is reasonable to assume that the PCs provide a more comprehensive view of community function, and it can be concluded that +OSS communities have increased PGPR potential.

Further, investigating phylogenetic conservation of PGPR traits among genomes will be valuable in accurate scaling from lineages and MAGs to system behaviors, which is key for agromicrobiome management for climate resilience (Tiedjie et al., 2022) , and for predicting shifting ecosystem function under climate change (as for traits more broadly, Allison 2012, Amend et al 2015).

Intercropping resulted in a consistent response among the current and prior field

studies and the Simulated Drought experiment in the soil chemistry and millet responses. Shrub presence in the field was associated with significantly larger millet, significantly higher soil C and N , and a significantly different microbial community, in agreement with prior field studies (Diedhiou et al., 2009; Debenport et al 2015; Bright et al., 2021). Although there were distinct visual improvements in the height, biomass, and health of the plants +OSS (Figure S7.) (Charles et al., 2024a), they were not significant, likely due to the small sample size (n=12).

Shrub residue soil amendments and microbial drought response

In the Simulated Drought experiment, the history of intercropping could be separated from shrub OM addition. The OSS comprises both shrubs and yearly applied shrub residues, which means that the microbial community is affected by the history of intercropping, the history of OM, and the impact of the fresh OM yearly. The Simulated Drought experiment, +OSS/+OM and -OSS/-OM treatments most closely represent the conditions of the field site, especially at the start of the drought and in the watered controls, but the +OSS/-OM and -OSS/+OM treatments provided an opportunity to study the differential impact of historical and new OM.

The OM amendment treatment played a significant role in determining community structure and function and was a significant driver in changes to community function (Figure 4, S7), similar to results of Leizaga (et al, 2020) ad Malik et al 2020. The imposed drought impacted PC composition of the total community at $p < 0.1$ and the PGPR related PCs at $p < 0.05$. This could be because the organisms are well adapted to drought (Leizaga et al 2020), or it could be due the effects of the physical effects of OM such as organic matter, such as water retention and increased soil C. These have been

well documented to affect microbial community function under drought stress (Felix et al 2018; Adamczyk et al, 2020; Che et al., 2020; Malik et al 2020). Notably per Malik et al (2020), OM may affect key functions related to drought stress amelioration in plants. Here, OM amendments influenced composition at gene- and genome levels of resolution and increased throughout the experiment (Figure 4), and OM control of variance in active target PC response to drought (Figure S7). Also, above: belowground biomass ratio of +OM millet plants was 60% higher than that of -OM (Charles et al., 2024a) at the time of harvest, possibly indicating that increase in the water holding capacity of the soil and the activation of potentially beneficial microbes (Diedhiou-Sall et al., 2013) supported millet growth.

It is also possible that the influence of the OM could also be due to shrub residue degradation over the course of the experiment, as hypothesized in Charles et al., 2024b and Mason et al., 2024a. Authors reported there that OM amendments increased in contribution to community variation through the post-drought and harvest phases of this experiment. Similarly, Deidhiou et al., 2009 reported an increase in total PLFAs as *G. senegalensis* residues decomposed, peaking at 15 days after residue amendment in *G. senegalensis* soils and a significant increase in total PLFA in non-amended *G. senegalensis* soils after 45 - 105 days than in soils from outside of the G. *senegalensis* canopy. They also reported significant clustering with amendment. They hypothesized that the residue amendments, and the increased moisture from HL, stimulate growth, and in the current study, OM had a significant impact on the composition of the active community after drought (Figure 4), indicating that there is a portion of this community that responds to the OM treatment. Degradation of OM in both the +/-OSS treatments and

the subsequent impacts on community function are worth further investigation as they indicate the importance of shrub residue incorporation to the use of the OSS, and increasing C storage in soils is a key need in the Sahel (Poppy et al., 2014).

Several MAGs were enriched under drought conditions -OSS/+OM in the Simulated Drought experiment that were also enriched under +OSS conditions. The shift in potential function indicates that there was a subset of microbes, present in both +/OSS soils, which are being activated by the increased soil C and then supported through drought by the OM, both for C and water. Further, although the total composition of target PGPR PCs in the community significantly differed +/-OSS and +/-OM as well as the imposed drought treatment, there were no significant differences in the amounts of each category of PGPR PC at post-drought by any treatment (Table S2). However, this may indicate that the overall potential function of the community may be an emergent property of the ecosystem. As the impacts of climate change may be challenging to predict and may include less frequent but more intense rainfall events (IPCC 2022), it is critical that the functional potential of these organisms be analyzed.

Insights from the active microbial community data

History of shrubs and the OM amendment the total and active communities differentially. Generally, greater consistency of the response to treatment was observed in the total community compared with the active community. This may represent a lag in the total community, and as it is possible to obtain relic DNA or the DNA of dormant cells, or it may indicate that only a small portion of the community is active; for example species richness, defined through singleM and the rplB gene, is also about double in the total community than the active community As soils in the Sahel are sandy, nutrient-

poor and tend to be low in microbial biomass, low activity would not be surprising (; Che et al., 2020, Bickel and Or, 2021; Liu et al., 2022). It also appears that active community is not simply a subset of the total community. For example, the top 50 lineages from rplB are not the same and there are only 4 overlapping lineages between the total and active communities. This indicates that there is, however, small, an active and responsive portion of the community, distinct from the total portion.

A history of intercropping and the current OM amendment treatment drove variation in the PGPR related PCs. First, treatment shifted and increased the counts of target PGPR PCs (Figures 4, S7) in both the total and active communities at the start of the drought. However, the active and total communities are differentially influenced by shrubs and OM at different points in the experiment. The pre-drought and post-drought watered active communities are significantly different +/-OSS, and the OM treatment significantly impacted composition of droughted communities. Also, a greater spread in the active PCs was observed in the ordinations at all stages of the experiment (both PGPR related and not, figure 4, S6), indicating that within the small portion of the community that is active, a suite of genes was upregulated under treatment. Finally, active genomes that transcribed PGPR related genes were present in +OSS field soils (dry and rainy seasons), and some had PGPR PCs enriched within their transcriptome under drought conditions (Table S6). However, low sequencing depth and this low biomass community may prevent us from making further conclusions.

MAGs of interest

Several MAGs from the phylum Actinobacteria, genus Palsa 739, were highly enriched in +OSS in both the field and the Simulated Drought experiment, and also

possess genes for osmolyte production, phytohormone manipulation, and exopolysaccharide production. Notably CSA4R.bin.3 (genus Palsa-739) is enriched in bulk soil in the dry and rainy seasons at the field study and at both the start and post-drought in +OSS treatments in the greenhouse (table S1). The lineage is also enriched in the rhizosphere in the field study, as determined by single copy marker gene analyses. The genome's abundance correlated positively to percent total C and N, and millet height in the field study (Table S3). PCs present include those related to proline and trehalose production, exopolysaccharide production, and phosphorus solubilization (Figure 2, Figure S4). Another MAG identified as Palsa_739, is significantly enriched in the Simulated Drought experiment +OSS at the start and post-drought, and in the field study: dry soil +OSS. The abundance of this MAG is moderately positively correlated with percent total C and N in field study millet rhizosphere samples with 0x fertilizer and total chlorophyll post-drought in samples that had experienced drought. PCs present include several related to glycine betaine production, trehalose production, and exopolysaccharide production, as well as an aldehyde dehydrogenase gene (adlH) gene related to phytohormone manipulation (Figure S4).

As the name suggests, members of genus Palsa_739 has been previously found in sub-arctic peatlands (V.I. Rich, personal communication), but a MAG identified as Palsa-739 was recently uncovered in the microbial community in soils contaminated by mining operations (Liu et al., 2023) and is also common in our study site. Given the varying potential functions that have been ascribed to this genus (Liu et al, 2023; current study) and its geographical and ecological spread, it is logical to assume that this genus may contain many different organisms whose ecological function has not been fully

uncovered with the tools at hand. It may, as previous studies on its family of origin suggest, be a key player in semi-arid soil community structure and function (Chowdhury et al., 2019) and a great adapter to rapidly shifting dry-rewet cycles (Walters et al., 2018), making it a key candidate organism for further study in sustainable agricultural systems.

A MAG from the genus *Dyella*, (13_2.bin.2, phylum: Proteobacteria) was enriched +OSS rhizosphere soils and in +OSS, +OM treatments in the greenhouse, and also possess genes for phosphorus solubilization (2 phoN, appA), beta-glucosidase production (3 E.C:3.2.1.21), and one chitinase gene (EC:3.2.1.14) as well as genes related to salicylic acid production (acnA, E.2.2.1.6L), trehalose production (otsB), glutathione peroxidase production (gpx), and mannose production (manB) (Figure S4). It had moderate to strong correlations with percent totalC, percent totalN, and millet height and fresh biomass as well as average yield 2011 -2015; (grain kg/ha) in the field study and total chlorophyll post-drought in the Simulated Drought experiment (Table S2).

While the millet endophyte communities displayed no changes with treatment overall, one MAG was enriched for in +OSS endophyte samples CSC3R_bin_11 (family Burkholderiaeae, genus *Triinickia*) was enriched in millet root samples, as well as +OSS samples in bulk rainy season soil, bulk dry season soil, rhizosphere and +OSS before and after the drought in the greenhouse study, and has genes related to osmolyte production, butane-diol volatile production (phytohormone manipulation), exopolysaccharide production, and ACC-deaminase production (Figure S4). Another MAG was enriched in the -OSS millet endosphere, and possessed genes related to antioxidant and osmolyte production (Figure S4). Very few MAGs were present in the endophyte community, and the lineage-resolved community composition shows little response to intercropping or

other treatment (Figure S1). However, the presence of MAGs with PGPR potential calls for further investigation.

No MAGs were statistically enriched in the metatranscriptome of the Simulated Drought experiment. However, three active MAGs have notable patterns of abundance with treatment in both studies (Figure S5). 01_2.bin1 (family: Ktedonobacteraceae) was significantly enriched in two out of three replicates in the Simulated Drought experiment post-drought, as well as the rainy and dry season bulk soil and +OSS rhizosphere samples. This organism's genome is strongly positively correlated to percent total C and percent total N ($R2 = 0.86$ and 0.85 respectively, $p < 0.001$) in +OSS samples that had not received fertilizer (Table S3). Its genome encodes two genes for alginate lyase & catalase. Active genes include genes related to the production of osmolytes, 2,3-butanediol, exopolysaccharide, and catalase (Figure S4). This genome was present under multiple treatments, both + and - shrub in the Simulated Drought experiment but was enriched in two out of three replicates in the metatranscriptome +OSS under drought conditions (Figure S5). Active PCs enriched under drought conditions include one for type 2 lantibiotic (related to disease prevention in host (Keswani et al., 2020)), and a thioredoxin (antioxidant response (Bianucci et al., 2017)) (Table S6).

Members of the family Ktedonobacteraceae are represented by multiple MAGs that are enriched +OSS under drought conditions (Figure S5). Chloroflexi, the phylum to which this family belongs, are well adapted to rapid drying and rewetting so, it is not surprising MAGs from the family Ktedonobacteraceae are abundant in drought conditions in this study (Karray et al. (2020), Sarkar et al, (2022), Miesner et al. 2018) Here, the Ktedonobacteraceae MAGs also possess PGPR genes and the active MAG

contains some active PGPR-related genes. Previously, however, members of this group were found in disease-conducive soils (Nisrina et al., 2021), and there is little other literature on the family. Further, all MAGs identified as members of Ktedonobacteraceae are related at< 65% ANI, and one MAG, unidentified beyond the family level clustered, many enriched lineages also from this family (Table S1, Figure S6). Therefore, it is possible that members of the family Ktedonobacteraceae may have some yet-overlooked PGPR capabilities, although further research is required to test this hypothesis (Rodreguiz-R and Konstantinidis, 2014)

Another MAG CSC3R.bin.7 (order Acidobacteriales; genus *Gp1-AA17*) is present in the metatranscriptome and appears to be depleted in drought conditions, both +/- shrub and +/-OM (Figure S5). This genome is enriched in the field +OSS millet rhizospheres, and +OSS rainy season and dry season soils, and enriched post-drought +OSS in the Simulated Drought experiment. It appears to respond strongly to drought, being nearly completely depleted in droughted samples. This genome's abundance correlated with percent total C and percent total N in the +OSSs treatment and to total chlorophyll production by millet post-drought. Genes present include three copies for NAG-ase and chitinase production, three copies of a gene phosphoesterase production, and three genes for the production of trehalose (Figure S4). Active genes of note include several related to trehalose production (Table S6).

Conclusions

Intercropping and its history had a significant impact on microbial community structure and function at lineage-, PC-, and genome-level resolutions, with an overlap in intercropping-enriched members and functions among studies. Targeted PGPR-related

functions were common in these systems and also significantly increased +OSS in the field - in both rainy and dry seasons - and Simulated Drought experiment pre-drought, indicating that the microbial community functional impact of intercropping remained, even without the effect of the living shrub. Notably, the lack of post-drought difference +/-OSS *or* +/-OM (derived from shrub) in the Simulated Drought experiment communities in PGPR PCs implies that the living shrub has some important influence on community function under drought. In the active post-drought communities in the Simulated Drought experiment, addition of shrub-derived OM significantly altered the composition - but not total abundance - of the PGPR PCs. Thus, under *ex situ* drought, neither intercropping legacy nor shrub OM recapitulate shrub-enrichment in the field of PGPR functions. The drought resilience conferred to the crop by living shrubs may thus be an emergent property of the intercropping system. These findings demonstrate that the shrub intercropping system fosters microbiota with increased PGPR potential and responsiveness during drought stress. A key next step is further experimentation during the drought state, with higher replication, and deeper quantification of plant stress-response molecules and of microbial system-resilience functions and activities.

This work is the first time in this shrub-intercropping system that traditional soil microbial ecology characterizations have been complemented by meta-omic sequencing, providing a unique and granular portrait of the complex shrub-crop-microbial interactions in an understudied, but highly climate-relevant, agricultural system. Taken together, these results provide a partial view of the microbial mechanisms behind a long standing sustainable agricultural system and pave the way for further research into microbially mediated dry land agriculture under a changing climate.

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Figure legends

Figure 4.1. Conceptual overview of experimental design and procedures. a) Optimized Shrub-Intercropping Study site, located in Senegal in the Sahel region of West Africa. Experiments on the interactions between intercropping, fertilizer, and plant and soil health outcomes have been ongoing since 2004. Microbial DNA was obtained from these soils and used for metagenomic analysis b) Simulated Drought experimental design, soils were transported from field site (both +/-OSS, 0x fertilizer) and stored at -20 C leading up to the experiment. Soils were then thawed, homogenized, and divided across 12 mesocosms with or without *G. senegalensis* residues (+/-OM), as pictured. Soils were moistened to 3.75% moisture by weight, and this moisture level was maintained throughout the course of the experiment, except during the imposed drought. After 10 days, a small soil core was taken, and three millet seeds were planted (Phase 0). When millet plants had grown five leaves (the 'five-leaf stage'), a small soil core and a leaf cutting were collected, and the drought began (Phase I). At this time, half of the mesocosms underwent the imposed drought, during which they received no water while the control samples' moisture levels were maintained. After 10 days of the imposed drought (or 10 days after the Phase I sample was taken for the control mesocosms), another soil sample was taken and the droughted samples were re-wet to 3.75% moisture w/w (Phase II). After a 10-day recovery period (or 10 days after the phase II sample was obtained from the control mesocosms), mesocosms were destructively harvested (Phase III). DNA and RNA were co-extracted from all soil samples obtained at all time points, but paired metagenome/ metatranscriptomes were only obtained from Phases I and II. c) Analytical workflow. Metagenomes and metatranscriptomes were analyzed through the pipeline below.

Figure 4.2. PCoA of lineage, Protein cluster and MAG variation across treatments. A) PCoA of field site lineages. Data clustered +/-OSS (R2=0.02179, p = 0.019), sample type (R2=0.32498, p = 0.001), and fertilizer: (R2= 0.07013, p =0.001) B) PCoA of field site protein clusters. Data cluster by +/- shrub (R2 = 0.075, p =0.001), fertilizer application (R2 = 0.030, p 0.020), sample type, and the interaction between shrub presence and sample type (R2 = 0.62, p = 0.001). PCoA of OSS MAGs. Data cluster by +/-OSS (R2 = 0.12, p =0.001), fertilizer application (R = 0.067, p =0.001), and sample type (R2 = 0.32, p = 0.001). C) Enriched MAGs (log10(LDA) > 2; p = 0.05) order was determined through clustering by Euclidean distances between LDA scores. LDA scores for -OSS enriched samples were multiplied by -1 to facilitate this clustering and for ease of visualization. D) Abundance (transcripts per million) of enriched MAG/ total TPM of MAGs in treatment. Intensity of color indicates increased abundance. E) Gene content per MAG (count gene/ count of genes in category: Antioxidant production, exopolysaccharide production, osmolyte production, nutrient acquisition, and phytohormone manipulation)

Figure 4.3 Simulated Drought experiment MAGs pre- and post-drought. A) Enriched MAGs (log10(LDA) > 2) $p < 0.05$. * indicate MAGs also enriched in the OSS rhizosphere. LDA scores of MAGs enriched -OSS were multiplied by -1 for ease of visualization. B) Abundance (transcripts per million) of enriched MAG/ total TPM of MAGs in treatment. Intensity of color indicates abundance. C) Gene content per MAG (count gene/ count of genes in category, Antioxidant production, exopolysaccharide production, osmolyte production, nutrient acquisition, and phytohormone manipulation) C) Enriched MAGs (log10(LDA) > 2), $p < 0.05$. * indicate MAGs also enriched in the

+OSS rhizosphere. LDA scores of MAGs enriched -OSS were multiplied by -1 for ease of visualization. D) Abundance (transcripts per million) of enriched MAG/ total TPM of MAGs in treatment. Intensity of color indicates increased abundance. C) Gene content per MAG (count gene/ count of genes in category, as described in a)

Figure 4.4 Lineage, MAG, and protein cluster abundance and spread in active and total community before and after drought. a) PCoA of Total Lineages. Top panel, Pre-drought: data cluster significantly by history of intercropping ($R2 = 0.37$, $p = 0.001$)and organic matter amendment ($R2=0.14$, $p =0.001$). Interaction between the treatments is significant at $p < 0.1$ ($R2 = 0.050$, $p= 0.066$). Bottom panels, post-drought: watered control data cluster significantly by history of intercropping ($R2 = 0.14$, $p = 0.001$) and organic matter amendment ($R2 = 0.11$, $p = 0.022$); droughted data cluster by history of intercropping ($R2 = 0.14$, $p =0.002$). Data cluster at $p < 0.1$ by organic matter amendment ($R2 = 0.11$, $p =0.053$). b) PCoA of Active Community: Top panel, Pre-drought: data cluster at $p < 0.1$ by history of intercropping ($R2 = 0.051$, $r = 0.052$). Bottom panel, Post drought. No significant clustering with any treatment. c) PCoA of Total MAGs. Top panel, Pre-drought: data cluster significantly by history of intercropping ($R2 = 0.71$, $p = 0.001$),organic matter amendment ($R2=0.06$, $p =0.001$), and the interaction between the treatments ($R2 = 0.058$, $p= 0.018$). Bottom panels, Post-drought: watered control data cluster significantly by history of intercropping ($R2 = 0.61$, $p = 0.001$), organic matter amendment ($R2 = 0.18$, $p = 0.006$), and the interaction between the treatments ($R2 = 0.10$, $p = 0.011$).; droughted data cluster by history of intercropping ($R2 = 0.48$, $p = 0.001$) and organic matter amendment ($R2 = 0.15$, $p =0.015$). d) PCoA of Active MAGs:

Top panel, Pre-drought: No significant clustering with any treatment. Bottom panel, Post drought. No significant clustering with any treatment e) PCoA of Total protein clusters. Top panel, Pre-drought: data cluster significantly by history of intercropping ($R2 = 0.29$, $p = 0.001$) and organic matter amendment ($R2=0.09$, $p = 0.005$). Bottom panels, post-drought: watered control data cluster significantly by history of intercropping ($R2 = 0.27$, $p = 0.003$); droughted data cluster by history of intercropping ($R2 = 0.32$, $p = 0.003$) and organic matter amendment ($R2 = 0.11$, $p = 0.052$). Not pictured: Data at drought end cluster by the imposed drought treatment $p < 0.1$ ($R2 = 0.052$,$p = 0.068$) f) PCoA of Active protein clusters.: Top panel, Pre-drought: No significant clustering with any treatment. Bottom panel, Post drought. No significant clustering with any treatment, although data cluster with organic matter amendment treatment at $P < 0.1$ ($R2 = 0.25$, $p = 0.059$).

Figure 4.1. Conceptual overview of experimental design and procedures

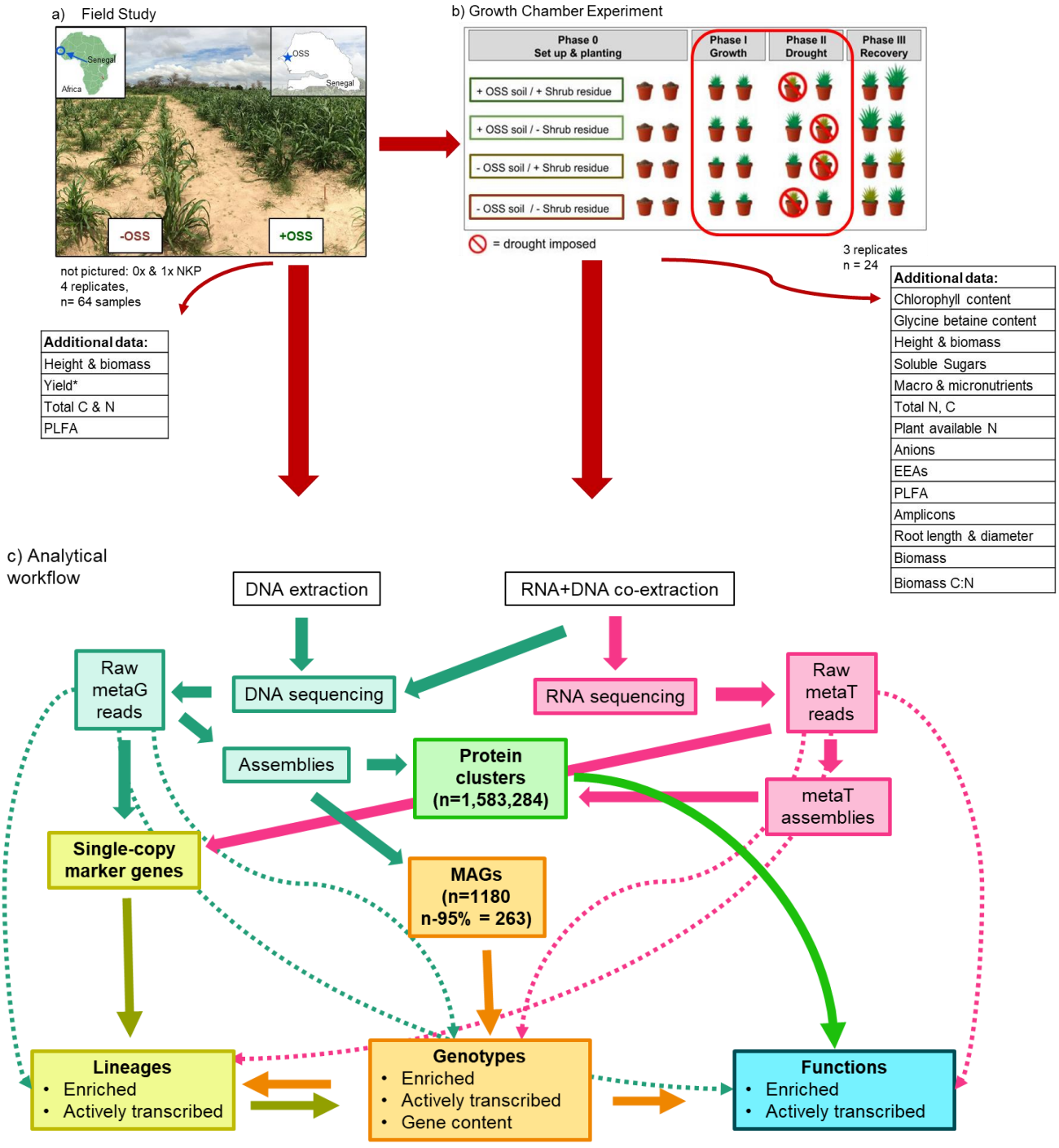


Figure 4.2 Field study lineage, MAG, and protein cluster abundance and variation across treatments, MAG enrichment, and genomic content

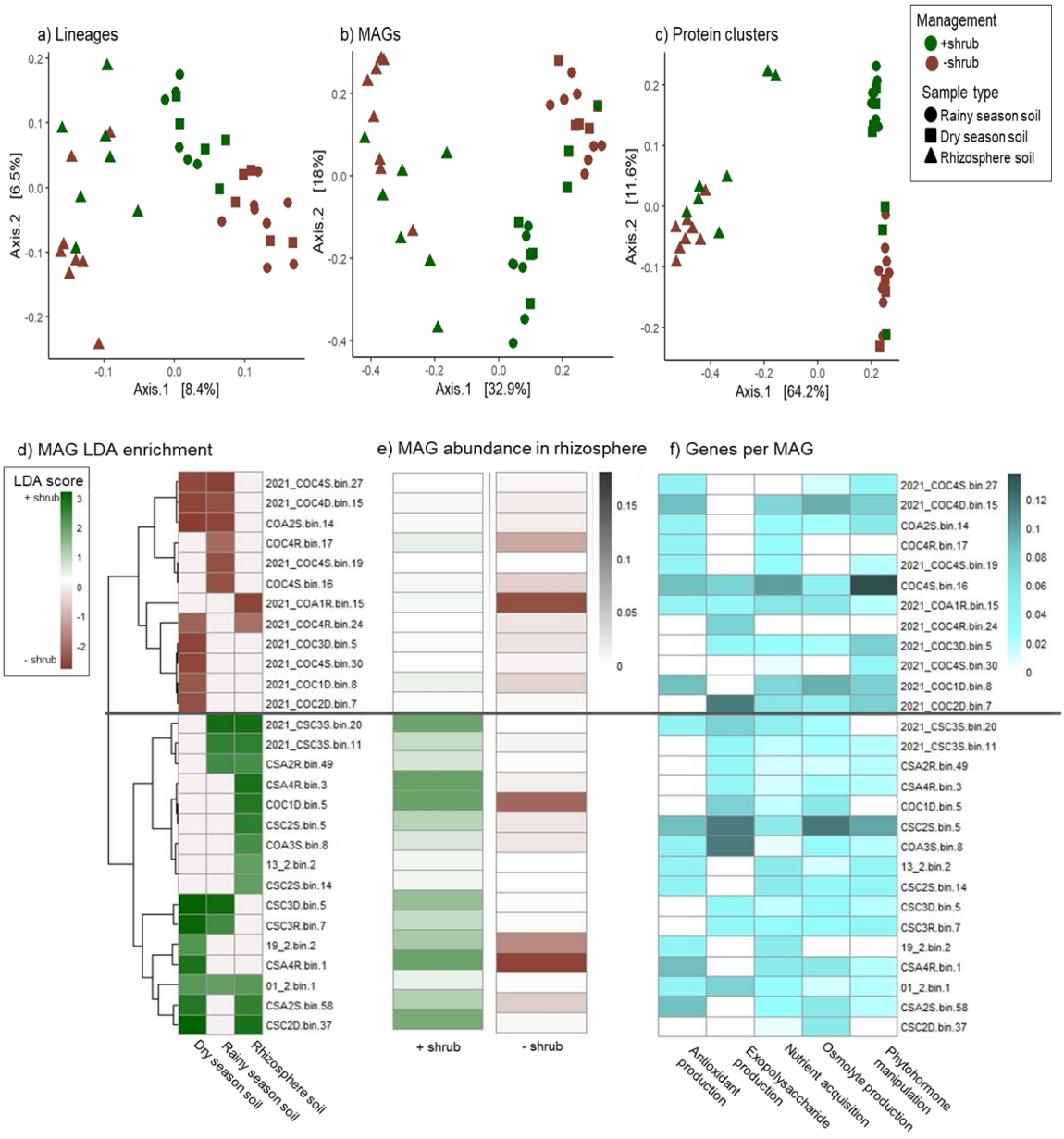


Figure 4.3 Simulated Drought experiment MAG enrichment, abundance, and gene content before and after drought

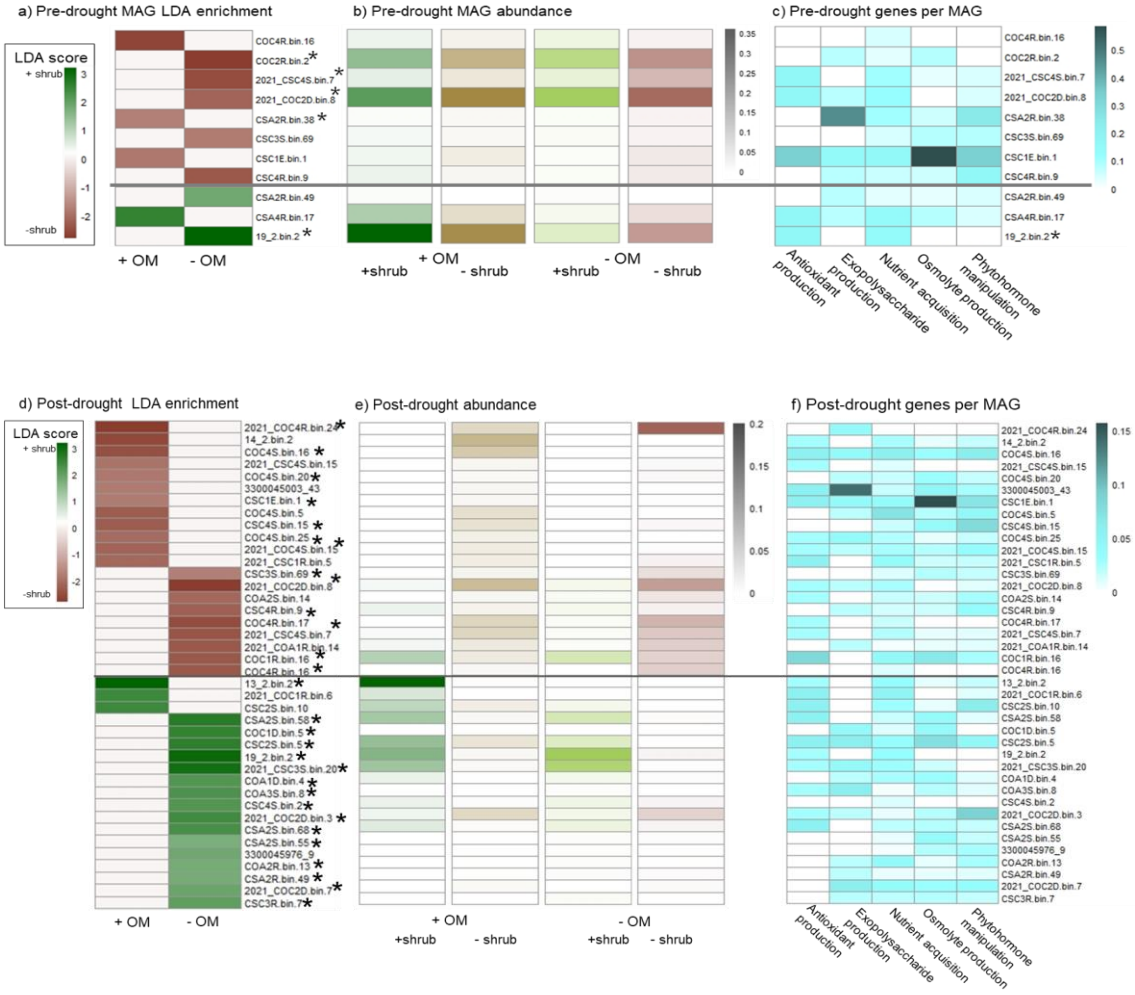
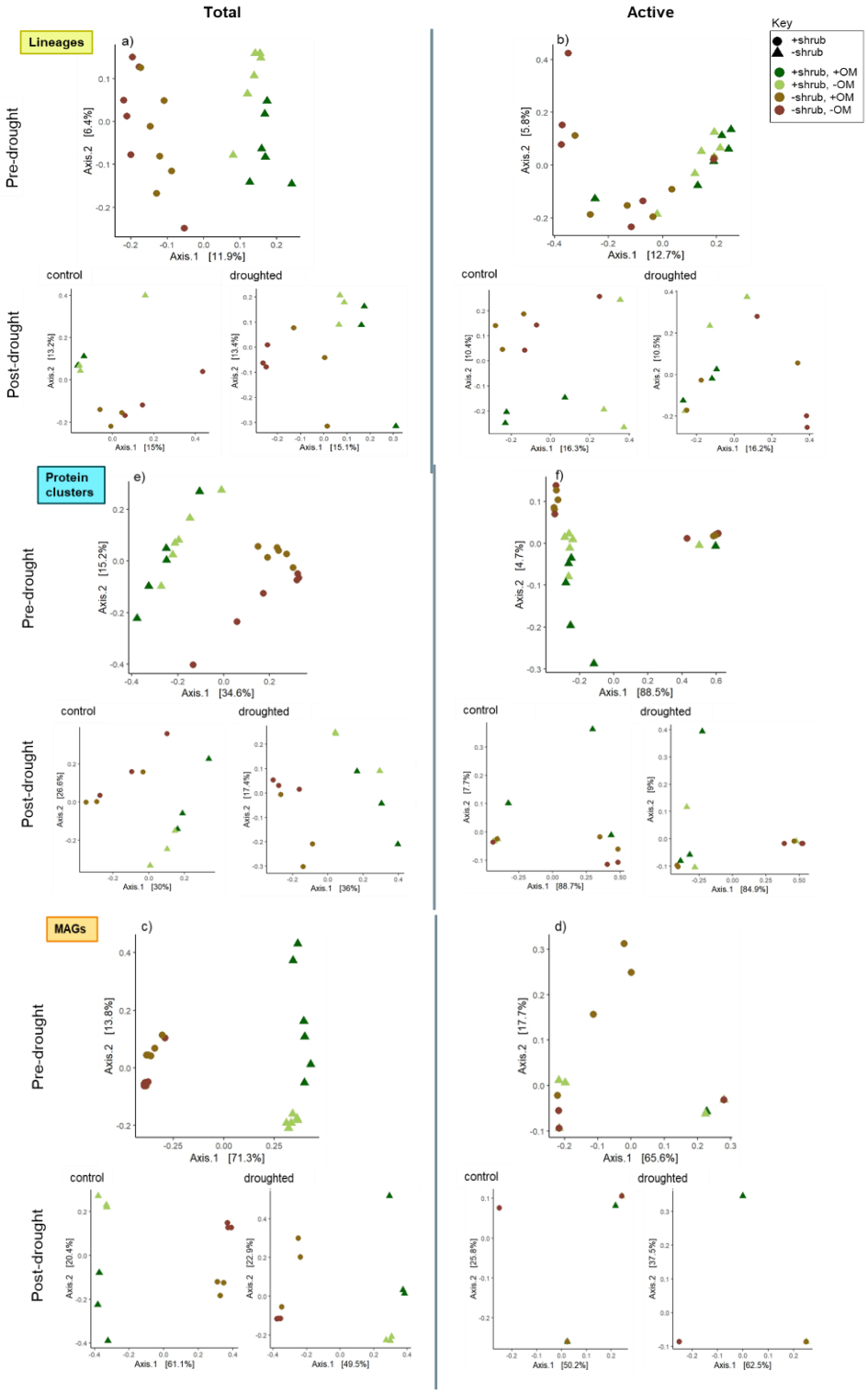


Figure 4.4 Lineage, MAG, and protein cluster abundance and spread in active and total communities



Supplemental Tables

Table S4.1A: List of enriched MAGs, origin, and taxonomy

Key: tbd: 'to be droughted', samples will go through drought, taken at the start of drought | droughted: samples that have gone through drought, taken at the end of drought | shrub: +OSS |noShrub: -OSS |OM: organic matter treatment | noOM: no orgranic matter treatment |rows in italics indicate MAGs that were not enriched under treatments | bold text: 73 MAGs selected for further analysis

MAG	MAG origin	Taxonomy (GTDB-tk)
01_2.bin.1	**Growth Chamber**	**d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_;s_**
02_2.bin.1	Growth Chamber	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Niastella;s_
04_2_bin.2	Growth Chamber	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Marmoricola;s_
08_2_bin.3	Growth Chamber	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_;s_
13_2.bin.2	Growth Chamber	**d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella;s_**
14_2.bin.2	Growth Chamber	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_
19_2.bin.2	Growth Chamber	**d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_**
2021_COA1R.bin.14	OSS, in-house analysis	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Dictyobacter;s_
2021_COA1R.bin.15	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_
2021_COA1R.bin.17	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_
2021_COA1R.bin.18	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Catenulisporaceae;g_Actinocrinis;s_
2021_COA1R.bin.4	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_CAIMXF01;s_
2021_COA1R.bin.9	OSS, in-house analysis	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Niastella;s_

2021_COA2R.bin.1	OSS, in-house analysis	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Bu33;s_
2021_COA2R.bin.19	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dokdonella_A;s_
2021_COA2R.bin.20	OSS, in-house analysis	d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_UBA11236;f_UBA11236;g_Chersky-265;s_
2021_COA2R.bin.5	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
2021_COA3D.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
2021_COA3R.bin.2	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_;s_
2021_COA4D.bin.2	**OSS, in-house analysis**	**d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_**
2021_COA4R.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
2021_COC1D.bin.14	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_Palsa-688;g_;s_
2021_COC1D.bin.8	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_;s_
2021_COC1D.bin.9	OSS, in-house analysis	d_Bacteria;p_Nitrospirota;c_Nitrospiria;o_Nitrospirales;f_Nitrospiraceae;g_;s_
2021_COC1R.bin.6	OSS, in-house analysis	**d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Puia;s_**
2021_COC2D.bin.12	OSS, in-house analysis	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_;s_
2021_COC2D.bin.3	**OSS, in-house analysis**	**d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_BOG-931;s_**
2021_COC2D.bin.7	OSS, in-house analysis	**d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Sulfotelmatobacter;s_**
2021_COC2D.bin.8	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_
2021_COC2R.bin.12	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_
2021_COC2R.bin.14	OSS, in-house analysis	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_;s_
2021_COC2R.bin.15	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_

2021_COC2R.bin.16	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_
2021_COC3D.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
2021_COC3D.bin.5	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_UBA8260;f_UBA8260;g_JAFALX01;s_
2021_COC4D.bin.15	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_Palsa-504;s_
2021_COC4D.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
2021_COC4R.bin.12	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Marmoricola;s_
2021_COC4R.bin.15	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Noviherbaspirillum;s_
2021_COC4R.bin.18	OSS, in-house analysis	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingod_Bacteriales;f_Sphingod_Bacteriaceae;g_Mucilaginibacter;s_
2021_COC4R.bin.19	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_Bradymillet rhizospherebium;s_
2021_COC4R.bin.24	OSS, in-house analysis	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_
2021_COC4R.bin.7	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales;f_Bryobacteraceae;g_Bog-105;s_
2021_COC4R.bin.8	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_
2021_COC4S.bin.1	OSS, in-house analysis	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_
2021_COC4S.bin.12	OSS, in-house analysis	d_Archaea;p_Thermoplasmatota;c_SW-10-69-26;o_JACQPN01;f_;g_;s_
2021_COC4S.bin.15	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Nevskiales;f_Nevskiaceae;g_Nevskia;s_
2021_COC4S.bin.18	OSS, in-house analysis	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_UBA10450;g_AV40;s_
2021_COC4S.bin.19	OSS, in-house analysis	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_;s_
2021_COC4S.bin.24	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_
2021_COC4S.bin.27	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-612;s_

2021_COC4S.bin.3	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_CF-121;f_CF-121;g_CF-13;s_
2021_COC4S.bin.30	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
2021_COC4S.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
2021_CSC1R.bin.17	OSS, in-house analysis	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_JAATET01;g_JAATET01;s_
2021_CSC1R.bin.5	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptacidiphilus_A;s_
2021_CSC2D.bin.4	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Casimicrobiaceae;g_VBCG01;s_
2021_CSC2S.bin.11	**OSS, in-house analysis**	**d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474;s_**
2021_CSC2S.bin.8	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Paraburkholderia;s_Paraburkholderia sabiae
2021_CSC3R.bin.1	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_;g_;s_
2021_CSC3S.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_
2021_CSC3S.bin.11	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_
2021_CSC3S.bin.17	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Acidothermales;f_;g_;s_
2021_CSC3S.bin.19	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Ramlibacter;s_
2021_CSC3S.bin.20	**OSS, in-house analysis**	**d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_**
2021_CSC3S.bin.23	OSS, in-house analysis	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Longimicrobiales;f_Longimicrobiaceae;g_;s_
2021_CSC3S.bin.8	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_;s_
2021_CSC4S.bin.15	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Koribacteraceae;g_Bog-257;s_
2021_CSC4S.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_GCA-003244245;s_
21_2.bin.2	Growth Chamber	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Bu33;s_

24_2_bin.1	Growth Chamber	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_JAFAQI01;g_JAFAQI01;s_
3300044652_17	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Iso899;s_
3300044654_37	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_GCA-003244245;s_
3300044658_31	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_
3300044667_14	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
3300044667_25	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_UBA9676;s_
3300044667_30	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_;s_
3300044684_27	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_
3300044689_1	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_AC-49;s_
3300044693_2	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Chromod_Bacteriaceae;g_;s_
3300044694_26	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_;s_
3300044694_9	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptomyces;s_
3300044705_27	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_
3300044741_25	OSS, JGI analysis	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_JAFAHZ01;s_
3300044842_12	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_
3300044842_42	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_
3300044901_10	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Baekduia;s_
3300045002_7	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
3300045003_14	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Acidobacterium_A;s_
3300045003_29	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Terracidiphilus;s_

3300045003_30	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_Bog-793;g_Palsa-601;s_
3300045003_43	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium;s_
3300045014_30	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_CAINCZ01;g_;s_
3300045014_31	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_
3300045049_17	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_
3300045049_56	OSS, JGI analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_
3300045838_42	OSS, JGI analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_
3300045976_9	OSS, JGI analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_
COA1D.bin.4	**OSS, in-house analysis**	**d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_;s_**
COA1R.bin.11	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Ramlibacter;s_
COA1R.bin.17	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_
COA1R.bin.2	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_
COA1R.bin.9	OSS, in-house analysis	d_Bacteria;p_Firmicutes;c_Bacilli;o_Paenibacillales;f_NBRC-103111;g_VKM-B-2647;s_
COA2R.bin.12	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_
COA2R.bin.13	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Catenulisporaceae;g_Catenulispora;s_
COA2R.bin.16	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Microbacterium;s_Microbacterium sp902506375
COA2R.bin.5	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Curtobacterium;s_
COA2S.bin.11	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
COA2S.bin.12	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_CAINCZ01;g_;s_

COA2S.bin.13	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_
COA2S.bin.14	OSS, in-house analysis	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_
COA2S.bin.18	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_UBA8260;f_UBA8260;g_;s_
COA2S.bin.3	OSS, in-house analysis	d_Bacteria;p_Chloroflexota;c_UBA5177;o_UBA5177;f_UBA5177;g_;s_
COA2S.bin.5	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_CF-121;f_CF-121;g_CF-13;s_
COA3D.bin.6	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_
COA3S.bin.8	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
COA4D.bin.4	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_
COA4R.bin.5	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia;s_Burkholderia dolosa
COC1D.bin.2	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_Dormibacterales;f_Dormibacteraceae;g_40CM-4-65-16;s_
COC1D.bin.5	OSS, in-house analysis	**d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_**
COC1R.bin.13	OSS, in-house analysis	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Deminuibacter;s_
COC1R.bin.16	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptomyces;s_
COC1R.bin.9	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Propionid_Bacteriaceae;g_Microlunatus_A;s_
COC1S.bin.4	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Micropepsales;f_Micropepsaceae;g_CAIYRG01;s_
COC1S.bin.50	OSS, in-house analysis	d_Archaea;p_Thermoplasmatota;c_SW-10-69-26;o_JACQPN01;f_;g_;s_
COC1S.bin.60	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-744;s_
COC2D.bin.6	OSS, in-house analysis	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_
COC2D.bin.9	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_

COC2R.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
COC2R.bin.2	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
COC2R.bin.22	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_I;s_
COC2S.bin.3	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_;o_;f_;g_;s_
COC2S.bin.5	OSS, in-house analysis	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_
COC2S.bin.6	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_
COC3D.bin.4	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_
COC3R.bin.17	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
COC3R.bin.18	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Beijerinckiaceae;g_Roseiarcus;s_
COC3R.bin.2	OSS, in-house analysis	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Chitinophaga;s_
COC3R.bin.26	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_Kutzneria;s_
COC3R.bin.27	OSS, in-house analysis	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Puia;s_
COC3R.bin.9	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Asticcacaulis;s_
COC4D.bin.15	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
COC4D.bin.17	OSS, in-house analysis	d_Bacteria;p_CSP1-3;c_CSP1-3;o_CSP1-3;f_NP-7;g_;s_
COC4D.bin.36	OSS, in-house analysis	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_;f_;g_;s_
COC4D.bin.7	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_QIAW01;g_;s_
COC4R.bin.16	OSS, in-house analysis	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_
COC4R.bin.17	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_

COC4S.bin.16	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_
COC4S.bin.20	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales;f_Bryobacteraceae;g_Bog-105;s_
COC4S.bin.25	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Edaphobacter;s_
COC4S.bin.5	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_
CSA1D.bin.22	OSS, in-house analysis	d_Bacteria;p_Chloroflexota;c_UBA6077;o_UBA6077;f_CF-72;g_;s_
CSA1D.bin.30	OSS, in-house analysis	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_JAFAQB01;s_
CSA2D.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_13-2-20CM-68-14;s_
CSA2D.bin.10	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_
CSA2D.bin.2	OSS, in-house analysis	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_UBA10450;g_Udaeobacter;s_
CSA2D.bin.6	OSS, in-house analysis	**d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrosocosmicus;s_**
CSA2D.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
CSA2D.bin.8	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_
CSA2D.bin.9	OSS, in-house analysis	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrososphaera;s_
CSA2R.bin.18	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
CSA2R.bin.36	OSS, in-house analysis	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_JAATET01;g_JAATET01;s_
CSA2R.bin.38	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Usitatibacteraceae;g_Usitatibacter;s_
CSA2R.bin.47	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Oxalicibacterium;s_
CSA2R.bin.49	**OSS, in-house analysis**	**d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_**
CSA2S.bin.33	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_

CSA2S.bin.54	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_IMCC26256;f_;g_;s_
CSA2S.bin.55	**OSS, in-house analysis**	**d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-744;s_**
CSA2S.bin.58	**OSS, in-house analysis**	**d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_JAFAQI01;g_JAFAQI01;s_**
CSA2S.bin.64	OSS, in-house analysis	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_AG2;s_
CSA2S.bin.68	**OSS, in-house analysis**	**d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_Pseudonocardia;s_**
CSA3D.bin.5	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_UBA8190;g_UBA8190;s_
CSA4R.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Nocardioides;s_
CSA4R.bin.14	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Nocardioides;s_
CSA4R.bin.17	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_
CSA4R.bin.3	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
CSA4R.bin.6	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_
CSA4S.bin.6	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_SG8-39;g_SCGC-AG-212-J23;s_
CSC1D.bin.5	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_
CSC1D.bin.7	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_
CSC1E.bin.1	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia;s_Burkholderia multivorans
CSC1R.bin.17	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_I;s_
CSC1R.bin.4	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
CSC1R.bin.6	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_
CSC2D.bin.3	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_

CSC2D.bin.37	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
CSC2S.bin.1	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_IMCC26256;f_;g_;s_
CSC2S.bin.10	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_Bradymillet rhizospherebium;s_
CSC2S.bin.12	OSS, in-house analysis	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_
CSC2S.bin.14	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Humibacter;s_
CSC2S.bin.3	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_
CSC2S.bin.5	OSS, in-house analysis	**d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_Reyranella;s_**
CSC3D.bin.5	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_
CSC3D.bin.7	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Thermoleophilaceae;g__;s__
CSC3R.bin.11	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_
CSC3R.bin.7	OSS, in-house analysis	**d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_**
CSC3S.bin.44	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_;g_;s_
CSC3S.bin.66	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_
CSC3S.bin.68	OSS, in-house analysis	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Longimicrobiales;f_RSA9;g_;s_
CSC3S.bin.69	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
CSC4R.bin.9	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_
CSC4S.bin.15	OSS, in-house analysis	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Acetobacterales;f_Acetobacteraceae;g_Acidisphaera;s_
CSC4S.bin.2	OSS, in-house analysis	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_UBA10452;s_UBA10452 sp009898475
CSC4S.bin.9	OSS, in-house analysis	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_

14_2_bin.1	Growth Chamber	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__Acidobacteriaceae;g__Terriglobus;s__
14_2_bin.3	Growth Chamber	d__Bacteria;p__Armatimonadota;c__Armatimonadia;o__Armatimonadales;f__Armatimonadaceae;g__JACMJB01;s__
2021_COA3D.bin.2	OSS, in-house analysis	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__Gp7-AA8;f__Gp7-AA8;g__;s__
2021_COA3R.bin.15	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Actinomycetales;f__Microbacteriaceae;g__Protaetiibacter;s__
2021_COA4R.bin.2	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__Lentzea;s__
2021_COA4R.bin.6	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides;s__
2021_COC4D.bin.4	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__
2021_COC4D.bin.9	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__Gandjariella;s__
2021_CSA1R.bin.10	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__VBDL01;s__
2021_CSA1R.bin.2	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Luteibacter;s__
2021_CSA1R.bin.9	OSS, in-house analysis	d__Bacteria;p__Chloroflexota;c__Chloroflexia;o__Chloroflexales;f__Roseiflexaceae;g__;s__
2021_CSC1R.bin.15	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Trinickia;s__
2021_CSC2S.bin.10	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Micromonosporaceae;g__Micromonospora;s__
2021_CSC2S.bin.2	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__;s__
2021_CSC2S.bin.6	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Streptomycetales;f__Catenulisporaceae;g__;s__
2021_CSC3S.bin.28	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-465;s__
2021_CSC3S.bin.7	OSS, in-house analysis	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Longimicrobiales;f__Longimicrobiaceae;g__;s__
21_2_bin.3	Growth Chamber	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Mucilaginibacter;s__
3300044652_29	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__70-9;g__;s__

3300044658_14	OSS, JGI analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__;s__
3300044658_7	OSS, JGI analysis	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Niastella;s__
3300044667_15	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Conexibacter;s__
3300044667_48	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides;s__
3300044667_53	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Streptosporangiales;f__Streptosporangiaceae;g__Spirillospora;s__Spirillospora meyerae
3300044672_2	OSS, JGI analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Dyella;s__
3300044685_11	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__Lentzea;s__
3300044686_6	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__GCA-003244245;s__
3300044689_21	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__GCA-003244245;s__
3300044705_15	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__70-9;g__;s__
3300045744_21	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-744;s__
3300045837_22	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-744;s__
3300045837_9	OSS, JGI analysis	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__Pyrinomonadaceae;g__QHXN01;s__
3300045958_27	OSS, JGI analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-744;s__
3300045976_17	OSS, JGI analysis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae_G;g__Bacillus_A;s__Bacillus_A cereus
COA1E.bin.1	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Ralstonia;s__Ralstonia mannitolilytica
COA2R.bin.6	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Rhizobium;s__Rhizobium sp003024605
COA2S.bin.1	OSS, in-house analysis	d__Archaea;p__Thermoplasmatota;c__SW-10-69-26;o__JACQPN01;f__;g__;s__
COA2S.bin.10	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-744;s__

COA2S.bin.19	OSS, in-house analysis	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__SbA1;g__Gp1-AA145;s__
COA2S.bin.8	OSS, in-house analysis	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales;f__UBA10450;g__AV40;s__
COA3E.bin.3	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Luteibacter;s__
COC1D.bin.1	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__SG8-39;g__SCGC-AG-212-J23;s__
COC1R.bin.12	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__Amycolatopsis;s__
COC1S.bin.57	OSS, in-house analysis	d__Bacteria;p__Dormibacterota;c__Dormibacteria;o__UBA8260;f__UBA8260;g__;s__
COC2R.bin.11	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Burkholderia;s__Burkholderia cenocepacia
COC2R.bin.18	OSS, in-house analysis	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Longimicrobiales;f__Longimicrobiaceae;g__;s__
COC4S.bin.13	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Palsa-744;s__
CSA1D.bin.14	OSS, in-house analysis	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__Gp7-AA8;f__Gp7-AA8;g__;s__
CSA1D.bin.7	OSS, in-house analysis	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__Pyrinomonadaceae;g__QHXN01;s__
CSA1E.bin.1	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Pandoraea;s__Pandoraea pulmonicola
CSA1R.bin.5	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas_N;s__
CSA1R.bin.9	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__GCA-003244245;s__
CSA1S.bin.4	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Propionibacteriales;f__Nocardioidaceae;g__Aeromicrobium;s__
CSA2R.bin.37	OSS, in-house analysis	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Niastella;s__
CSA2S.bin.6	OSS, in-house analysis	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__70-9;g__VAYN01;s__
CSC2E.bin.1	OSS, in-house analysis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter sichuanensis

CSC2S.bin.11	*OSS, in-house analysis*	*d__Bacteria;p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Pseudonocardiaceae;g__;s__*
CSC4R.bin.4	*OSS, in-house analysis*	*d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Magnetospirillaceae;g__;s__*
CSC4S.bin.6	*OSS, in-house analysis*	*d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Longimicrobiales;f__Longimicrobiaceae;g__;s__*

Table S4.1B: MAG enrichment in Simulated Drought study

Key: tbd: 'to be droughted', samples will go through drought, taken at the start of drought | droughted: samples that have gone through drought, taken at the end of drought | shrub: +OSS |noShrub: -OSS |OM: organic matter treatment | noOM: no orgranic matter treatment |rows in italics indicate MAGs that were not enriched under treatments | red text: 73 MAGs selected for further analysis			
	Simulated Drought		
MAG	enriched under treatment:	phase & sample type	LDA score
01_2.bin.1	**shrub**	**droughStart, tbd**	**3.202097933**
02_2.bin.1			
04_2_bin.2	noShrub	droughStart, tbd	2.395465928
08_2_bin.3	shrub	droughStart, tbd	2.718810228
	shrubOM	**droughtEnd, droughted**	**3.813021**
13_2.bin.2	**shrubOM**	**drought start, tbd**	**3.560071067**
14_2.bin.2	noShrubOM	droughtEnd, droughted	3.173930197
	shrubnoOM	**droughtEnd, droughted**	**3.632721958**
	shrub	**droughStart, tbd**	**3.539946463**
	ShrubnoOM	**drought start, tbd**	**3.642405551**
19_2.bin.2	**shrub**	**droughtEnd, droughted**	**3.415041344**
	noShrub	**droughStart, tbd**	**3.003159856**
	noShrub	**droughtEnd, droughted**	**2.778936345**
	noShrubnoOM	**droughtEnd, droughted**	**2.885373709**
2021_COA1R.bin.14	**droughtEnd**	**shrub**	**2.399617237**
2021_COA1R.bin.15			
2021_COA1R.bin.17	noShrub	droughStart, tbd	2.546834402

	noShrubnoOM	droughStart, tbd	2.592840277
2021_COA1R.bin.18	noShrub	droughtEnd, droughted	2.163139445
2021_COA1R.bin.4			
2021_COA1R.bin.9	noShrub	droughStart, tbd	2.157727965
	noShrubOM	droughtEnd, droughted	2.558651706
2021_COA2R.bin.1	**noShrub**	**droughStart, tbd**	**2.733114629**
	shrub	**droughtEnd, droughted**	**2.492296034**
2021_COA2R.bin.19			
2021_COA2R.bin.20			
2021_COA2R.bin.5	noShrub	droughtEnd, droughted	2.121503855
2021_COA3D.bin.1	noShrub	droughtEnd, droughted	
2021_COA3R.bin.2			
	shrub	**droughStart, tbd**	**3.052949443**
2021_COA4D.bin.2	**shrub**	**droughtEnd, droughted**	**3.011386404**
2021_COA4R.bin.7			
2021_COC1D.bin.14	noShrub	droughStart, tbd	2.840565645
	noShrub	**droughStart, tbd**	**2.758882176**
	noShrub	**droughtEnd, droughted**	**2.718863727**
2021_COC1D.bin.8	**drought start**	**noshrub**	**2.251170802**
	noShrub	droughStart, tbd	2.177458513
	shrub	droughtEnd, droughted	2.021284338
2021_COC1D.bin.9	noShrubnoOM	droughtEnd, droughted	0.025419183
	shrub	**droughtEnd, droughted**	**2.353257886**
2021_COC1R.bin.6	**shrubOM**	**droughtEnd, droughted**	**2.868636491**
	noShrub	droughStart, tbd	2.627404926
2021_COC2D.bin.12	noShrub	droughtEnd, droughted	2.536808992
	noShrub	**droughStart, tbd**	**2.649788428**
	noShrub	**droughtEnd, droughted**	**2.699750866**
2021_COC2D.bin.3	**noShrubOM**	**droughtEnd, droughted**	**2.853892901**
	noShrub	**droughStart, tbd**	**2.34342527**
	noShrub	**droughtEnd, droughted**	**2.346498713**
	noShrubOM	**droughtEnd, droughted**	**2.230004149**
2021_COC2D.bin.7	**watered**	**noshrub, drought end**	**2.09293934**
	noShrub	droughStart, tbd	3.379852632
	noShrub	droughtEnd, droughted	3.137688065
	noShrubnoOM	droughtStart, tbd	3.386814049
	noShrubnoOM	drought Start, tbd	2.592840277
2021_COC2D.bin.8	drought start	noshrub	2.932175717
2021_COC2R.bin.12			
2021_COC2R.bin.14	noShrub	droughtEnd, droughted	2.28338859
2021_COC2R.bin.15			
	noShrub	**droughStart, tbd**	**2.03822019**
2021_COC2R.bin.16	**noShrub**	**droughtEnd, droughted**	**2.263889008**

	noShrubOM	**droughtEnd, droughted**	**2.493654041**
2021_COC3D.bin.1	noShrub	droughStart, tbd	2.662360044
2021_COC3D.bin.5	**noShrub**	**droughStart, tbd**	**2.219609332**
	noShrub	**droughtEnd, droughted**	**2.263298781**
2021_COC4D.bin.15	**noShrub**	**droughStart, tbd**	**2.634579372**
	noShrub	**droughtEnd, droughted**	**2.575225335**
2021_COC4D.bin.7	noShrub	droughStart, tbd	2.315319487
	noShrub	droughtEnd, droughted	2.40968994
2021_COC4R.bin.12	noShrub	droughStart, tbd	2.633414253
	noShrub	droughStart, tbd	2.634579372
2021_COC4R.bin.15	noShrub	droughtEnd, droughted	2.575225335
2021_COC4R.bin.18			
2021_COC4R.bin.19			
	noShrub	**drought start, tbd**	**3.379419925**
	noShrub	**droughtEnd, droughted**	**3.270480019**
2021_COC4R.bin.24	**noShrubnoOM**	**droughtEnd, droughted**	**3.458122747**
	noShrub	drought start, tbd	2.315319487
2021_COC4R.bin.7	noShrub	droughtEnd, droughted	2.40968994
	noShrub	**droughStart, tbd**	**2.735750944**
2021_COC4R.bin.8	**noShrubnoOM**	**droughtEnd, droughted**	**2.982843735**
	noShrub	droughStart, tbd	2.633343056
	noShrub	droughtEnd, droughted	2.518728652
	noShrubnoOM	droughtEnd, droughted	2.71181986
2021_COC4S.bin.1	noShurbnoOM	2.714951427	droughtStart, tbd
	noShrub	droughStart, tbd	2.919645246
2021_COC4S.bin.12	noShrub	droughtEnd, droughted	2.526462952
	noShrub	**droughStart, tbd**	**2.475445525**
	noShrub	**droughtEnd, droughted**	**2.386367988**
2021_COC4S.bin.15	**noShrubOM**	**droughtEnd, droughted**	**2.664910283**
2021_COC4S.bin.18			
2021_COC4S.bin.19	**noShrub**	**droughStart, tbd**	**2.275612269**
2021_COC4S.bin.24			
	noShrub	**droughStart, tbd**	**2.817818921**
2021_COC4S.bin.27	**noShrub**	**droughtEnd, droughted**	**2.700486919**
	noShrub	droughStart, tbd	2.745196329
	noShrub	droughtEnd, droughted	2.507907029
2021_COC4S.bin.3	noShrubnoOM	drought Start, tbd	2.797150342
2021_COC4S.bin.30	**noShrub**	**droughtEnd, droughted**	**2.073291547**
2021_COC4S.bin.7			
2021_CSC1R.bin.17			
2021_CSC1R.bin.5	**noShrub**	**drought start, tbd**	**2.586105481**

	noShrub	**droughtend, droughted samples**	**2.510550067**
	noShrubOM	**droughtEnd, droughted**	**2.613533067**
	shrub	droughStart, tbd	2.456006422
2021_CSC2D.bin.4	ShrubnoOM	drought start, tbd	2.541214755
	shrub	**droughStart, tbd**	**2.842782172**
	shrub	**droughtEnd, droughted**	**2.535959056**
2021_CSC2S.bin.11	**drought start**	**shrub**	**2.529550353**
	shrub	droughStart, tbd	2.917741053
	shrub	droughtEnd, droughted	2.681465596
	shrubOM	droughtEnd, droughted	3.061266169
2021_CSC2S.bin.8	ShrubOM	drought start, tbd	3.102757638
2021_CSC3R.bin.1			
	noShrub	droughStart, tbd	2.744015387
2021_CSC3S.bin.1	noShrub	droughtEnd, droughted	2.763732578
	shrub	**drought start, tbd**	**2.334890943**
2021_CSC3S.bin.11	**drought**	**shrub, drought end**	**2.030878758**
	noShrub	droughStart, tbd	2.469909964
	noShrub	droughtEnd, droughted	2.417907219
2021_CSC3S.bin.17			
	shrub	droughStart, tbd	2.976136139
	shrubOM	drought end, droughted	3.480605967
2021_CSC3S.bin.19	ShrubOM	drought Start, tbd	3.217325824
	ShrubnoOM	**drought end, droughted**	**3.464741486**
2021_CSC3S.bin.20			
	noShrub	droughStart, tbd	2.206990632
2021_CSC3S.bin.23	noShrub	droughtEnd, droughted	2.108954361
	shrubnoOM	droughtEnd, droughted	2.278532623
	ShrubnoOM	drought start, tbd	2.394592793
2021_CSC3S.bin.8			
	noShrub	**droughStart, tbd**	**2.362383495**
	noShrub	**droughtEnd, droughted**	**2.233562431**
2021_CSC4S.bin.15	**noShrubOM**	**droughtEnd, droughted**	**2.437823061**
	noShrub	**droughStart, tbd**	**2.884753401**
	noShrub	**droughtEnd, droughted**	**2.956727635**
	noShrubnoOM	**drought start, tbd**	**2.99956651**
2021_CSC4S.bin.7	**drought**	**shrub, drought end**	**2.003166404**
21_2.bin.2	**noShrubOM**	**droughtEnd, droughted**	**3.448015233**
	noShrub	**droughStart, tbd**	**3.621491657**
24_2_bin.1	**noShrub**	**droughtEnd, droughted**	**3.508456297**
3300044652_17			
3300044654_37	noShrub	droughtEnd, droughted	2.073335105
3300044658_31	shrub	drought start, tbd	2.575249704

	shrub	droughtEnd, droughted	2.189066541
	noShrub	drought start, tbd	2.56032871
	ShrubnoOM	drought start, tbd	2.482385405
3300044667_14	ShrubnoOM	drought Start, tbd	2.482385405
	noShrub	drought start, tbd	2.55256313
3300044667_25	noShrub	droughtEnd, droughted	2.344094408
3300044667_30			
3300044684_27	noShrub	droughStart, tbd	2.201672825
	shrub	droughStart, tbd	2.524368791
3300044689_1	noShrub	droughStart, tbd	2.486000646
3300044693_2			
3300044694_26			
	shrub	droughStart, tbd	2.588440534
3300044694_9	shrub	droughtEnd, droughted	2.46649608
3300044705_27	ShrubnoOM	2.434589569	
	noShrub	droughStart, tbd	2.55256313
3300044741_25	noShrub	droughtEnd, droughted	2.344094408
3300044842_12	noShrub	droughtEnd, droughted	
3300044842_42			
3300044901_10			
3300045002_7			
	noShrub	droughStart, tbd	2.56032871
3300045003_14	noShrubnoOM	drought start, tbd	2.746828096
	noShrub	droughStart, tbd	2.128093865
3300045003_29	noShrubOM	droughtend, droughted samples	2.196205064
	noShrub	droughStart, tbd	2.485117966
3300045003_30	noShrub	droughStart, tbd	2.300448839
	noShrub	droughtEnd, droughted	2.034532583
3300045003_43	noShrubOM	droughtend, droughted samples	2.26149282
	shrub	droughStart, tbd	2.441789701
3300045014_30	shrub	droughtEnd, droughted	2.314160169
	shrub	droughStart, tbd	2.575249704
	shrub	droughtEnd, droughted	2.189066541
3300045014_31	ShrubnoOM	drought Start, tbd	2.626164522
3300045049_17	noShrub	droughStart, tbd	2.520496259
3300045049_56	**shrub**	**droughtEnd, droughted**	**2.609082068**
	noShrub	droughStart, tbd	2.479221677
3300045838_42	noShrub	droughtEnd, droughted	2.259735151
3300045976_9	ShrubnoOM	droughtEnd, droughted	2.1427265
	shrub	**droughStart, tbd**	**2.612149105**
	shrub	**droughtEnd, droughted**	**2.508173383**
COA1D.bin.4	**shrubnoOM**	**droughtEnd, droughted**	**2.592390837**

COA1R.bin.11			
COA1R.bin.17			
COA1R.bin.2			
COA1R.bin.9			
	shrub	droughStart, tbd	2.505904232
COA2R.bin.12	shrub	droughtEnd, droughted	2.351181076
COA2R.bin.13	**shrubnoOM**	**droughtEnd, droughted**	**2.084439443**
COA2R.bin.16			
COA2R.bin.5			
COA2S.bin.11			
	noShrub	drought start, tbd	2.37173857
	noShrub	droughtEnd, droughted	2.103895614
COA2S.bin.12	watered	noshrub, drought end	2.027476604
COA2S.bin.13	shrub	droughStart, tbd	2.429749068
COA2S.bin.14	**noShrubnoOM**	**droughtEnd, droughted**	**2.617539666**
	noShrub	droughStart, tbd	2.179043119
COA2S.bin.18	noShrub	droughtEnd, droughted	2.057007468
COA2S.bin.3			
	shrub	droughStart, tbd	2.400453091
	ShrubnoOM	droughtend, droughted samples	2.293618237
COA2S.bin.5	ShrubnoOM	drought Start, tbd	2.367193484
COA3D.bin.6			
	shrub	**drought start, tbd**	**2.624008256**
	shrub	**droughtEnd, droughted**	**2.624008256**
COA3S.bin.8	**shrubnoOM**	**droughtEnd, droughted**	**2.659573589**
COA4D.bin.4			
COA4R.bin.5			
COC1D.bin.2			
	shrub	**droughtEnd, droughted**	**2.831132268**
COC1D.bin.5	**ShrubnoOM**	**droughtend, droughted samples**	**3.042814591**
COC1R.bin.13			
	shrub	**droughStart, tbd**	**2.516085089**
	noShrub	**drought end, droughted**	**2.463751343**
COC1R.bin.16	**noShrubnoOM**	**droughtEnd, droughted**	**2.941842535**
COC1R.bin.9			
COC1S.bin.4			
COC1S.bin.50	noShrub	droughStart, tbd	2.357262006
COC1S.bin.60			
COC2D.bin.6			
	noShrub	droughtEnd, droughted	3.031759728
COC2D.bin.9	noShrub	droughtEnd, droughted	2.659027741

COC2R.bin.1			
	noShrub	**droughStart, tbd**	**3.324252232**
	noShrub	**droughtEnd, droughted**	**3.330737233**
COC2R.bin.2	**noShrubnoOM**	**drought Start, tbd**	**3.326531491**
COC2R.bin.22			
COC2S.bin.3			
	shrub	droughtEnd, droughted	2.883879727
	shrub	droughtEnd, droughted	2.881142378
COC2S.bin.5	ShrubnoOM	drought Start, tbd	2.964334782
COC2S.bin.6			
COC3D.bin.4	drought	shrub, DE	2.060072169
	noShrub	droughStart, tbd	2.784469639
COC3R.bin.17	noShrub	droughtEnd, droughted	2.806611473
	noShrub	**droughStart, tbd**	**2.290937035**
COC3R.bin.18	**noShrub**	**droughtEnd, droughted**	**2.273242684**
COC3R.bin.2			
COC3R.bin.26			
COC3R.bin.27			
COC3R.bin.9	**noShrub**	**droughtEnd, droughted**	**2.10422908**
COC4D.bin.15			
	noShrub	droughStart, tbd	2.327154567
COC4D.bin.17	noShrub	droughtEnd, droughted	2.013668574
COC4D.bin.36			
	noShrub	droughStart, tbd	2.447057708
COC4D.bin.7	noShrub	droughtEnd, droughted	2.380520982
	noShrub	**droughStart, tbd**	**2.719582835**
	noShrub	**droughtEnd, droughted**	**2.732726616**
COC4R.bin.16	**noShrubnoOM**	**droughtEnd, droughted**	**2.941842535**
	noShrub	**droughStart, tbd**	**3.030010625**
	noShrub	**droughtEnd, droughted**	**3.019754367**
	noShrubnoOM	**droughtEnd, droughted**	**3.115151364**
COC4R.bin.17	**noShrubOM**	**drought start, tbd**	**3.172148317**
	noShrub	**droughStart, tbd**	**2.321080332**
	noShrub	**droughtEnd, droughted**	**2.723321322**
COC4S.bin.16	**noShrubOM**	**droughtEnd, droughted**	**3.070992506**
	noShrub	**droughStart, tbd**	**2.486173903**
	noShrub	**droughtEnd, droughted**	**2.37886629**
	noShrubOM	**droughtEnd, droughted**	**2.31202499**
COC4S.bin.20	**drought start**	**shrub**	**2.203182695**
	noShrub	**droughStart, tbd**	**2.57573301**
COC4S.bin.25	**noShrubOM**	**droughtEnd, droughted**	**2.551406569**
COC4S.bin.5	**noShrubOM**	**droughtEnd, droughted**	**2.844984214**
CSA1D.bin.22	shrub	droughStart, tbd	2.668319544

	shrub	droughtEnd, droughted	2.562989757
	ShrubnoOM	drought Start, tbd	2.652312061
	shrub	droughStart, tbd	2.865155361
	shrub	droughtEnd, droughted	2.848939734
	ShrubnoOM	droughtEnd, droughted	2.945490593
CSA1D.bin.30	ShrubnoOM	drought start, tbd	2.912616058
	shrub	droughStart, tbd	2.988962226
CSA2D.bin.1	shrub	droughtEnd, droughted	2.922570312
	shrub	droughStart, tbd	2.732475853
CSA2D.bin.10	shrub	droughtEnd, droughted	2.444232366
	shrub	droughStart, tbd	2.967478532
CSA2D.bin.2	shrub	droughtEnd, droughted	2.903396704
CSA2D.bin.6			
CSA2D.bin.7			
CSA2D.bin.8			
CSA2D.bin.9			
CSA2R.bin.18			
CSA2R.bin.36			
	noShrub	**droughtEnd, droughted**	**2.241893321**
CSA2R.bin.38	**noShrubOM**	**drought end, droughted**	**2.121683477**
CSA2R.bin.47			
	shrubnoOM	**droughtEnd, droughted**	**2.093255401**
CSA2R.bin.49	**ShrubnoOM**	**drought start, tbd**	**2.106614514**
CSA2S.bin.33			
CSA2S.bin.54	shrub	droughtEnd, droughted	2.703811187
CSA2S.bin.55	**shrubnoOM**	**droughtEnd, droughted**	**2.02447965**
	shrub	**droughtEnd, droughted**	**2.878942742**
	shrub	**drought end, droughted**	**3.091226394**
CSA2S.bin.58	**shrubnoOM**	**droughtEnd, droughted**	**3.193570277**
	shrub	droughStart, tbd	2.525511462
CSA2S.bin.64	shrub	drought end, droughted	2.429020041
	shrub	**droughStart, tbd**	**2.682479509**
	shrub	**drought end, droughted**	**2.581728534**
CSA2S.bin.68	**ShrubnoOM**	**droughtEnd, droughted**	**2.773973821**
	noShrub	droughStart, tbd	2.454057937
CSA3D.bin.5	noShrub	drought end, droughted	2.322145389
CSA4R.bin.1	**shrub**	**droughStart, tbd**	**2.699339716**
	shrub	droughStart, tbd	2.785247011
CSA4R.bin.14	shrub	droughtEnd, droughted	2.802029605
	shrub	**droughStart, tbd**	**2.853663101**
	shrub	**droughtEnd, droughted**	**2.824723235**
CSA4R.bin.17	**ShrubOM**	**droughtStart, tbd**	**2.912536366**
CSA4R.bin.3	**shrub**	**droughStart, tbd**	**3.114184199**

	shrub	**droughtEnd, droughted**	**3.059455664**
	shrub	droughStart, tbd	2.857630182
CSA4R.bin.6	shrub	droughtEnd, droughted	2.635534065
	shrub	droughStart, tbd	2.753813734
CSA4S.bin.6	shrub	droughtEnd, droughted	2.483964017
	noShrub	**droughStart, tbd**	**3.170442822**
CSC1D.bin.5	**noShrub**	**droughStart, tbd**	**3.065035598**
CSC1D.bin.7			
CSC1E.bin.1	**noShrubOM**	**droughtEnd, droughted**	**2.228232956**
CSC1R.bin.17			
CSC1R.bin.4	noShrub	drought start, tbd	2.245426732
CSC1R.bin.6			
CSC2D.bin.3			
	shrub	**droughStart, tbd**	**2.589059394**
CSC2D.bin.37	**shrub**	**droughtEnd, droughted**	**2.512234543**
	shrub	droughStart, tbd	2.662236583
CSC2S.bin.1	shrub	droughtEnd, droughted	2.528761581
	shrub	**droughStart, tbd**	**2.783944061**
	drought start	**shrub**	**2.372570768**
CSC2S.bin.10	**ShrubOM**	**droughtEnd, droughted**	**2.896159596**
CSC2S.bin.12			
CSC2S.bin.14			
CSC2S.bin.3			
	shrub	**droughStart, tbd**	**3.115586634**
CSC2S.bin.5	**shrub**	**droughtEnd, droughted**	**2.924744238**
	ShrubnoOM	**droughtEnd, droughted**	**3.114571141**
	shrub	**droughStart, tbd**	**2.995666944**
CSC3D.bin.5	**shrub**	**droughtEnd, droughted**	**2.901300573**
CSC3D.bin.7	ShrubnoOM	droughStart, tbd	2.463802938
CSC3R.bin.11			
	shrub	**droughStart, tbd**	**3.540069218**
	shrub	**droughtEnd, droughted**	**3.421830173**
CSC3R.bin.7	**shrubnoOM**	**droughtEnd, droughted**	**2.401469824**
	noShrub	droughStart, tbd	2.544819464
	noShrub	droughtEnd, droughted	2.521264401
CSC3S.bin.44	noShrubnoOM	droughtStart, tbd	2.547036658
CSC3S.bin.66			
	noShrub	**droughtEnd, droughted**	**2.005581465**
CSC3S.bin.68	**noShrubnoOM**	**droughtEnd, droughted**	**2.158421297**
	noShrub	**droughStart, tbd**	**2.405975494**
	noShrub	**droughStart, tbd**	**2.63385028**
CSC3S.bin.69	**noShrubnoOM**	**droughtEnd, droughted**	**2.77407661**
CSC4R.bin.9			

	noShrub	**droughStart, tbd**	**2.492433675**
	noShrub	**droughtEnd, droughted**	**2.627173369**
CSC4S.bin.15	**noShrubOM**	**droughtEnd, droughted**	**2.865121136**
	shrub	**droughStart, tbd**	**2.492433675**
	shrub	**droughtEnd, droughted**	**2.627173369**
CSC4S.bin.2	**ShrubnoOM**	**droughtEnd, droughted**	**2.645053975**
CSC4S.bin.9			

Table S4.1C MAG enrichment in OSS field study

OSS MAG enrichment			
MAG	enriched under treatment:	sample type	LDA score
	shrub	**bulk soil (dry season)**	**2.16327038**
	shrub	**bulk soil (rainy season)**	**2.005833637**
	shrub	**millet rhizosphere**	**2.142180184**
01_2.bin.1	**millet rhizosphere**	**shrub**	**2.206979109**
02_2.bin.1	millet rhizosphere	shrub	2.025299206
04_2_bin.2			
08_2_bin.3			
13_2.bin.2	**Shrub**	**millet rhizosphere**	**2.018326992**
14_2.bin.2	millet rhizosphere	shrub	2.043311313
	Shrub	**bulk soil (dry season)**	**2.185242378**
19_2.bin.2	**millet rhizosphere**	**shrub**	**2.779081033**
2021_COA1R.bin.14	**millet rhizosphere**	**noshrub**	**2.870441908**
	noShrub	**millet rhizosphere**	**2.65449963**
2021_COA1R.bin.15	**millet rhizosphere**	**noshrub**	**2.693072735**
2021_COA1R.bin.17			
	millet rhizosphere	shrub	2.551571137
2021_COA1R.bin.18	millet rhizosphere	noshrub	2.598865769
2021_COA1R.bin.4	**millet rhizosphere**	**shrub**	**2.999663108**
2021_COA1R.bin.9			
2021_COA2R.bin.1			
2021_COA2R.bin.19	**millet rhizosphere**	**noShrub**	**2.466667324**
2021_COA2R.bin.20	millet rhizosphere	noShrub	2.364358969
	millet rhizosphere	noShrub	2.857217844
2021_COA2R.bin.5	millet rhizosphere	shrub	2.707145595
	noShrub	bulk soil (dry season)	2.851599541
2021_COA3D.bin.1	noShrub	bulk soil (rainy season)	2.894706906

	bulk soil (dry season)	shrub	2.56102466
	bulk soil (dry season)	noShrub	3.084981777
2021_COA3R.bin.2	millet rhizosphere	noShrub	2.543923816
2021_COA4D.bin.2	**bulk soil (dry season)**	**shrub**	**2.821380384**
2021_COA4R.bin.7	millet rhizosphere	noShrub	2.714413772
	bulk soil (rainy season)	noShrub	2.880507316
2021_COC1D.bin.14	bulk soil (rainy season)	shrub	2.546526809
	Shrub	**bulk soil (dry season)**	**2.353901448**
2021_COC1D.bin.8			
	Shrub	bulk soil (dry season)	2.055482806
	bulk soil (dry season)	shrub	2.289221965
2021_COC1D.bin.9	bulk soil (dry season)	noShrub	2.493233793
2021_COC1R.bin.6			
2021_COC2D.bin.12	bulk soil (dry season)	noShrub	2.27418847
	bulk soil (dry season)	**shrub**	**2.888102074**
2021_COC2D.bin.3	**bulk soil (dry season)**	**noShrub**	**2.787422455**
	noShrub	**bulk soil (dry season)**	**2.455190983**
2021_COC2D.bin.7	**bulk soil (rainy season)**	**shrub**	**2.177458174**
2021_COC2D.bin.8			
2021_COC2R.bin.12	millet rhizosphere	noShrub	2.723282104
	millet rhizosphere	shrub	2.253685011
2021_COC2R.bin.14	millet rhizosphere	noShrub	2.465616934
	millet rhizosphere	shrub	2.785712978
2021_COC2R.bin.15	millet rhizosphere	noShrub	2.954190118
	millet rhizosphere	**shrub**	**2.555030098**
2021_COC2R.bin.16	**millet rhizosphere**	**noShrub**	**2.50828804**
	bulk soil (rainy season)	shrub	2.751577424
2021_COC3D.bin.1	bulk soil (dry season)	noShrub	3.178832289
2021_COC3D.bin.5	**noShrub**	**bulk soil (dry season)**	**2.620834289**
	noShrub	**bulk soil (dry season)**	**2.659645957**
	noShrub	**bulk soil (rainy season)**	**2.474438909**
	bulk soil (dry season)	**noShrub**	**2.759736738**
2021_COC4D.bin.15	**bulk soil (rainy season)**	**shrub**	**2.347908619**
2021_COC4D.bin.7	noShrub	bulk soil (dry season)	2.38158967
	millet rhizosphere	shrub	2.651981833
2021_COC4R.bin.12	millet rhizosphere	noShrub	2.690858584
	millet rhizosphere	shrub	2.135065553
2021_COC4R.bin.15	millet rhizosphere	noShrub	2.553996588
	millet rhizosphere	shrub	2.212223008
2021_COC4R.bin.18	millet rhizosphere	noShrub	2.314687753
	millet rhizosphere	shrub	2.254785715
2021_COC4R.bin.19	millet rhizosphere	noShrub	2.577106643

	noShrub	**bulk soil (dry season)**	**2.188338814**
2021_COC4R.bin.24	**noShrub**	**millet rhizosphere**	**2.000263119**
	Shrub	bulk soil (dry season)	2.006587127
	bulk soil (dry season)	shrub	2.342976365
2021_COC4R.bin.7	millet rhizosphere	noShrub	2.180131487
2021_COC4R.bin.8	**millet rhizosphere**	**shrub**	**2.180035805**
2021_COC4S.bin.1			
2021_COC4S.bin.12			
2021_COC4S.bin.15			
	noShrub	bulk soil (dry season)	2.296956281
2021_COC4S.bin.18	noShrub	bulk soil (rainy season)	2.457722429
2021_COC4S.bin.19	**noShrub**	**bulk soil (rainy season)**	**2.431528312**
2021_COC4S.bin.24	noShrub	bulk soil (rainy season)	2.379935644
	noShrub	**bulk soil (rainy season)**	**2.68407047**
	noshrub	**bulk soil (dry season)**	**2.550424223**
2021_COC4S.bin.27	**bulk soil (rainy season)**	**noShrub**	**2.805660564**
2021_COC4S.bin.3	bulk soil (dry season)	noShrub	2.563065777
	noShrub	**bulk soil (dry season)**	**2.560317888**
2021_COC4S.bin.30	**bulk soil (rainy season)**	**noShrub**	**2.651062327**
	millet rhizosphere	shrub	2.14340594
2021_COC4S.bin.7	bulk soil (rainy season)	noShrub	2.465855257
	millet rhizosphere	shrub	2.707992515
2021_CSC1R.bin.17	millet rhizosphere	noShrub	2.241894858
2021_CSC1R.bin.5	millet rhizosphere	noShrub	2.623552485
2021_CSC2D.bin.4	Shrub	bulk soil (rainy season)	2.181206984
	Shrub	millet rhizosphere	
2021_CSC2S.bin.11	Shrub	bulk soil (rainy season)	
2021_CSC2S.bin.8			
	shrub	bulk soil (rainy season)	2.347475086
	shrub	millet rhizosphere	2.247538759
	shrub	bulk soil (dry season)	2.360418732
2021_CSC3R.bin.1	bulk soil (rainy season)	shrub	2.341541888
2021_CSC3S.bin.1			
	Shrub	**millet rhizosphere**	**2.60128153**
	shrub	**bulk soil (rainy season)**	**2.536368347**
2021_CSC3S.bin.11	**bulk soil (rainy season)**	**shrub**	**2.740228298**
2021_CSC3S.bin.17			

2021_CSC3S.bin.19	Shrub	bulk soil (rainy season)	2.281330866
	shrub	**bulk soil (rainy season)**	**2.923531709**
2021_CSC3S.bin.20	**shrub**	**millet rhizosphere**	**2.933256366**
2021_CSC3S.bin.23			
2021_CSC3S.bin.8			
2021_CSC4S.bin.15			
	bulk soil (dry season)	**shrub**	**3.203391673**
2021_CSC4S.bin.7	**bulk soil (dry season)**	**noShrub**	**3.010847255**
21_2.bin.2			
24_2_bin.1			
	Shrub	bulk soil (dry season)	2.687192442
	Shrub	bulk soil (dry season)	2.013318734
3300044652_17	bulk soil (rainy season)	shrub	2.687654177
3300044654_37			
	millet rhizosphere	shrub	2.222048679
3300044658_31	millet rhizosphere	noShrub	2.596422374
	Shrub	bulk soil (dry season)	2.633496378
	shrub	bulk soil (rainy season)	2.075370297
	shrub	millet rhizosphere	2.983711971
3300044667_14	bulk soil (rainy season)	shrub	3.002812788
	bulk soil (dry season)	noShrub	2.912147172
3300044667_25	bulk soil (rainy season)	shrub	2.891415572
3300044667_30	bulk soil (rainy season)	shrub	2.180229128
3300044684_27			
3300044689_1			
	millet rhizosphere	shrub	2.182158523
3300044693_2	millet rhizosphere	noShrub	2.531733051
3300044694_26	Shrub	bulk soil (dry season)	2.003298811
	millet rhizosphere	noShrub	2.971439398
3300044694_9	shrub	bulk soil (dry season)	2.440398192
3300044705_27			
3300044741_25			
	Shrub	bulk soil (dry season)	2.071250318
3300044842_12	millet rhizosphere	shrub	2.053435102
3300044842_42			
3300044901_10	millet rhizosphere	noShrub	2.646939502
	bulk soil (rainy season)	shrub	2.863831472
3300045002_7	bulk soil (rainy season)	noShrub	2.605689182
3300045003_14			
3300045003_29	bulk soil (rainy season)	noShrub	2.336943441
3300045003_30	bulk soil (dry season)	noShrub	2.146231604

3300045003_43	**bulk soil (rainy season)**	**noShrub**	**2.508378573**
3300045014_30			
3300045014_31	bulk soil (dry season)	shrub	2.666191713
3300045049_17			
	millet rhizosphere	**shrub**	**3.263672267**
3300045049_56	**millet rhizosphere**	**noShrub**	**3.315698857**
3300045838_42	noShrub	millet rhizosphere	2.485666887
3300045976_9	**bulk soil (rainy season)**	**noShrub**	**2.68494619**
	bulk soil (dry season)	**shrub**	**2.668700326**
COA1D.bin.4	**bulk soil (dry season)**	**noShrub**	**3.155313828**
	noShrub	**millet rhizosphere**	**2.581779574**
	millet rhizosphere	shrub	2.243180112
COA1R.bin.11	millet rhizosphere	noShrub	2.734792389
COA1R.bin.17	millet rhizosphere	noShrub	2.241902943
	millet rhizosphere	shrub	2.796627407
COA1R.bin.2	millet rhizosphere	noShrub	2.749266491
	noShrub	bulk soil (dry season)	2.258218445
	noShrub	bulk soil (rainy season)	2.155836993
	millet rhizosphere	shrub	2.40157484
COA1R.bin.9	millet rhizosphere	noShrub	2.456447288
COA2R.bin.12			
	millet rhizosphere	**shrub**	**2.260926931**
COA2R.bin.13	**millet rhizosphere**	**noShrub**	**2.500667906**
COA2R.bin.16	millet rhizosphere	shrub	2.269084298
	noShrub	millet rhizosphere	2.423482224
COA2R.bin.5	millet rhizosphere	noShrub	2.488675442
COA2S.bin.11	bulk soil (dry season)	shrub	2.454685529
COA2S.bin.12	bulk soil (rainy season)	noShrub	2.58674738
	bulk soil (rainy season)	shrub	2.937403696
COA2S.bin.13	bulk soil (rainy season)	noShrub	3.144513454
	noShrub	**bulk soil (dry season)**	**2.789469759**
	noShrub	**bulk soil (rainy season)**	**2.648268088**
	bulk soil (dry season)	**noShrub**	**2.893631555**
COA2S.bin.14	**bulk soil (rainy season)**	**shrub**	**2.348723073**
COA2S.bin.18			
	noShrub	bulk soil (rainy season)	2.746058984
COA2S.bin.3	bulk soil (rainy season)	noShrub	2.885711215
COA2S.bin.5			
	noShrub	bulk soil (dry season)	2.576719212
COA3D.bin.6	noShrub	bulk soil (rainy season)	2.314751871

	bulk soil (dry season)	noShrub	2.740922166
	bulk soil (dry season)	**shrub**	**2.878526139**
	bulk soil (dry season)	**noShrub**	**2.996951354**
COA3S.bin.8	**shrub**	**millet rhizosphere**	**2.32280243**
	bulk soil (dry season)	shrub	2.75197541
COA4D.bin.4	bulk soil (dry season)	noShrub	3.011034912
COA4R.bin.5	**Endo**	**noShrub**	**3.850850238**
COC1D.bin.2	noShrub	bulk soil (rainy season)	2.696821634
	bulk soil (rainy season)	noShrub	2.756449263
	Shrub	**millet rhizosphere**	**2.726212118**
	bulk soil (rainy season)	**shrub**	**3.428237436**
COC1D.bin.5	**bulk soil (rainy season)**	**noShrub**	**3.419683967**
	millet rhizosphere	shrub	2.055250485
COC1R.bin.13	millet rhizosphere	noShrub	2.684076161
	millet rhizosphere	**shrub**	**2.26233043**
COC1R.bin.16	**millet rhizosphere**	**noShrub**	**2.863994068**
	Shrub	**bulk soil (dry season)**	**2.533208766**
	bulk soil (dry season)	**shrub**	**2.657637276**
COC1R.bin.9	**millet rhizosphere**	**noShrub**	**2.743575032**
COC1S.bin.4	bulk soil (rainy season)	shrub	2.380342245
COC1S.bin.50			
COC1S.bin.60	noShrub	bulk soil (dry season)	2.00433935
COC2D.bin.6			
COC2D.bin.9			
	bulk soil (rainy season)	shrub	2.40174525
COC2R.bin.1	bulk soil (rainy season)	noShrub	2.635466976
	bulk soil (dry season)	**noShrub**	**2.863117638**
COC2R.bin.2	**bulk soil (rainy season)**	**shrub**	**2.711094707**
COC2R.bin.22	millet rhizosphere	shrub	2.499978534
COC2S.bin.3	noShrub	bulk soil (dry season)	2.360283584
COC2S.bin.5			
COC2S.bin.6			
	noShrub	bulk soil (dry season)	2.810272972
	bulk soil (dry season)	shrub	2.70008083
COC3D.bin.4	bulk soil (dry season)	noShrub	3.063722222
	bulk soil (dry season)	noShrub	2.860161267
COC3R.bin.17	bulk soil (rainy season)	shrub	2.762222265
	millet rhizosphere	**shrub**	**2.28565539**
COC3R.bin.18	**millet rhizosphere**	**noShrub**	**2.213658734**
	millet rhizosphere	shrub	2.014118112
COC3R.bin.2	millet rhizosphere	noShrub	2.149486611
COC3R.bin.26	millet rhizosphere	shrub	2.114165502

	millet rhizosphere	noShrub	2.764113431
	millet rhizosphere	shrub	2.365926299
COC3R.bin.27	millet rhizosphere	noShrub	2.299066593
COC3R.bin.9	**millet rhizosphere**	**shrub**	**2.72581492**
	bulk soil (rainy season)	shrub	2.688313901
COC4D.bin.15	bulk soil (rainy season)	noShrub	3.123834975
COC4D.bin.17			
	noShrub	bulk soil (dry season)	2.433965801
COC4D.bin.36	bulk soil (dry season)	noShrub	2.315356446
COC4D.bin.7			
	millet rhizosphere	**noShrub**	**2.246284631**
COC4R.bin.16	**noshrub**	**bulk soil (rainy season)**	**2.019003608**
	millet rhizosphere	**shrub**	**2.224876826**
	noShrub	**bulk soil (dry season)**	**2.151893747**
COC4R.bin.17	**bulk soil (rainy season)**	**noShrub**	**2.459882652**
	noShrub	**bulk soil (rainy season)**	**2.484466789**
COC4S.bin.16	**bulk soil (rainy season)**	**noShrub**	**2.543203027**
COC4S.bin.20			
COC4S.bin.25			
COC4S.bin.5			
CSA1D.bin.22			
CSA1D.bin.30			
CSA2D.bin.1	bulk soil (dry season)	shrub	2.984485873
	bulk soil (dry season)	shrub	2.627482474
CSA2D.bin.10	bulk soil (dry season)	noShrub	2.471696958
CSA2D.bin.2	bulk soil (dry season)	shrub	2.669376286
	bulk soil (dry season)	shrub	2.599416733
CSA2D.bin.6	bulk soil (dry season)	noShrub	2.508721938
CSA2D.bin.7	bulk soil (dry season)	shrub	2.474176123
CSA2D.bin.8	bulk soil (dry season)	shrub	2.570627573
CSA2D.bin.9	bulk soil (dry season)	noShrub	2.497265184
	millet rhizosphere	shrub	2.780765432
CSA2R.bin.18	millet rhizosphere	noShrub	3.074300149
	shrub	millet rhizosphere	2.062260606
CSA2R.bin.36	millet rhizosphere	shrub	2.146763075
	millet rhizosphere	**shrub**	**2.451251607**
CSA2R.bin.38	**millet rhizosphere**	**noShrub**	**2.167195922**
CSA2R.bin.47	millet rhizosphere	noShrub	2.106786429
	Shrub	**millet rhizosphere**	**2.31324354**
CSA2R.bin.49	**shrub**	**bulk soil (rainy season)**	**2.369659833**
CSA2S.bin.33	bulk soil (rainy season)	shrub	2.868059678

	bulk soil (rainy season)	noShrub	2.971407719
	bulk soil (rainy season)	shrub	2.41507072
CSA2S.bin.54	bulk soil (rainy season)	noShrub	2.423648863
	bulk soil (rainy season)	**shrub**	**2.436246548**
CSA2S.bin.55	**bulk soil (rainy season)**	**noShrub**	**2.721256855**
	Shrub	**bulk soil (dry season)**	**2.75342915**
	shrub	**millet rhizosphere**	**2.551334414**
	bulk soil (dry season)	**shrub**	**2.851628276**
CSA2S.bin.58	**bulk soil (rainy season)**	**noShrub**	**2.254064459**
	bulk soil (rainy season)	shrub	2.692550727
	shrub	millet rhizosphere	2.248346442
	shrub	bulk soil (dry season)	2.255319282
CSA2S.bin.64	bulk soil (rainy season)	noShrub	2.422305408
	bulk soil (rainy season)	**shrub**	**2.924195915**
CSA2S.bin.68	**bulk soil (rainy season)**	**noShrub**	**2.733572892**
CSA3D.bin.5			
	bulk soil (dry season)	**shrub**	**3.009343335**
	shrub	**bulk soil (dry season)**	**2.887155671**
CSA4R.bin.1	**millet rhizosphere**	**noShrub**	**2.790860279**
	Shrub	bulk soil (dry season)	2.727137277
CSA4R.bin.14	shrub	bulk soil (rainy season)	2.317043911
	millet rhizosphere	**shrub**	**3.113374293**
	bulk soil (dry season)	**shrub**	**2.90744407**
CSA4R.bin.17	**millet rhizosphere**	**noShrub**	**2.797640521**
	bulk soil (dry season)	**shrub**	**3.038246786**
CSA4R.bin.3	**shrub**	**bulk soil (rainy season)**	**2.871061663**
CSA4R.bin.6	shrub	bulk soil (rainy season)	2.299474768
	bulk soil (rainy season)	shrub	2.840034816
CSA4S.bin.6	shrub	millet rhizosphere	2.445694368
CSC1D.bin.5	**bulk soil (dry season)**	**noShrub**	**3.018669514**
	noShrub	bulk soil (dry season)	2.680991001
	noShrub	bulk soil (rainy season)	2.666170903
	bulk soil (rainy season)	shrub	2.373179113
CSC1D.bin.7	bulk soil (rainy season)	noShrub	2.837163545
CSC1E.bin.1			
	Shrub	millet rhizosphere	2.529454369
	millet rhizosphere	shrub	2.724021768
CSC1R.bin.17	millet rhizosphere	noShrub	2.215497886
	millet rhizosphere	shrub	2.67690397
CSC1R.bin.4	millet rhizosphere	noShrub	2.391462616

CSC1R.bin.6	millet rhizosphere	noShrub	2.529451825
	Shrub	millet rhizosphere	2.573388908
	bulk soil (rainy season)	shrub	3.044218457
CSC2D.bin.3	bulk soil (rainy season)	noShrub	2.807082565
	bulk soil (dry season)	**shrub**	**3.220994304**
	shrub	**millet rhizosphere**	**2.889159393**
CSC2D.bin.37	**shrub**	**bulk soil (dry season)**	**3.192218446**
	bulk soil (rainy season)	shrub	2.828376912
	bulk soil (rainy season)	noShrub	2.608046163
CSC2S.bin.1	shrub	millet rhizosphere	2.114445355
CSC2S.bin.10			
CSC2S.bin.12	Shrub	bulk soil (rainy season)	2.533786754
CSC2S.bin.14	**Shrub**	**millet rhizosphere**	**2.017813965**
	Shrub	bulk soil (dry season)	2.034596379
CSC2S.bin.3	bulk soil (rainy season)	shrub	2.844955868
	millet rhizosphere	**shrub**	**2.694630573**
CSC2S.bin.5	**bulk soil (rainy season)**	**noShrub**	**2.044135646**
	bulk soil (dry season)	**shrub**	**3.175714032**
CSC3D.bin.5	**shrub**	**bulk soil (rainy season)**	**2.998250587**
CSC3D.bin.7			
CSC3R.bin.11	**Endo**	**shrub**	**3.999450802**
CSC3R.bin.7			
CSC3S.bin.44			
CSC3S.bin.66	shrub	bulk soil (rainy season)	2.353960445
CSC3S.bin.68			
CSC3S.bin.69			
	bulk soil (rainy season)	**shrub**	**3.031496785**
CSC4R.bin.9	**bulk soil (rainy season)**	**noShrub**	**2.772667727**
	bulk soil (dry season)	**noShrub**	**2.133727881**
CSC4S.bin.15	**bulk soil (rainy season)**	**shrub**	**2.27184377**
	bulk soil (dry season)	**shrub**	**2.736585475**
CSC4S.bin.2	**bulk soil (dry season)**	**noShrub**	**2.482210497**
	bulk soil (rainy season)	shrub	2.659191953
CSC4S.bin.9	bulk soil (rainy season)	noShrub	3.094574927

Table S4.1D MAGs with conspecific lineages

MAG	

	Clusters at >=95% with SCMG clusters with these taxonomies (bolded ones were Lefse-enriched, in parentheses enrichment pattern)
01_2.bin.1	d_Archaea;p_Asgardarchaeota;c_Heimdallarchaeia;o_Hodarchaeales;f_S146-22;g_S146-22 | d_Archaea;p_Hydrothermarchaeota;c_Hydrothermarchaeia;o_Hydrothermarchaeales;f_BMS3B;g_BMS3B | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_UBA2241;f_UBA2241;g_FEN-672 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9sp005888435 | **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae (Study: OSS; sample type: soil, dry season soil, millet rhizosphere; enrichment: -OSS)** | **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Dictyobacter (Study: GC metaG; sample time: droughtEnd, drought Start; Enrichment: -OSS)**| **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_CF-154 (Study: GC metaT; sample time: drought start, drought end; enrichment: +OSS)** | d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Thermogemmatispora | d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_JAFATZ01| **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_DTNP01 (Study: GC metaG; sample type: droughtEnd, droughted; enrichment noShrub noOM)** | d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Bu33 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_Midichloriaceae;g_Jidaibacter | d_Bacteria;p_Chloroflexota;c_Anaerolineae | d_Bacteria;p_Bacteroidota;c_Chlorobia;o_Chlorobiales;f_Chlorobiaceae;g_Prosthecochloris | d_Bacteria;p_Desulfobacterota_B;c_Binatia;o_UBA9968;f_UBA9968;g_UBA9968 | d_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus | d_Bacteria;p_Marinisomatota;c_Marinisomatia;o_Marinisomatales;f_UBA1611;g_GCA-2722105 |
08_2_bin.3	**d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella (study: GC metG; sample type: droughtEnd, droughted; enrichement ShrubOM**) | **d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B (study: GC metG; sample type: droughtEnd, droughted; enrichement noShrubOM)|**

	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium (Study: GC metaG; sample type: droughtEnd, droughted; enrichement: shrub noOM)| d_Bacteria;p_Proteobacteria; | d_Bacteria;p_Armatimonadota;c_UBA5377;o_UBA5377;f_UBA11051;g_JAAYSP01_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Croceibacterium;s_Croceibacterium;s | d_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UBA3738_ | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_JACDAN01_ | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_SKUG01;g_SKUG01_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_N;s_Sphingomonas_N;sp0 | d_Bacteria;p_Armatimonadota;c_Chthonomonadetes;o_Chthonomonadales;f_Chthonomonadaceae;g_CAIXIX01_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_D;s_Sphingomonas_D;san | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_N;s_Sphingomonas_N;chu | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_XMGL2;s_XMGL2;sp018863195 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Erythrobacter;s_Erythrobacter;sp900 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Allosphingosinicella;s_Allosphingos | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Qipengyuania;s_Qipengyuania;seohaen | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas;sp01774 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_B;s_Sphingomonas_B_hor | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_BOG-932;f_BOG-932;g_BOG-932;s_BOG-932;sp003165335 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_ rhizohabdus;s_rhizohabdus;sp01104 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas;sp01419 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria| d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas;sp00434 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Tsuneonella;s_Tsuneonella;sp0070658 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas_yanting |
14_2.bin.2	

	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_ rhizosbiales;f_Beijerinckiaceae;g_Rhabdaerophilum;s_Rhabdaerophilum;calidif | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Casp-alpha2;g_UBA1479;s_UBA1479;sp002433335 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas_
2021_COA1R.bin.14	**d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae (study: OSS; sample type: millet rhizosphere; enrichment: -OSS; study: GC metaG, sample type: droughtEnd, droughted; enrichd noShrubOM, shrubnoOM)** | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Schlegelella_A |
2021_COA1R.bin.9	**d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae** (Study: GC; sample type: droughted, droughtEnd; enriched: noShrub, noOM; Study: OSS; sample type: soil, dry season soil, millet rhizosphere; enrichment: -OSS) | **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Ktedonosporobacter (Study: GC; sample type: droughted, droughtEnd; enriched: Shrub, OM)** | **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_UBA11361 (Study: GC; sample type: droughted, droughtEnd; enriched: noShrub, noOM)** | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_UBA2241;f_UBA2241;g_FEN-672 |
2021_COA2R.bin.1	**d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrososphaera (study: GC metaG; sample type droughtEnd, droughted: enrichment: shrub noOM)**
2021_COC1D.bin.14	**d_Bacteria;p_Actinobacteriota;c_Actinomycetia (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM)**|

2021_COC1D.bin.9	**d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae (study: GC metaG, sample type: droughtEnd, droughted; enricment: Shrub OM)**| Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Puia;s_Puia _dinghuensis | d_Bacteria_p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae; g_Puia_| **d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae ;g_Flavisolibacter_ (study: GC metaG, sample type: droughtEnd, droughted; enricment: Shrub OM)** | **d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae ;g_Puia;s_Puia;sp017307755 (study: GC metaG, sample type: droughtEnd, droughted; enricment: Shrub OM)** | d_Bacteria;p_Bacteroidota;c_Bacteroidia | d_Bacteria;p_Firmicutes_B;c_Desulfitobacteriia;o_Desulfitobacteriales;f_Desulfito bacteriaceae;g_PLLO_| **d_Bacteria;p_Firmicutes;c_Bacilli_ (Study: GC metaG; sample type: droughtEnd, droughted: enriched noshrubnoOM)**| d_Bacteria;p_Firmicutes;c_Bacilli;o_Alicyclobacillales;f_Alicyclobacillaceae;g_Alicy clobacillus_B_ | d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae; g_Puia;s_Puia;sp018267585
2021_COC2D.bin.3	d_Bacteria | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_UBA2241;f_UBA2241;g_FEN-672 | d_Bacteria;p_Acidobacteriota;c_Acidobacteria;o_Acidobacteriales;f_SbA1;g_Sulfo telmatobacter | d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Sulf otelmatobacter;s_Sulfotelmatobactersp003134655 |
2021_COC3D.bin.1	**d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedono bacteraceae;g_UBA11361 (Study: OSS; sample type: dry soil, soil; enrichment: -OSS; Study: GC metaG; sample time: drought start; enrichment: -OSS; Study G: sample type: drought End, droughted; enrichment: noShrub, noOM)** | d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_V1-33;g_JAGNEJ01 | d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_UBA8260;f_UBA8260 |
2021_COC3D.bin.5	**d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophih abitantaceae;g_FW021-bin43;s_FW021-bin43sp004299665 (study: GC metaG, sample type: droughtEnd, drougted; enrichment: shrub no OM)** | CSA4R.bin.17.fa | **d_Bacteria;p_Actinobacteriota;c_Actinomycetia (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM)| d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales(study: GC metaG, sample type: droughtEnd, droughted; enrichment shrubOM)** | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocar dioidaceae;g_WHTJ01;s_WHTJ01sp009377795 |
2021_COC4R.bin.19	**d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobact eraceae;g_Rubrimentiphilum (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM)** | **p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM**) | **d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobact eraceae;g_Aquilonibacter (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM)** |

2021_COC4S.bin.18	**d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrososphaera (study: GC metaG; sample type droughtEnd, droughted: enrichment: shrub noOM)** | d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_TA-21 | d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrosopumilaceae;g_Nitrosotalea
2021_COC4S.bin.19	
2021_COC4S.bin.24	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-612 | ;d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_PALSA-600sp009702325 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_Palsa-739sp003161615| **d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrososphaera (study: GC metaG; sample type droughtEnd, droughted: enrichment: shrub noOM)** | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7;s_GMQP-bins7sp004366385 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_AC-32 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_AC-50;s_AC-50sp005885565 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7;s_GMQP-bins7sp013812465
2021_COC4S.bin.3	**d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae (study: GC metaG; sample type droughtEnd, droughted: enrichment: noshrub noOM) |** **d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465 (study: GC metaG; sample type droughtEnd, droughted: enrichment: noshrub noOM, noShrub OM)**| d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Hyphomonadaceae;g_UBA5336;s_UBA5336sp009909065 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Acetobacterales;f_Acetobacteraceae;g_Roseomonas_A;s_Roseomonas_Atokyonensis | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_rhizobiales;f_rhizobiaceae;g_Mesorhizobium_B;s_Mesorhizobium_Bamorphae_A | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Euzebyales;f_Egibacteraceae;g_SLAO01;s_SLAO01sp007126835 | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae;g_Rathayibacter;s_Rathayibactersp013204985 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_rhizobiales;f_Im1;g_Rhodoligotrophos;s_Rhodoligotrophossp005281615 | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Euzebyales;f_Egibacteraceae;g_SLAO01;s_SLAO01sp007126835

	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_KBS-83_ | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_GCA-2729495;f_GCA-2729495;g_QUBU01;s_QUBU01;sp014337915 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas;s_Luteimonas_aestuarii | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria; | **d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales_d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae_ (study: GC metaG; sample type droughtEnd, droughted: enrichment: noshrub OM**) | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Thiobacillaceae;g_Thiobacillus;s_Thiobacillus;sp01139128 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Rhodanobacter;s_Rhodanobacter;sp004 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Arenimonas;s_Arenimonas;soli | d_Bacteria;p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_UBA1924;g_GCA-2706885;s_GCA-2706885;sp002706885 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Rhodanobacter;s_Rhodanobacter;sp004 | d_Bacteria;p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_UBA1924;g_JAEUIW01;s_JAEUIW01;sp016794925 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Usitatibacteraceae;g_FEB-7_ | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas;s_Stenotrophomonas_m | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Succinivibrionaceae;g_Succinivibrio;s_Succinivibrio;sp9 | d_Bacteria;p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_UBA1924;g_GCA-2706885;s_GCA-2706885;sp002706885 | d_Bacteria;p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_UBA1924;g_JAEUIW01;s_JAEUIW01;sp016794925 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Comamonas_C;s_Comamonas_C_badia | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas;s_Luteimonas;sp013425525 | **d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria (study: GC metaG; sample type droughtEnd, droughted: enrichment: noshrub OM**) | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Acidiferrobacterales;f_Sulfurifustaceae;g_MFSY01;s_MFSY01;sp001785175 | d_Bacteria;p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_UBA1924;g_GCA-2706885;s_GCA-2706885;sp002706885 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Rhodoferax;s_Rhodoferax;sp903920695 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus_ | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Thermomonas;s_Thermomonas_hydrotherma |
2021_CSC2D.bin.4	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rho

	danobacteraceae;g_Mizugakiibacter;s_Mizugakiibacter;s | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474;s_66-474;sp001899805 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Arenimonas;s_Arenimonas_terrae | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas;s_Luteimonas_huabeiensis | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_rhizobiales; f_rhizobiaceae;g_DUSC01;s_DUSC01;sp016756615 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Rudaea;s_Rudaea;sp018240545 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474;s_66-474;sp018241365 |
2021_CSC3S.bin.1	**d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae (Study: OSS. Sample type: millet rhizosphere, enrichment: -OSS)**

	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium_ | d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_KBS-83_ | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474;s_66-474;sp018971925| _d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Pacificimonas;s_Pacificimonas;flava | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_GCA-014117445;s_GCA-014117445;sp014 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sandaracinobacter;s_Sandaracinobact | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas_lenta | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_N;s_Sphingomonas_N;sp0 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium;s_Novosphingobium_k | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Tsuneonella;s_Tsuneonella_dongtanen | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Caenibius;s_Caenibius;sp017744735 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Alteraurantiacibacter;s_Alteraurant | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Croceibacterium;s_Croceibacterium;s | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Tsuneonella;s_Tsuneonella;sp0070658 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Bin65;f_Bin65;g_Bin65;s_Bin65;sp011523655 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474_| d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_CAHJWT01;s_CAHJWT01;sp903643075 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Bin65;f_Bin65;g_Bin65;s_Bin65;sp011523655 | d_Bacteria;p_Planctomycetota;c_Planctomycetia;o_Pirellulales;f_Thermoguttaceae;g_DSXM01;s_DSXM01;sp011332595 | Eukaryota_Rhodophyta_ | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis;s_Sphingopyxis_macrogo | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas_hominis | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium;s_Sphingobium;scionense | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas;s_Sphingomonas;spermid | **d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis_ (study: GC, metaG; sample type: drought end, droughed; enricment: shrub OM)**| d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Thermaurantiacus;s_Thermaurantiacus |
2021_CSC3S.bin.19	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis;s_Sphingopyxis_macrogo |

	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium;s_Sphingobium;sp0186038 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis;s_Sphingopyxis;sp01646 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Tsuneonella;s_Tsuneonella_rigui | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_rhizohabdus;s_rhizohabdus_wittich | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_I;s_Sphingomonas_I;sp9 | d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingopyxis;s_Sphingopyxis_indica | d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Acidobacterium_| d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_SCMT01;s_SCMT01;sp008015835 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae_ | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Rhodanobacter;s_Rhodanobacter;sp001 | d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Luteibacter;s_Luteibacter_jiangsuen
2021_CSC4S.bin.7	**d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae (Study: GC; sample type: droughted, droughtEnd; enriched: noShrub, noOM; Study: OSS; sample type: soil, dry season soil, millet rhizosphere; enrichment: -OSS)**| d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Ktedonobacter | d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Bu33_ | **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Dictyobacter_ (Study: GC metaG, droughEnd droughted, shrub no OM)**| **d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_CADDYT01;s_CADDYT01;sp902810755 (Study: GC metaG, droughEnd droughted, no shrub no OM**)| d_Bacteria;p_Chloroflexota;c_Dehalococcoidia;o_JACVQG01;f_JAHKAY01;g_JAHKAY01_ | d_Bacteria;p_Chloroflexota;c_FW602-bin22;o_FW602-bin22;f_DSKJ01;g_DSKJ01_ | d_Bacteria;p_Chloroflexota d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_JACDAE01_ |

	d_Bacteria;p_Marinisomatota;c_UBA2242;o_UBA2242;f_B5-G15;g_B5-G15_ | d_Bacteria;p_Chloroflexota;c_Chloroflexia;o_Chloroflexales;f_Herpetosiphonaceae;g_Herpetosiphon_
24_2_bin.1	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Cellulomonadaceae;g_Cellulomonas;s_Cellulomonassp018623035 | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_FW021-bin43;s_FW021-bin43sp004299665 |
COA3D.bin.6	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_JACVSB01;s_JACVSB01sp013697275
CSA2R.bin.47	**d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_Aquilonibacter (study: GC metaG, sample type: droughtEnd, droughted; enricment noShrub noOM)** | p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_JACRUB01
CSA4R.bin.14	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_FW021-bin43 | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_QHCC01 | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides;s_Nocardioidesspeluncae | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Geodermatophilaceae;g_Geodermatophilus;s_Geodermatophilus nigrescens | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Micromonosporaceae;g_Stackebrandtia;s_Stackebrandtiaalbiflava | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae: d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptomyces;s_Streptomycesharbinensis
CSA4R.bin.17	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Thermoleophilaceae;g_AC-37 | ;d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_JACCTQ01| d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-612;s_PALSA-612sp003134505 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7 | CSC3D.bin.5 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9sp005888435
CSC2S.bin.12	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae;g_Humibacter | p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae
CSC2S.bin.14	
CSC2S.bin.3	
CSC2S.bin.5	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Thermoleophilaceae;g_AC-37 |

	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_JACVRU01;s_JACVRU01sp014534295 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_AC-50;s_AC-50sp005885565 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae | CSA4R.bin.3 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_Palsa-739sp003161615 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9sp005885085 | **d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600 (Study: GC metaG, sample type: droughtEnd, droughted; enrichment: shrub OM)** | d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_WHSL01;s_WHSL01sp009380095 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_JACCTQ01 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_AC-32 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_GMQP-bins7 | d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9sp005888435

Table S4.2 Genes of interest

		Abbreviation	Description	citations
Antioxidant production	glutathione peroxidase	gpx	gpx, glutathione peroxidase (EC:1.11.1.9); K00432 glutathione peroxidase [EC:1.11.1.9]	https://www.bluepenjournals.org/ijaar/pdf/2015/August/Sen_and_Chandrasekhar.pdf https://www.sciencedirect.com/science/article/pii/S0147651314001134?casa_token=wM58Uj83KdgAAAAA:G1epydAH5aIL3V7wvVZX189Rw-IVeJl_YJ4LYvY3qNuJlktiL3gXXoaV-HYZOu4s2XyrZWtl68U
	Catalase	katE	katE, catalase (EC:1.11.1.6); K03781 catalase [EC:1.11.1.6]	https://www.annualreviews.org/doi/abs/10.1146/annurev.micro.57.030502.090938
		katG	katG; catalase/peroxidase; K03782 catalase-peroxidase [EC:1.11.1.21]	
	Superoxide dismutase	sodA	sodA; superoxide dismutase, Mn (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	https://pubmed.ncbi.nlm.nih.gov/7592406/
		sodB	sodB; superoxide dismutase (EC:1.15.1.1); K04564 superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	
Exopolysaccharide production	Aliginate lyase production	algC	algC; phosphomannomutase (EC:5.4.2.8); K01840 phosphomannomutase [EC:5.4.2.8]	https://www.frontiersin.org/articles/10.3389/fmicb.2021.730980/full https://journals.asm.org/doi/10.1128/jb.178.7.1800-1808.1996
		algL	algL; poly(beta-D-mannuronate) lyase; K01729 poly(beta-D-mannuronate) lyase [EC:4.2.2.3]	
		algG	algG, alginate-c5-mannuronan-epimerase AlgG	
		algI	algI, alginate O-acetyltransferase complex protein AlgI	
		alginate lyase 2	alginate lyase 2	
		algL	algL; poly(beta-D-mannuronate) lyase (EC:4.2.2.3); K01729 poly(beta-D-mannuronate) lyase [EC:4.2.2.3]	

			manB; beta-mannosidase precursor (EC:3.2.1.25); K01192 beta-mannosidase [EC:3.2.1.25]	
		algW	algW; serine protease AlgW	
		algZ	algZ; two-component system sensor protein, alginate biosynthesis (EC:2.7.3.-); K08082 two-component system, LytT family, sensor histidine kinase AlgZ [EC:2.7.13.3]	
	Xanthan production	gumB	gumB; polysaccharide export protein; K01991 polysaccharide export outer membrane protein	https://link-springer-com.proxy.lib.ohio-state.edu/referenceworkentry/10.1007/978-3-642-31331-8_25
		gumC	gumC; uncharacterized protein involved in exopolysaccharide biosynthesis	
	Mannose production	manB	manB; beta-mannosidase precursor (EC:3.2.1.25); K01192 beta-mannosidase [EC:3.2.1.25]	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4443731/
		manC	manC; mannose-1-phosphate guanyltransferase; putative capsular polysaccharide biosynthesis protein	
	misc.	noeL	noeL; GDP-mannose 4,6-dehydratase; K01711 GDPmannose 4,6-dehydratase [EC:4.2.1.47]	https://www.mdpi.com/2076-2607/9/1/91
		rfbB	rfbB; dTDP-D-glucose 4,6-dehydratase (EC:4.2.1.46); K01710 dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	https://www.mdpi.com/2076-2607/9/1/91
		zwf	zwf; glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49); K00036 glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]	https://pubmed.ncbi.nlm.nih.gov/25450881/
Nutrient status	beta-1,4-glucosidase	bglB	bglB, beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase; K05350 beta-glucosidase [EC:3.2.1.21]	https://www.sciencedirect.com/science/article/abs/pii/B9780323918053000046
		blgX	blgX, exported beta-glucosidase; K05349 beta-glucosidase [EC:3.2.1.21]	
		EC:3.2.1.21	beta-glucosidase (EC:3.2.1.21); K01188 beta-glucosidase [EC:3.2.1.21]	
	Iron acquisition	afuA	afuA; iron (III)-binding protein	https://bmcmicrobiol.biomedcentral.com/articles/10.1186/s12866-019-1536-1
		afuB	afuB; ABC transporter, iron(III) transport system permease protein	
		afuC	afuC; ABC transporter ATP-binding protein; K02010 iron(III) transport system ATP-binding protein [EC:3.6.3.30]	

		fbpA	fbpA; fe(3+)-binding periplasmic protein	
		fbpC1	fbpC1; Fe(3+) ions import ATP-binding protein FbpC 1 (EC:3.6.3.30)	
		fepA	fepA; TonB-dependent receptor	
		fepB	fepB; Iron(III) dicitrate-binding protein; K02016 iron complex transport system substrate-binding protein	
		fepC	fepC; ferric-enterobactin ABC transporter ATPase; K15738 ATP-binding cassette, subfamily F, uup	
		fepD	fepD; Iron(III) dicitrate-binding protein; K02015 iron complex transport system permease protein	
		fhuA	fhuA; TonB-dependent receptor	
		fepG	fepG; ferrichrome ABC transport system permease protein; K02015 iron complex transport system permease protein	https://link.springer.com/article/10.1007/s11103-010-9691-7
	Nitrogen acquisition, SOM degradation	chitinase	chitinase (EC:3.2.1.14); K01183 chitinase [EC:3.2.1.14]	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6604996/ https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6604996/
		nagA	nagA; N-acetylglucosamine-6-phosphate deacetylase (EC:3.5.1.25); K01443 N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]	https://bmcmicrobiol.biomedcentral.com/articles/10.1186/s12866-019-1536-1
		nagB	nagB; glucosamine-6-phosphate deaminase; K02564 glucosamine-6-phosphate deaminase [EC:3.5.99.6]	https://link.springer.com/article/10.1007/s11103-010-9691-7
		narB	narB, Nitrate reductase., Nitrite reductase (NAD(P)H)	
		nifS	nifS; pyridoxal-phosphate-dependent aminotransferase (EC:2.6.1.44 2.6.1.51); K04487 cysteine desulfurase [EC:2.8.1.7]	
		nifU	nifU; SUF system FeS cluster assembly protein	https://pubmed.ncbi.nlm.nih.gov/1538703/
		nirA	nirA; ferredoxin-nitrite reductase; K00366 ferredoxin-nitrite reductase [EC:1.7.7.1]	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC101460/ https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9751815/
		nirB1	nirB1; nitrite reductase (EC:1.7.1.4); K00362 nitrite reductase (NAD(P)H) large subunit [EC:1.7.1.4]	

		nirC	nirC; nitrite transporter NirC	
		nirD	nirD; nitrite reductase, [NAD(P)H] small subunit	
		NAG-ase	N-beta-d-acetylglucosaminidase, K01207 beta-N-acetylhexosaminidase [EC:3.2.1.52]	https://www.microbiologyresearch.org/content/journal/ijsem/10.1099/ijsem.0.005640
		amoA	amoA; ammonia monooxygenase subunit A	
		amoB	amoB; ammonia monooxygenase subunit B (EC:1.14.13.25)	https://www.sciencedirect.com/science/article/pii/S0038071718300415
	Phosphorus mineralization and acquisition	acid phosphatase AcpA	acid phosphatase	https://www.sciencedirect.com/science/article/pii/S1877705816004562 https://ami-journals.onlinelibrary.wiley.com/doi/10.1111/1758-2229.13040?af=R
		appA	appA; acid phosphatase precursor (EC:3.1.3.2); K01093 4-phytase / acid phosphatase [EC:3.1.3.26 3.1.3.2]	https://ami-journals.onlinelibrary.wiley.com/doi/10.1111/1758-2229.13040?af=R
		phnC	phnC; phosphonates ABC transporter ATP-binding protein; K02041 phosphonate transport system ATP-binding protein [EC:3.6.3.28]	
		phnD	phnD; phosphonate transport protein, binding protein; K02044 phosphonate transport system substrate-binding protein	
		phnE	phnE; phosphonate transport system permease; K02042 phosphonate transport system permease protein	
		phnF	phnF; PhnF; K02043 GntR family transcriptional regulator, phosphonate transport system regulatory protein	
		phnG	phnG; phosphonate C-P lyase system protein PhnG; K06166 PhnG protein	
		phnH	phnH; carbon-phosphorus lyase complex subunit; K06165 PhnH protein	
		phnI	phnI; phosphonate metabolism protein; K06164 PhnI protein	
		phnJ	phnJ; phosphonate metabolism protein PhnJ; K06163 PhnJ protein	
		phnK	phnK; phosphonate C-P lyase system protein PhnK; K05781 putative phosphonate transport system ATP-binding protein	

		phnL	phnL; ABC-type transport system involved in lipoprotein release, ATPase component	
		phnM	phnM; phosphonate metabolism protein PhnM	
		phnO	phnO; Protein phnO (EC:2.3.1.-)	
		phnW	phnW; 2-aminoethylphosphonate--pyruvate transaminase (EC:2.6.1.37); K03430 2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]	
		AP	phosphoesterase; K01078 acid phosphatase [EC:3.1.3.2]	https://doi.org/10.2136/sssabookser9.c8 https://ami-journals.onlinelibrary.wiley.com/doi/10.1111/1758-2229.13040?af=R
		phoD	phoD; alkaline phosphatase (EC:3.1.4.1); K01113 alkaline phosphatase D [EC:3.1.3.1]	https://www.frontiersin.org/articles/10.3389/fmicb.2022.1045919/full https://ami-journals.onlinelibrary.wiley.com/doi/10.1111/1758-2229.13040?af=R
		phoN	phoN, acid phosphatase (EC:3.1.3.2); K09474 acid phosphatase (class A) [EC:3.1.3.2]	https://doi.org/10.2136/sssabookser9.c8 https://ami-journals.onlinelibrary.wiley.com/doi/10.1111/1758-2229.13040?af=R
		phoP	phoP, alkaline phosphatase; K01077 alkaline phosphatase [EC:3.1.3.1]	https://www.frontiersin.org/articles/10.3389/fmicb.2020.588605/full
		phoR	phoR, alkaline phosphatase synthesis sensor protein PhoR (EC:2.7.13.3)	https://journals.asm.org/doi/10.1128/jb.186.4.1182-1190.2004
		pstA	pstA; phosphate ABC transporter permease; K02038 phosphate transport system permease protein	
		pstB	pstB; phosphate transporter ATP-binding protein; K02036 phosphate transport system ATP-binding protein [EC:3.6.3.27]	https://www.nature.com/articles/srep21329
		pstC	pstC; phosphate ABC transporter permease; K02037 phosphate transport system permease protein	
		pstS	pstS; high-affinity phosphate ABC transporter substrate-binding protein; K02040 phosphate transport system substrate-binding protein	https://cdn.techscience.cn/uploads/attached/file/20220530/20220530141123_11797.pdf
	sulfur acquisition	sufD	sufD; sufD, needed for fhuF Fe-S center production/stability	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8610958/

Osmolyte production	osmoproctectant	malK	malK; sugar ABC transporter ATP-binding protein; K10111 maltose/maltodextrin transport system ATP-binding protein [EC:3.6.3.19]	https://www.frontiersin.org/articles/10.3389/fmicb.2016.01577/full
	Glycine betaine/ choline	betA	betA, glucose-methanol-choline oxidoreductase; K00108 choline dehydrogenase [EC:1.1.99.1]	https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-022-08738-8
		betB	betB, betaine-aldehyde dehydrogenase (EC:1.2.1.8); K00130 betaine-aldehyde dehydrogenase [EC:1.2.1.8]	https://link-springer-com.proxy.lib.ohio-state.edu/article/10.1007/BF02936140
		opuABC	opuABC; glycine betaine ABC transport system permease protein; K02001 glycine betaine/proline transport system permease protein; K02002 glycine betaine/proline transport system substrate-binding protein	https://www.pnas.org/doi/abs/10.1073/pnas.97.13.7102
		opuBCD	opuBCD; substrate-binding region of ABC-type glycine betaine transport system; K05845 osmoprotectant transport system substrate-binding protein; K05846 osmoprotectant transport system permease protein	
	proline production	proA	proA; gamma-glutamyl phosphate reductase; K00147 glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]	https://onlinelibrary.wiley.com/doi/full/10.1111/brv.12146 https://pubmed.ncbi.nlm.nih.gov/26284090/ https://journals.asm.org/doi/10.1128/msphere.00613-19
		proB	proB; glutamate 5-kinase; K00931 glutamate 5-kinase [EC:2.7.2.11]	
		proC	proC; pyrroline-5-carboxylate reductase; K00286 pyrroline-5-carboxylate reductase [EC:1.5.1.2]	
		proP	proP; proline/glycine betaine transporter major facilitator superfamily	https://journals.asm.org/doi/10.1128/msphere.00613-19
		proV	proV; glycine betaine/L-proline ABC transporter ATP-binding protein; K02000 glycine betaine/proline transport system ATP-binding protein [EC:3.6.3.32]	
		proW	proW; choline ABC transporter, permease protein; K02001 glycine betaine/proline transport system permease protein	

		proX	proX; glycine betaine/proline transporter substrate-binding protein; K02002 glycine betaine/proline transport system substrate-binding protein	https://academic.oup.com/bbb/article/65/6/1419/5945228
	Trehalose production	otsA	alpha, alpha-trehalose-phosphate synthase [EC:2.4.1.15 2.4.1.347]	https://www.frontiersin.org/articles/10.3389/fmicb.2020.567768/full https://www.frontiersin.org/articles/10.3389/fmicb.2016.01577/full https://link.springer.com/article/10.1007/s11816-019-00554-z
		otsB	otsB;K01087 trehalose 6-phosphate phosphatase [EC:3.1.3.12]	
		treS	treS; trehalose synthase (EC:5.4.99.16); K05343 maltose alpha-D-glucosyltransferase [EC:5.4.99.16]	https://www.frontiersin.org/articles/10.3389/fmicb.2015.00937/full https://apsjournals.apsnet.org/doi/abs/10.1094/MPMI-07-10-0148
		treT	treT; Trehalose synthase; K13057 trehalose synthase [EC:2.4.1.245]	https://www.frontiersin.org/articles/10.3389/fmicb.2019.01779/full
		treZ	treZ; malto-oligosyltrehalose trehalohydrolase; K01236 maltooligosyltrehalose trehalohydrolase [EC:3.2.1.141]	https://www.sciencedirect.com/science/article/pii/S2214662816300135
Phytohormone manipulation		acnA	acnA; aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [EC:4.2.1.3]	https://apsjournals.apsnet.org/doi/abs/10.1094/MPMI-07-10-0148
		aldH	aldH; aldehyde dehydrogenase; K00128 aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9281055/
	Butainediol producuton	alsD	alsD; alpha-acetolactate decarboxylase; K01575 acetolactate decarboxylase [EC:4.1.1.5]	https://www.sciencedirect.com/science/article/pii/S0944501320300173?via%3Dihub https://www.frontiersin.org/articles/10.3389/fmicb.2015.00937/full
		budA	budA; acetoin reductase; K03366 (R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4 1.1.1.303]	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4151105/
		E2.2.1.6L	E2.2.1.6L; acetolactate synthase 3 catalytic subunit (EC:2.2.1.6); K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	https://www.sciencedirect.com/science/article/pii/S0038071718300415
	ACC degredation	ACC-Deaminase	1-aminocyclopropane-1-carboxylate deaminase; K01505 1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]	https://www.frontiersin.org/articles/10.3389/fmicb.2015.00937/full

		mdlC	mdlC; benzoylformate decarboxylase (EC:4.1.1.7); K01576 benzoylformate decarboxylase [EC:4.1.1.7]	https://journals.asm.org/doi/full/10.1128/aem.00226-22
		nirK	nirK; copper-containig nitrite reductase (EC:1.7.2.1)	https://www.sciencedirect.com/science/article/pii/S0038071718300415
		pqqB	pqqB; pyrroloquinoline quinone biosynthesis protein PqqB; K06136 pyrroloquinoline quinone biosynthesis protein B	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2245851/ https://www.sciencedirect.com/science/article/pii/S0038071718300415
		pchA	isochorismatase synthase	
		pchB		
	Aux-in	iaaM		
		iaaH		

Table S4.3: Detailed statistical results

	shrub	OM	shrub * OM	sample type	fertilizer	shrub* fertilizer	season	drought
Millet height								
Millet Biomass								
total C (wilcox signed rank)	p= 0.01, higher +shrub							
total N (wilcox signed rank)	p=0.022, higher+shrub							
Field study: PERMANOVA Resuts								
Lineages	R2=0.02179, p = 0.019; rhizo: 0.1945, soil: 0.3324 dry soil: 0.31401			R2=0.32498, p = 0.001	All samples: R2= 0.07013, p =0.001; dry soil R2 = 0.1992, p = 0.0010		R2=0.0830, p=0.0020	
Protein cluster	R2=0.075, p =			R2=62, p = 0.001	R2=0.03, p = 0.01			
PGPR protein	bothsoils: R2 = 0.25548 0.001				both soils: R2 = 0.10869 p= 0.002		both soils: R2= 0.11481; p =	
						endo: R2= 0.16066 p = 0.003		
	rainy soil: R2 =							
	drySoil: R2 = 0.27657 0.001				dry Soil R2= 0.16247 p =0.010			
	rhizo: R2 = 0.34117							
MAGs	R2=0.12, p = 0.001			R2=0.32, p=0.001	R2=0.067, p			

Growth Chamber - PERMANOVA								
Metagenomes	pre-drought: R2= 0.37, p = 0.001, post drought drought ed: R2 =	R2 = 0.014, p =0.001; post drought watered: R2 =						
PCs total	pre drought R2 = 0.35, p =.001; post drought R2 = 0.31	predrought: R2 = 0.077, p = 0.022						R2= 0.052, p = 0.052
PCs selected	R2=0.34,p = 0.001; watered: R2 = 0.26, p = 0.005;	R2 = 0.07, p = 0.027						R2 = 0.05, p = 0.065
MAGs	R2 = 0.71, p = 0.001; post drought: R2 = 0.49	R2 =0.067, p = 0.006	R = 0.048, p = 0.018; watered R2= 0.11, p = 0.011					
Growth Chamber - PERMANOVA								
Metatranscript	pre drought: R2 = 0.078, p = 0.004; post drought both	post drought watered: R = 0.13,p = 0.015						R2=0.048, p <0.1
PCs total								
PCs selected	R2=0.10, p = 0.001; end of							

Table S4.4A: significant correlation between MAGs and site metrics (Field)

	percent total C		percent total N		height (cm)		fresh Biomass (g)		Grain (kg/ha)*	
Genome	rho	p	rho	p	rho	p	rho	p	rho	p
01_2.bin.1										
13_2.bin.2	0.755	0.001	0.732	0.001	0.731	0.001	0.735	0.001	0.836	0.000
2021_COC3D.bin.5	-0.732	0.001	-0.661	0.005						
2021_COC4R.bin.24	-0.7496	0.0008								
2021_COC4S.bin.15	-0.7080	0.0021								
2021_COC4S.bin.27	-0.7227	0.0016								
2021_COC4S.bin.30	-0.7706	0.0005	-0.651	0.006						
2021_CSC1R.bin.5										
2021_CSC3S.bin.11									0.746	0.001
2021_CSC3S.bin.20									0.872	0.000
COC2D.bin.9	-0.677	0.004								
COC4S.bin.5	-0.723	0.002								
CSA2R.bin.49									0.773	0.000
CSA2S.bin.58									0.703	0.002
CSA4R.bin.3	0.686	0.003	0.655	0.006	0.674	0.004				
CSC2D.bin.37									0.717	0.002
CSC2S.bin.10					0.651	0.006			0.728	0.001
CSC2S.bin.14									0.700	0.003
CSC2S.bin.5									0.885	0.000
CSC3D.bin.5									0.765	0.001
CSC3R.bin.7	0.760	0.001	0.720	0.002					0.704	0.002

Table S4.4B significant correlation between MAGs and site metrics (pre-drought)

	Growth Chamber Mescosm: pre-drought									
	percent total C		percent total N		Na		K		b-1,4-d-glucosidase activity	
Genome	rho	p	rho	p	rho	p	rho	p	rho	p
19_2.bin.2							0.706	0.010		
2021_COC4S.bin.15									-0.657	0.020
2021_COC4S.bin.30			-0.65	0						
3300045003_43									-0.672	0.017
COC4S.bin.16									-0.6942	0.0123
COC4S.bin.25									-0.6706	0.0170
CSC3R.bin.11	0.022	0.650			0.725	0.008				

Table S4.4C significant correlation between MAGs and site metrics (post-drought)

Growth Chamber Mescosm: post-drought										
	total chlorophyll		percent total N		GAE		chlA/chlB		height (cm)	
Genome	rho	p	rho	p	rho	p	rho	p	rho	p
01_2.bin.1	0.608	0.036	-0.653	0.021						
13_2.bin.2	0.732	0.007								
19_2.bin.2	0.587	0.045								
2021_COA4D.bin.2	0.662	0.019								
2021_COC1R.bin.6	0.717	0.009								
2021_COC2D.bin.3	-0.650	0.022								
2021_COC2D.bin.7	-0.679	0.015								
2021_COC2R.bin.16	-0.732	0.007								
2021_CSC3S.bin.11	0.671	0.017								
2021_CSC3S.bin.20	0.594	0.042								
2021_CSC4S.bin.15	-0.784	0.003								

2021_CSC4S.bin.7	-0.739	0.006								
21_2.bin.2	-0.642	0.024								
3300045003_43	-0.814	0.001								
COA1D.bin.4	0.682	0.015								
COA2R.bin.13							0.698	0.012		
COA3S.bin.8	0.664	0.018								
COC1R.bin.16	0.591	0.043								
COC2D.bin.9	-0.694	0.012								
COC3R.bin.18	-0.769	0.003								
COC4R.bin.16	-0.709	0.010								
COC4S.bin.20	-0.709	0.010								
COC4S.bin.25	-0.657	0.020								
COC4S.bin.5	-0.754	0.005								
CSA2R.bin.38	-0.799	0.002								
CSA2S.bin.55					0.640	0.025				
CSA2S.bin.58									0.666	0.018
CSA2S.bin.68	0.769	0.003								
CSA4R.bin.3	0.696	0.012								
CSC1D.bin.5	-0.672	0.017								
CSC2D.bin.37	0.662	0.019								
CSC3D.bin.5	0.696	0.012								
CSC3R.bin.11										
CSC3R.bin.7	0.672	0.017								
CSC4S.bin.15	-0.784	0.003								
CSC4S.bin.2	0.666	0.018								

Table S4.5: enriched lineages

Taxonomy (singleM -pipe)	log(mean)	enriched	sample type	LDA	mean	study
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__JAFAQI01_g__JAFAQI01	2.6547	Shrub	soil	2.0061	0.0106	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__JAFAQI01_g__JAFAQI01	2.7006	Shrub	drySoil	2.1093	0.0016	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae_g__Pseudonocardia	2.8264	Shrub	drySoil	2.0337	0.0008	OSS

d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Propionibacteriales_f__Nocardioidaceae_g__Nocardioides	3.2072	Shrub	drySoil	2.4381	0.0063	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptomycetales_f__Streptomycetaceae_g__Streptomyces	2.9954	Shrub	soil	2.1852	0.0106	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptomycetales_f__Streptomycetaceae_g__Streptomyces	3.0802	Shrub	drySoil	2.2949	0.0008	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae	3.0595	Shrub	soil	2.3037	0.0106	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae	3.0132	Shrub	drySoil	2.2372	0.0087	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.3212	Shrub	soil	2.6707	0.0062	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.2427	Shrub	drySoil	2.5365	0.0008	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739	3.6503	Shrub	soil	2.9443	0.0062	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739	3.5759	Shrub	drySoil	2.9136	0.0016	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739_s__Palsa_739sp005883365	2.9236	Shrub	soil	2.2456	0.0062	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739_s__Palsa_739sp005883365	2.8923	Shrub	drySoil	2.3037	0.0016	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__70_9_g__VAYN01	2.7009	Shrub	soil	2.3500	0.0106	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__70_9_g__VAYN01	2.5800	Shrub	drySoil	2.0874	0.0008	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Solirubrobacter	3.0043	Shrub	soil	2.5361	0.0106	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Solirubrobacter	3.0373	Shrub	drySoil	2.2771	0.0157	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Micropepsales_f__Micropepsaceae_g__Rhizomicrobium	2.5898	Shrub	drySoil	2.1019	0.0008	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Bradyrhizobium	2.9228	Shrub	soil	2.1995	0.0446	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Bradyrhizobium	2.8891	Shrub	drySoil	2.1681	0.0033	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Pseudolabrys	2.6925	Shrub	soil	2.0823	0.0106	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Pseudolabrys	2.7018	Shrub	drySoil	2.0950	0.0011	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Sphingomonadales_f__Sphingomonadaceae	2.7664	Shrub	drySoil	2.0401	0.0011	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Sphingomonadales_f__Sphingomonadaceae_g__Sphingomicrobium	3.2588	Shrub	drySoil	2.6243	0.0008	OSS
d__Bacteria	3.0746	noShrub	soil	2.2709	0.0062	OSS

d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Microbacteriaceae	2.8864	noShrub	rhizo	2.2436	0.0026	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Microbacteriaceae_g__Leifsonia	2.5472	noShrub	rhizo	2.0850	0.0055	OSS
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Microbacteriaceae_g__Leifsonia_s__Leifsoniasp003367665	2.5351	noShrub	rhizo	2.0748	0.0151	OSS
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Palsa_465	3.8153	noShrub	drySoil	3.0828	0.0274	OSS
d__Bacteria_p__Chloroflexota	2.7131	noShrub	soil	2.2015	0.0062	OSS
d__Bacteria_p__Chloroflexota	2.5982	noShrub	drySoil	2.0707	0.0008	OSS
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae	2.7528	noShrub	drySoil	2.2130	0.0008	OSS
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__UBA11361	2.7986	noShrub	soil	2.1429	0.0285	OSS
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__UBA11361	2.8137	noShrub	drySoil	2.2730	0.0008	OSS
d__Bacteria_p__Chloroflexota_c__UBA5177_o__UBA5177_f__UBA5177_g__QHBP01	2.8624	noShrub	soil	2.2632	0.0285	OSS
d__Bacteria_p__Chloroflexota_c__UBA5177_o__UBA5177_f__UBA5177_g__UBA5177	2.9730	noShrub	soil	2.3591	0.0285	OSS
d__Bacteria_p__Chloroflexota_c__UBA6077_o__UBA6077_f__CF_72_g__CF_72	3.3037	noShrub	soil	2.7572	0.0062	OSS
d__Bacteria_p__Chloroflexota_c__UBA6077_o__UBA6077_f__CF_72_g__CF_72	3.2540	noShrub	drySoil	2.6657	0.0008	OSS
d__Bacteria_p__Dormibacterota_c__Dormibacteria_o__CF_121_f__CF_121_g__CF_13	2.9009	noShrub	soil	2.5194	0.0062	OSS
d__Bacteria_p__Dormibacterota_c__Dormibacteria_o__CF_121_f__CF_121_g__CF_13	2.6686	noShrub	drySoil	2.3352	0.0008	OSS
d__Bacteria_p__Dormibacterota_c__Dormibacteria_o__Dormibacterales_f__Dormibacteraceae_g__40CM_4_65_16	2.6731	noShrub	soil	2.2258	0.0062	OSS
d__Bacteria_p__Dormibacterota_c__Dormibacteria_o__Dormibacterales_f__Dormibacteraceae_g__40CM_4_65_16	2.5399	noShrub	drySoil	2.0825	0.0008	OSS
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae	2.8294	noShrub	soil	2.0388	0.0062	OSS
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae	2.8842	noShrub	drySoil	2.2087	0.0008	OSS
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Beijerinckiaceae_g__Microvirga	2.6630	noShrub	rhizo	2.1013	0.0026	OSS
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae	3.4271	noShrub	rhizo	2.7272	0.0491	OSS
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae_g__Ramlibacter	2.9223	noShrub	rhizo	2.2576	0.0055	OSS
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae_g__Trinickia_s__Trinickiasymbiotica	2.5005	noShrub	rhizo	2.0595	0.0491	OSS
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Xanthomonadales_f__Rhodanobacteraceae	2.8027	noShrub	rhizo	2.3710	0.0078	OSS

d__Archaea_p__Thermoplasmatota	2.4121	noShrub	droughtStart, to be drought ed	2.1091	0.0028	GC_metaG
d__Archaea_p__Thermoplasmatota_c__Thermoplasmata	2.3822	noShrub	droughtStart, to be drought ed	2.0843	0.0028	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__Acidobacteriaceae_g__Palsa_343	2.4517	noShrub	droughtStart, to be drought ed	2.0790	0.0039	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__Gp1_AA112_g__Gp1_AA112	2.4125	noShrub	droughEnd, drought ed	2.0455	0.0037	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__Gp1_AA112_g__Gp1_AA112	2.6353	noShrub	droughtStart, to be drought ed	2.2747	0.0039	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__SbA1_g__Gp1_AA145	2.5699	noShrub	droughEnd, drought ed	2.0214	0.0374	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__SbA1_g__Gp1_AA145	2.7522	noShrub	droughtStart, to be drought ed	2.0873	0.0039	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__SbA1_g__Sulfotelmatobacter	2.5176	noShrub	droughEnd, drought ed	2.0439	0.0039	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__SbA1_g__Sulfotelmatobacter	2.6812	noShrub	droughtStart, to be drought ed	2.1315	0.0039	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Bryobacterales_f__Bryobacteraceae_g__Bog_105	2.9812	noShrub	droughtStart, to be drought ed	2.0569	0.0163	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Blastocatellia_o__Pyrinomonadales_f__Pyrinomonadaceae_g__OLB17	2.7712	Shrub	droughEnd, drought ed	2.4644	0.0033	GC_metaG
d__Bacteria_p__Acidobacteriota_c__Blastocatellia_o__Pyrinomonadales_f__Pyrinomonadaceae_g__OLB17	2.8214	Shrub	droughtStart, to be drought ed	2.5004	0.0028	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia	2.9999	noShrub	droughtStart, to be drought ed	2.1579	0.0250	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales	2.9985	noShrub	droughEnd, drought ed	2.1107	0.0163	GC_metaG

d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Geodermatophilaceae	2.7912	noShrub	droughtStart, to be drought ed	2.0917	0.0104	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Geodermatophilaceae_g__Geodermatophilus	2.9557	noShrub	droughtStart, to be drought ed	2.3122	0.0065	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__JAFAQI01_g__JAFAQI01	3.0219	noShrub	droughtStart, to be drought ed	2.5141	0.0065	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae	2.9038	noShrub	droughtStart, to be drought ed	2.2195	0.0065	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae_g__Actinosynnema	2.9093	noShrub	droughtStart, to be drought ed	2.6441	0.0132	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae_g__GCA_003244245	2.7992	noShrub	droughEnd, drought ed	2.3714	0.0061	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae_g__GCA_003244245	2.5948	noShrub	droughtStart, to be drought ed	2.2467	0.0103	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptosporangiales_f__Streptosporangiaceae	3.0148	noShrub	droughEnd, drought ed	2.2022	0.0163	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptosporangiales_f__Streptosporangiaceae	3.0131	noShrub	droughtStart, to be drought ed	2.2010	0.0065	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptosporangiales_f__Streptosporangiaceae_g__Palsa_504	2.5644	noShrub	droughEnd, drought ed	2.0781	0.0163	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptosporangiales_f__Streptosporangiaceae_g__Palsa_504	2.6445	noShrub	droughtStart, to be drought ed	2.2224	0.0039	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae	3.1667	Shrub	droughtStart, to be drought ed	2.4115	0.0039	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.3520	Shrub	droughtStart, to be drought ed	2.7539	0.0039	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__70_9_g__VAYN01	2.7215	Shrub	droughEnd,	2.2367	0.0247	GC_metaG

			drought ed			
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__70_9_g__VAYN01	2.5738	Shrub	droughtStart, to be drought ed	2.2128	0.0039	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Palsa_465	3.5425	noShrub	droughEnd, drought ed	2.9503	0.0104	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Palsa_465	3.4554	noShrub	droughtStart, to be drought ed	2.9176	0.0065	GC_metaG
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Solirubrobacter	2.5577	Shrub	droughtStart, to be drought ed	2.0539	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae	3.0279	noShrub	droughtStart, to be drought ed	2.4300	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__CADDYT01	2.4699	noShrub	droughtStart, to be drought ed	2.0367	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__Dictyobacter	2.7576	noShrub	droughEnd, drought ed	2.1940	0.0374	GC_metaG
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__Dictyobacter	2.6917	noShrub	droughtStart, to be drought ed	2.3166	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae_g__UBA11361	2.8268	noShrub	droughtStart, to be drought ed	2.3548	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Limnocylindria_o__Limnocylindrales_f__CSP1_4	2.3384	Shrub	droughEnd, drought ed	2.0450	0.0028	GC_metaG
d__Bacteria_p__Chloroflexota_c__Limnocylindria_o__Limnocylindrales_f__CSP1_4	2.4332	Shrub	droughtStart, to be drought ed	2.0871	0.0039	GC_metaG
d__Bacteria_p__Chloroflexota_c__Limnocylindria_o__Limnocylindrales_f__CSP1_4_g__UBA5189	2.3259	Shrub	droughtStart, to be drought ed	2.0370	0.0021	GC_metaG
d__Bacteria_p__Chloroflexota_c__UBA5177_o__UBA5177_f__UBA5177_g__QHBP01	2.4851	noShrub	droughtStart, to be drought ed	2.0598	0.0104	GC_metaG

d__Bacteria_p__Chloroflexota_c__UBA5177_o__UBA5177_f__UBA5177_g__UBA5177	2.7684	noShrub	droughtEnd, drought	2.3211	0.0104	GC_metaG
d__Bacteria_p__Dormibacterota_c__Dormibacteria_o__Dormibacterales_f__Dormibacteraceae	2.5286	noShrub	droughtStart, to be drought	2.0630	0.0039	GC_metaG
d__Bacteria_p__Eremiobacterota_c__Eremiobacteria_o__Baltobacterales_f__Baltobacteraceae	3.1798	noShrub	droughtStart, to be drought	2.6520	0.0374	GC_metaG
d__Bacteria_p__Eremiobacterota_c__Eremiobacteria_o__Baltobacterales_f__Baltobacteraceae_g__Cybelea	2.6805	noShrub	droughtStart, to be drought	2.2282	0.0104	GC_metaG
d__Bacteria_p__Eremiobacterota_c__Eremiobacteria_o__Baltobacterales_f__Baltobacteraceae_g__Elarobacter	2.4358	noShrub	droughtEnd, drought	2.0429	0.0099	GC_metaG
d__Bacteria_p__Eremiobacterota_c__Eremiobacteria_o__Baltobacterales_f__Baltobacteraceae_g__Elarobacter	2.4131	noShrub	droughtStart, to be drought	2.0747	0.0037	GC_metaG
d__Bacteria_p__Eremiobacterota_c__Eremiobacteria_o__Baltobacterales_f__Baltobacteraceae_g__Rubrimentiphilum	2.9417	noShrub	droughtStart, to be drought	2.5211	0.0163	GC_metaG
d__Bacteria_p__Gemmatimonadota_c__Gemmatimonadetes_o__Gemmatimonadales_f__Gemmatimonadaceae	2.9249	Shrub	droughtStart, to be drought	2.0129	0.0374	GC_metaG
d__Bacteria_p__Myxococcota_c__Polyangia_o__Polyangiales_f__Polyangiaceae_g__Palsa_1150	2.3763	noShrub	droughtStart, to be drought	2.0623	0.0037	GC_metaG
d__Bacteria_p__Patescibacteria_c__Paceibacteria_o__UBA9983_A	2.5920	Shrub	droughtStart, to be drought	2.1251	0.0039	GC_metaG
d__Bacteria_p__Patescibacteria_c__Saccharimonadia_o__Saccharimonadales	2.7158	drought	shrub	2.0455	0.0163	GC_metaG
d__Bacteria_p__Planctomycetota_c__Phycisphaerae_o__Tepidisphaerales_f__Tepidisphaeraceae	2.6366	Shrub	droughtStart, to be drought	2.0725	0.0104	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae	2.9066	noShrub	droughtEnd, drought	2.2999	0.0039	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae	2.9029	noShrub	droughtStart, to be drought	2.3150	0.0039	GC_metaG

d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae_g__JACOUH01	2.4960	noShrub	drought End, drought ed	2.1528	0.0037	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae_g__JACOUH01	2.4487	noShrub	drought tStart, to be drought ed	2.1287	0.0037	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae_g__SIAQ01	2.4167	noShrub	drought End, drought ed	2.0080	0.0039	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae_g__UBA4732	2.3926	noShrub	drought tStart, to be drought ed	2.0905	0.0028	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Isosphaerales_f__Isosphaeraceae	2.5890	noShrub	drought End, drought ed	2.0131	0.0039	GC_metaG
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Isosphaerales_f__Isosphaeraceae_g__Paludisphaera	2.4456	noShrub	drought End, drought ed	2.0010	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Acetobacterales_f__Acetobacteraceae	3.0414	noShrub	drought End, drought ed	2.3379	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Acetobacterales_f__Acetobacteraceae	3.0231	noShrub	drought tStart, to be drought ed	2.2516	0.0065	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__ATCC43930_f__Stellaceae_g__AP_15	2.7631	noShrub	drought End, drought ed	2.2785	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__ATCC43930_f__Stellaceae_g__AP_15	2.8448	noShrub	drought tStart, to be drought ed	2.4215	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Reyranellales_f__Reyranellaceae_g__Reyranella	2.4402	Shrub	drought tStart, to be drought ed	2.0286	0.0037	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Devosiaceae_g__Devosia_A	2.6301	Shrub	drought End, drought ed	2.2639	0.0099	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Devosiaceae_g__Devosia_A	2.6457	Shrub	drought tStart, to be drought ed	2.2805	0.0225	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Rhizobiaceae	2.6708	Shrub	drought End, drought ed	2.1008	0.0163	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae	3.0174	Shrub	drought tStart, to be	2.2701	0.0374	GC_metaG

			drough ed			
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Bradyrhizobium	3.2640	Shrub	droughtStart, to be drough ed	2.6916	0.0065	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Pseudolabrys	2.9521	Shrub	droughEnd, drough ted	2.4319	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae_g__Pseudolabrys	2.9927	Shrub	droughtStart, to be drough ed	2.5056	0.0065	GC_metaG
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Sphingomonadales_f__Sphingomonadaceae	3.1734	Shrub	droughEnd, drough ted	2.4136	0.0065	GC_metaG
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae	3.2082	Shrub	droughEnd, drough ted	2.5219	0.0374	GC_metaG
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae_g__Ramlibacter	2.3877	Shrub	droughEnd, drough ted	2.0562	0.0033	GC_metaG
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Casimicrobiaceae_g__VBCG01	2.4884	Shrub	droughEnd, drough ted	2.1392	0.0039	GC_metaG
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Casimicrobiaceae_g__VBCG01	2.5005	Shrub	droughtStart, to be drough ed	2.1384	0.0039	GC_metaG
d__Bacteria_p__Verrucomicrobiota_c__Verrucomicrobiae_o__Pedosphaerales	2.5841	Shrub	droughEnd, drough ted	2.0719	0.0039	GC_metaG
d__Bacteria_p__Verrucomicrobiota_c__Verrucomicrobiae_o__Pedosphaerales	2.6632	Shrub	droughtStart, to be drough ed	2.1961	0.0039	GC_metaG
d__Bacteria_p__Bacteroidota_c__Bacteroidia	3.2716	ShrubnoOM	droughtEnd, drough ted	3.2784	0.0132	GC_metaT
d__Bacteria_p__Actinobacteriota	3.5173	noShrubOM	droughtStart, to be drough ed	3.5508	0.0324	GC_metaT

Table S4.6: Enriched Genes in Active MAGs

MAG	log(mean)	enriched	LDA	mean		ko_id
01_2_bin_1_	2.3275	droughtStart	2.081	0.01320	noshrub	K03545 dru:Desru_1004 dru:Desru_1004 factor; K03545 trigger factor; bacterial trigger factor protein
01_2_bin_1	2.5027	watered	2.378	0.02223	drought end, noshrub	sth:STH3146 plastoquinol--plastocyanin reductase
01_2_bin_1	2.7040	droughtStart	2.353	0.00911	noshrub	gob:Gobs_1044 **cyclase/dehydrase**
01_2_bin_1	2.5679	Shrub	2.284	0.00209	drought end, droughted	
01_2_bin_1	3.1826	Shrub	2.881	0.00740	drought end, droughted	
01_2_bin_1	3.3995	Shrub	3.027	0.01448	drought end, droughted	nop:Nos7524_0492 **type 2 lantibiotic**, mersacidin/lichenicidin family
01_2_bin_1	2.3466	Shrub	2.057	0.00740	drought end, droughted	
01_2_bin_1	2.6510	Shrub	2.353	0.00476	drought end, droughted	
01_2_bin_1	2.6074	Shrub	2.329	0.00740	drought end, droughted	
01_2_bin_1	2.7875	noShrub	2.419	0.04495	drought end, droughted	chl:Chy400_2405 hypothetical protein
01_2_bin_1	2.3934	Shrub	2.064	0.03263	drought end, droughted	ccx:COCOR_05393 trx1; thioredoxin; K03671 thioredoxin 1

01_2_bin_1	3.0413	droughtStart	2.725	0.01320	noshrub	
01_2_bin_1	2.3901	Shrub	2.063	0.02223	drought end, droughted	
01_2_bin_1	2.5007	droughtStart	2.004	0.00395	shrub	cai:Caci_0397 hypothetical protein
01_2_bin_1	2.6973	Shrub	2.419	0.00740	drought end, droughted	
01_2_bin_1	2.4164	Shrub	2.090	0.00209	drought end, droughted	ttr:Tter_0708 DNA-directed RNA polymerase subunit beta; K03043 DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
01_2_bin_1	2.1448	watered	2.095	0.02223	drought end, noshrub	
01_2_bin_1	2.8524	Shrub	2.523	0.00740	drought end, droughted	
01_2_bin_1	3.3143	droughtEnd	2.917	0.02497	shrub	
01_2_bin_1	2.8844	droughtStart	2.509	0.00911	noshrub	cow:Calow_0656 translation elongation factor tu (EC:2.7.7.4); K02358 elongation factor Tu
01_2_bin_1	3.1029	droughtStart	2.753	0.00911	noshrub	
01_2_bin_1	2.2742	droughtStart	2.037	0.02223	noshrub	chl:Chy400_0496 peptidase C26; K07010 putative glutamine amidotransferase
01_2_bin_1	2.7076	Shrub	2.457	0.02223	drought end, droughted	
01_2_bin_1	2.4652	Shrub	2.149	0.02223	drought end, droughted	
01_2_bin_1	2.3978	Shrub	2.074	0.02223	drought end, droughted	amz:B737_5129 **cellulose 1,4-beta-cellobiosidase**
01_2_bin_1	2.4515	Shrub	2.094	0.02103	drought end, droughted	msv:Mesil_1626 hypothetical protein
01_2_bin_1	2.3658	Shrub	2.046	0.00209	drought end, droughted	
01_2_bin_1	2.3347	Shrub	2.036	0.00209	drought end, droughted	dly:Dehly_1387 ribosomal 5S rRNA E-loop-binding protein Ctc/L25/TL5; K02897 large subunit ribosomal protein L25

01_2_bin_1	3.8140	Shrub	3.401	0.02497	drought end, droughted	
01_2_bin_1	2.6779	droughtStart	2.233	0.01041	shrub	tbi:Tbis_2786 50S ribosomal protein L28; K02902 large subunit ribosomal protein L28
01_2_bin_1	4.0812	noShrub	3.672	0.00649	drought end, droughted	
01_2_bin_1	2.7168	droughtStart	2.364	0.04934	noshrub	aym:YM304_04010 putative menaquinol-cytochrome c reductase cytochrome b subunit
01_2_bin_1	2.5700	Shrub	2.291	0.00740	drought end, droughted	
01_2_bin_1	2.5700	droughtEnd	2.247	0.04160	shrub	
01_2_bin_1	3.0034	noShrub	2.547	0.00649	drought end, droughted	ttr:Tter_0673 RpoD subfamily RNA polymerase sigma-70 subunit; K03086 RNA polymerase primary sigma factor
01_2_bin_1	2.5043	Shrub	2.214	0.00740	drought end, droughted	afw:Anae109_2114 hypothetical protein
21_2_bin_2	3.6293	Shrub	3.337	0.01320	drought end, droughted	
21_2_bin_2	2.3608	Shrub	2.113	0.02223	drought end, droughted	
21_2_bin_2	2.7118	Shrub	2.441	0.00740	drought end, droughted	K01937, hau:Haur_1743 pyrG; CTP synthetase; K01937 CTP synthase [EC:6.3.4.2]
21_2_bin_2_	3.2435	Shrub	2.947	0.02010	drought end, droughted	sma:SAV_3598 hypothetical protein
21_2_bin_2	2.7817	Shrub	2.501	0.02010	drought end, droughted	chl:Chy400_2405 hypothetical protein
21_2_bin_2	3.8309	Shrub	3.554	0.00335	drought end, droughted	

21_2_bin_2	2.7738	Shrub	2.465	0.02397	drought end, droughted	K09014; ttr:Tter_1698 FeS assembly protein SufB; K09014 Fe-S cluster assembly protein SufB
21_2_bin_2	4.9734	noShrub	4.207	0.00395	drought end, droughted	
21_2_bin_2	2.3073	Shrub	2.078	0.04951	drought end, droughted	tro:trd_1635 Transcriptional regulator superfamily
21_2_bin_2	2.2979	Shrub	2.103	0.00280	drought end, droughted	K03043 gpo:GPOL_c37680 rpoB; DNA-directed RNA polymerase subunit beta (EC:2.7.7.6); K03043 DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
21_2_bin_2	3.2377	Shrub	2.970	0.00370	drought end, droughted	K02950 cag:Cagg_3030 rpsL; 30S ribosomal protein S12; K02950 small subunit ribosomal protein S12
21_2_bin_2	2.4890	Shrub	2.211	0.00209	drought end, droughted	
21_2_bin_2	2.7226	Shrub	2.494	0.00370	drought end, droughted	K01358 sul:SYO3AOP1_0322 ATP-dependent Clp protease, proteolytic subunit ClpP (EC:3.4.21.92); K01358 ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
21_2_bin_2	3.1312	Shrub	2.892	0.00209	drought end, droughted	cyj:Cyan7822_1726 resolvase domain-containing protein
21_2_bin_2	2.2321	Shrub	2.026	0.02223	drought end, droughted	K05576 dev:DhcVS_801 nuoK; NADH:quinone oxidoreductase subunit 11 or 4L (chain K); K05576 NAD(P)H-quinone oxidoreductase subunit 4L [EC:1.6.5.3]
21_2_bin_2	2.2241	Shrub	2.038	0.01320	drought end, droughted	K02111 ttr:Tter_0065 ATP synthase F1 subunit alpha (EC:3.6.3.14); K02111 F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]

21_2_bin_2	2.2147	Shrub	2.014	0.02223	drought end, droughted	atm:ANT_13160 hypothetical protein
21_2_bin_2	3.0236	Shrub	2.762	0.00209	drought end, droughted	oni:Osc7112_1291 transposase, IS605 OrfB family
CSC3R_bin_7	2.9275	drought	3.014	0.04951	noshrub, drought end	aba:Acid345_3850 ECF subfamily RNA polymerase sigma-24 factor
CSC3R_bin_7	3.1350	droughtStart	2.898	0.02223	noshrub	sus:Acid_3036 ArsR family transcriptional regulator

Supplemental Figure Legends

Figure S4.1. Field study lineage, PC, and MAG abundance variation across treatments, including endophyte samples. a) Lineages, derived from single copy marker genes, b) MAGs and c) protein clusters. In Figure S2, we show the same ordinations with the endophyte samples removed. This is because of the high degree of divergence between endophyte and soil and millet rhizosphere communities, as in a. In a linear mixed effects model including endophyte samples, the effect of sample type accounts for 62% of community variation, obscuring the effects of other notable factors ($p < 0.05$). For this reason, endophyte samples were not included in further statistical analyses in this manuscript.

Figure S4.2. Ordinations with at lineage-, gene-, and genome- resolved data from field study and the Simulated Drought experiment a) Lineage abundance. All lineages were derived from SingleM, using all 59 single copy marker genes. The abundance of each has been relative abundance transformed b) PC abundance: protein clusters were made from all field study and active Simulated Drought assemblies via a Markov Clustering Algorithm. CoverM0.6.1 was used to map metagenomic reads from both studies to the

PCs in transcripts per million (TPM). This value was relative abundance transformed c) MAG abundance: Metagenomic reads were mapped to the 263 dereplicated MAGs in CoverM0.6.1 in TPM. This value was then normalized to the length of each MAG

Figure S4.3. Abundance of MAGs of interest and gene counts by MAG and category. MAGs of interest were selected out of the 208 enriched MAGs by virtue of their enrichment > 2.9 LDA in the field study and/or the Simulated Drought experiment and/or their activity in the Simulated Drought experiment. Despite our selection of these 73 MAGs, we recognize that there are many possible combinations of MAGs of interest and numerous MAGs in this dataset that are worthy of intensive study. a) Abundance of the 73 MAGs of interest in the field study rhizosphere (TPM). Clustering based on euclidean distances. This order is maintained in panels b) MAGs abundance (TPM) pre-drought; c) post-drought; and d) Gene content per MAG (count of gene/ count of gene in category: Antioxidant production, exopolysaccharide production, osmolyte production, nutrient acquisition, and phytohormone manipulation)

Figure S4.4. Genes of interest present in all MAGs of interest (counts gene/MAG). Genes of interest were selected from literature. See table S3 for more info

Figure S4.5. MAGs present in the Active Community a) pre-drought and b) post-drought abundances of active MAGs TPM

Figure S4.6. ANI/ AAI matrix of MAGs described as a) Ktedonobacteraceae and b) Palsa-73.9. Enriched MAGs taxonomically defined as members of the same lineage were clustered via FASTANI at 95% at EDGAR 3.2.

Figure S4.7. Abundance and spread Protein clusters related to PGPR function and drought resilience (n =752) in active and total communities before and after drought a) PCoA of Total Community. Top panel, Pre-drought: data cluster significantly by history of intercropping ($R^2 = 0.43$, $p = 0.001$)and organic matter amendment ($R^2=0.07$, $p =0.024$). Bottom panels, Post-drought: watered control data cluster significantly by history of intercropping ($R^2 = 0.42$, $p = 0.001$); droughted data cluster by history of intercropping ($R^2 = 0.17$, $p = 0.011$). Not pictured: Data at drought end cluster by the imposed drought treatment $p < 0.1$ ($R^2 = 0.053$,$p = 0.065$) b) PCoA of Active Community: Top panel, Pre-drought:data cluster significantly by history of intercropping ($R^2=0.10$, $p = 0.001$). Bottom panel, Post drought. No significant clustering with any treatment, although the history of intercropping influences active protein clusters within the droughted community at $P < 0.1$ ($R^2=0.16$, $p = 0.066$).

Figure S4.8. Millet plants from all OSS/OM combinations at harvest. From left to right: +OSS/+OM; +OSS/-OM; -OSS/+OM; -OSS/-OM

Supplemental Figures

Figure S4.1 Field study MAG and gene abundance variation across treatments, including endophyte samples

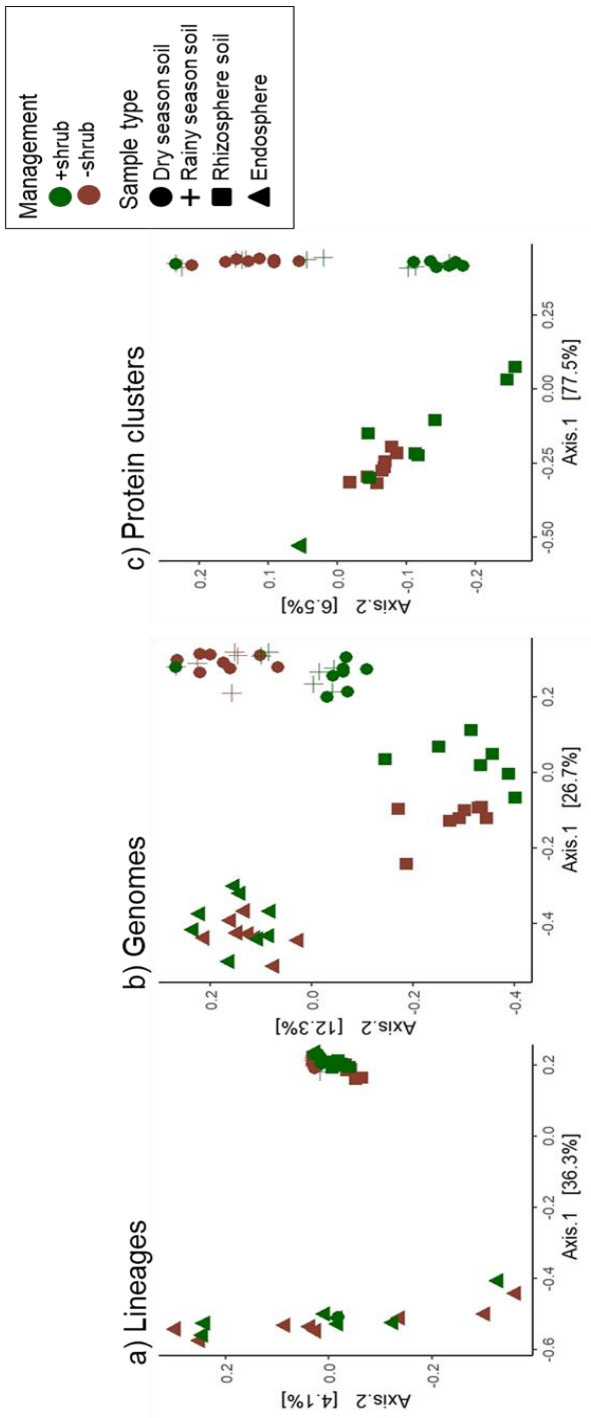


Figure S4.2. Abundance of MAGs of interest and gene counts by MAG and category

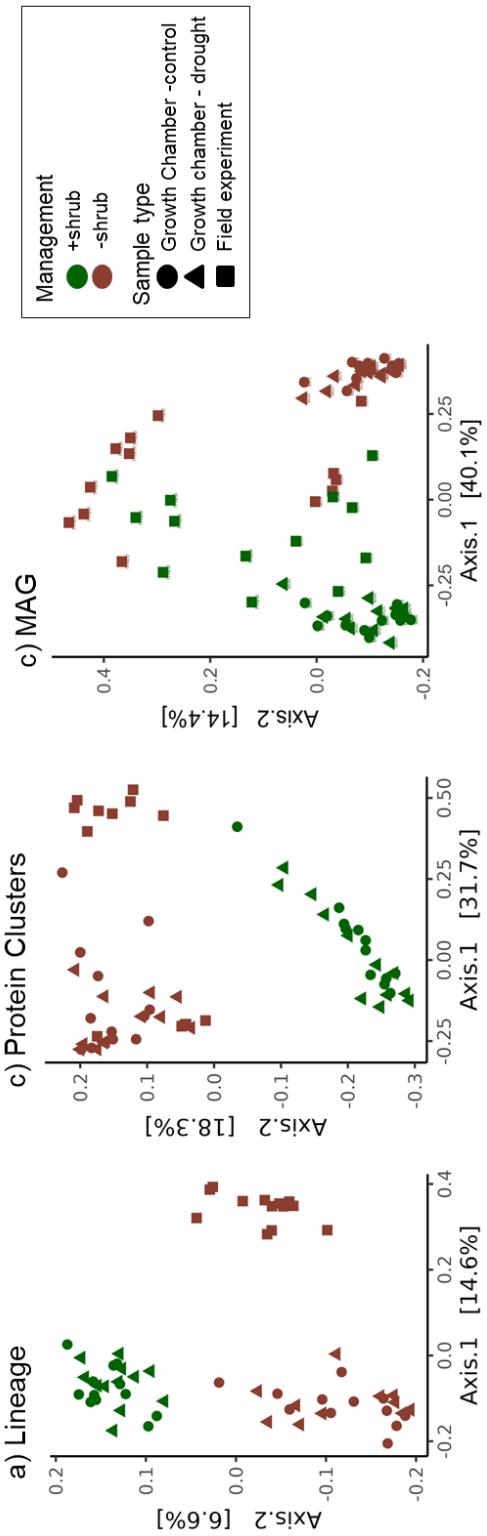


Figure S4.3. Abundance of MAGs of interest and gene counts by MAG and category

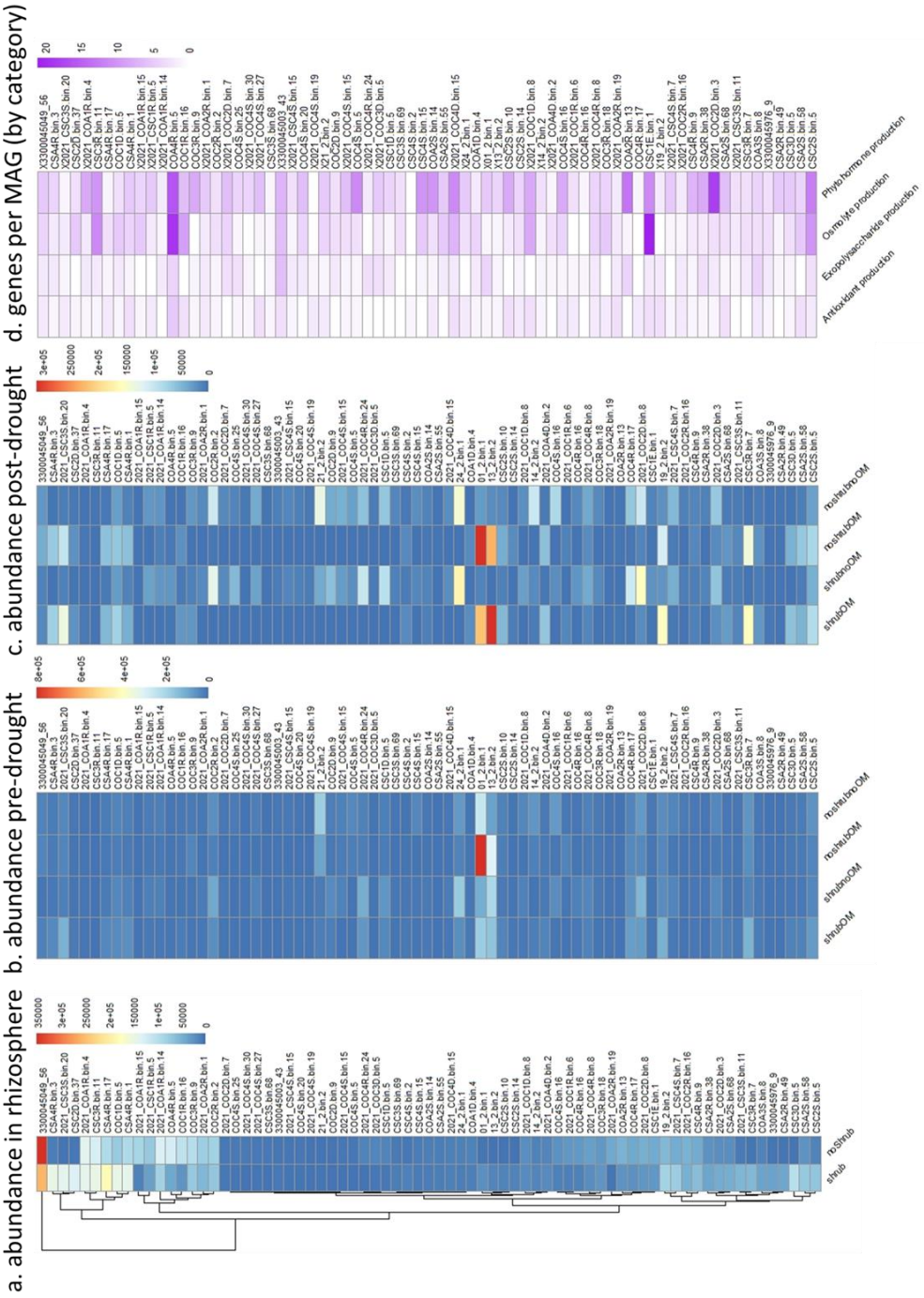


Figure S4.4. Genes of interest present in all MAGs of interest

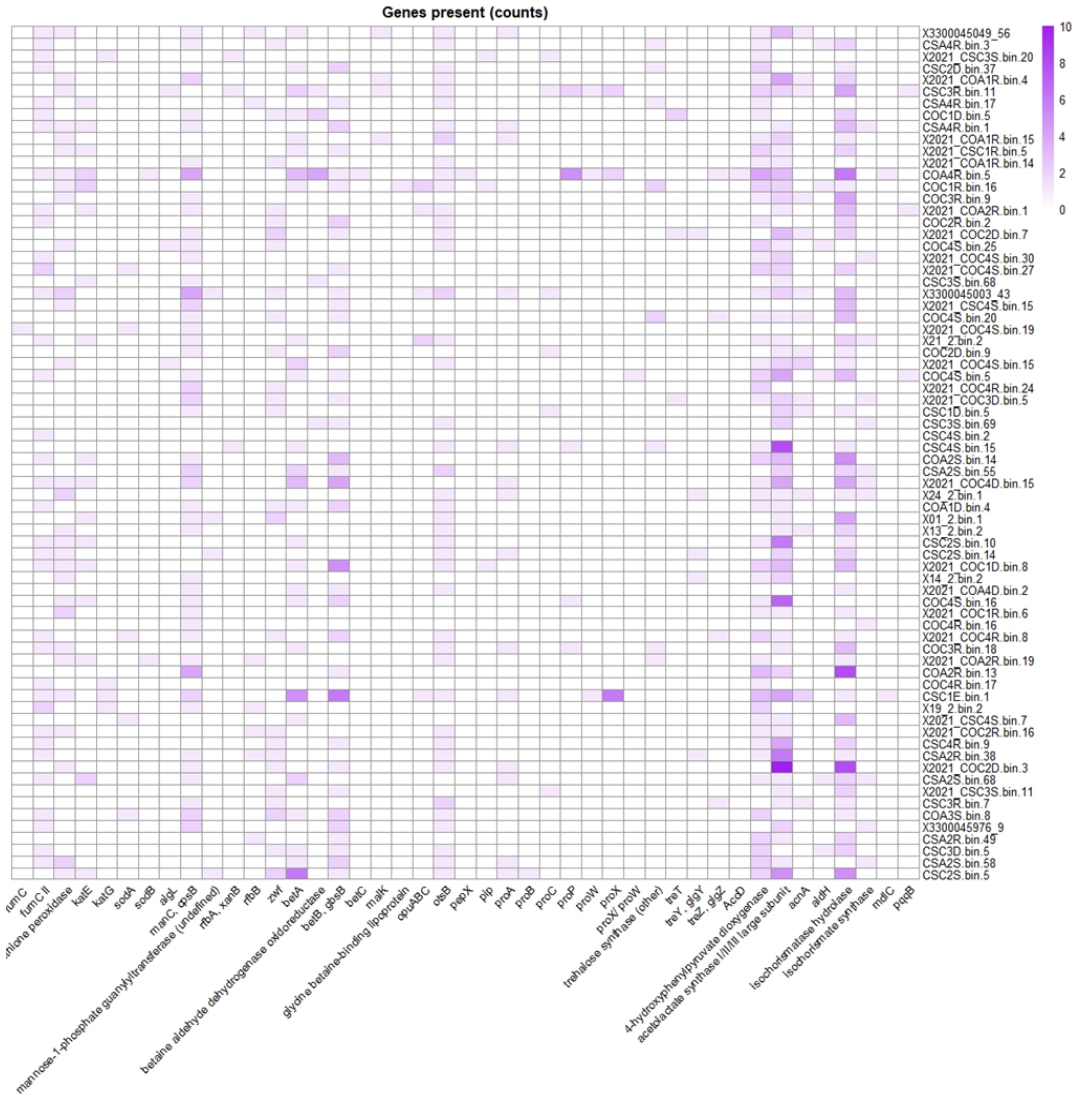


Figure S4.5. MAGs present in the Active Community

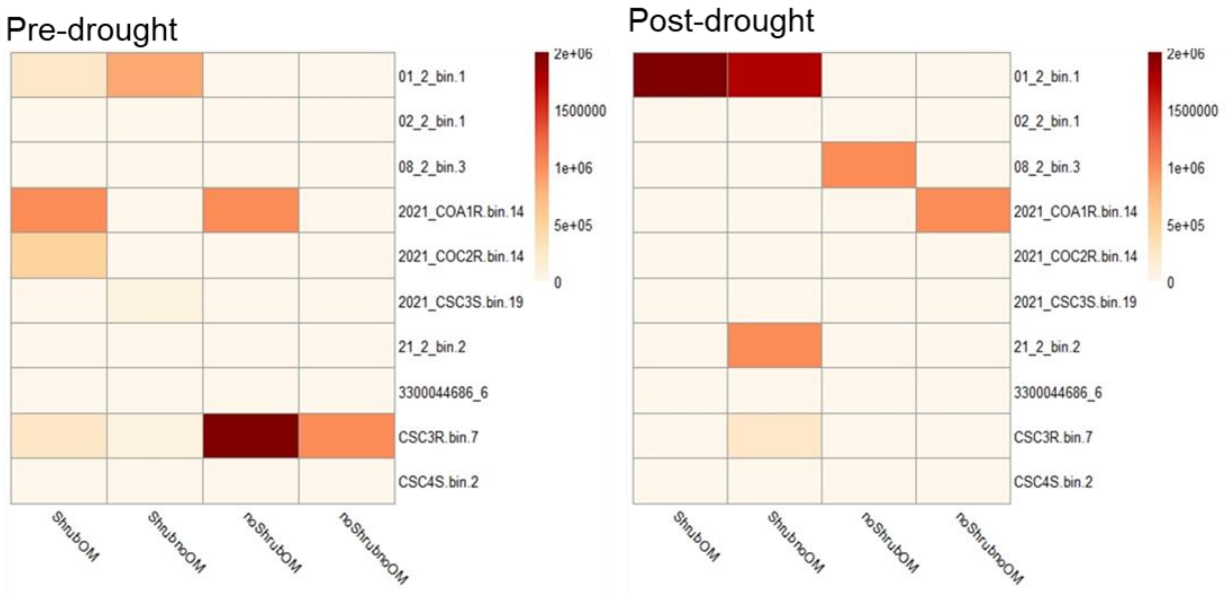


Figure S4.6. ANI/ AAI matrix of MAGs of Interest

A) Ktedonobacteraceae

100	81.29	65.00	65.00	65.00	21_2.bin.2	% ANI
87.99	100	65.00	65.00	65.00	2021_COA2R.bin1	
71.21	70.97	100	65.00	65.00	01_2.bin.1	
69.05	68.93	69.05	100	65.00	2021_COC2R.bin.14	
68.04	68.07	67.87	68.60	100	2021_COA1R.bin.14	
21_2.bin.2	2021_COA2R.bin1	01_2.bin.1	2021_COC2R.bin.14	2021_COA1R.bin.14		
% AAI						

B) Palsa-739

100	89.18	82.72	83.69	83.53	83.29	83.03	82.74	81.72	COC3R.bin.17	%ANI
91.90	100	82.23	81.24	83.31	83.00	82.77	82.57	81.50	CSC3D.bin.5	
83.39	83.08	100	82.89	83.23	83.11	82.86	82.62	81.37	3300044667_14	
82.91	82.68	86.82	100	82.08	81.98	81.70	81.66	80.59	COC2R.bin.2	
83.44	83.19	86.07	85.49	100	84.91	84.26	84.67	83.02	COA3S.bin.8	
82.77	83.00	85.26	84.94	86.02	100	84.82	83.98	82.40	COC1D.bin.5	
82.37	82.35	83.98	83.85	84.49	84.17	100	83.61	82.32	CSC2R.bin.37	
78.48	78.64	79.16	78.91	78.81	78.70	78.12	100	82.49	CSA4R.bin.3	
77.97	77.71	78.14	77.93	78.12	78.26	77.39	77.62	100	2021_COA4D.bin.2	
COC3R.bin.17	CSC3D.bin.5	3300044667_14	COC2R.bin.2	COA3S.bin.8	COC1D.bin.5	CSC2R.bin.37	CSA4R.bin.3	2021_COA4D.bin.2		
%AAI										

Figure S4.7 Abundance and spread Protein clusters related to PGPR function and drought resilience (n =752) in active and total communities before and after drought

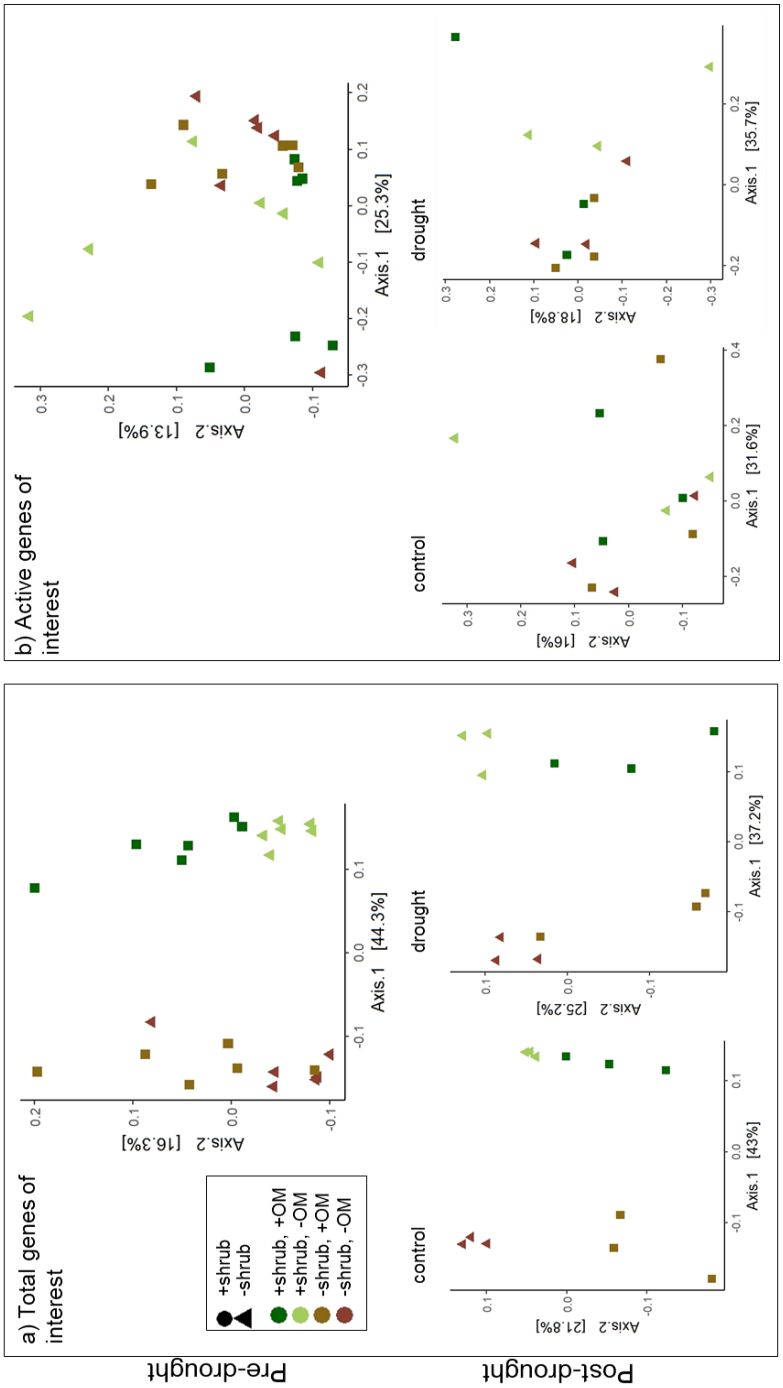


Figure S4.8. Millet plants from all OSS/OM combinations at harvest

Chapter 5. Three nested metagenomic studies describe crop-shrub-microbe interactions in a sustainable agroecology system in the Sahel

In prep for submission to *Nature Scientific Data*

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Abstract

The Sahel of West Africa is a vulnerable eco-region, where climate change will exacerbate drought. Due to a rapidly growing rural population, cropping and livestock grazing has greatly intensified, resulting in degraded soils. Local and biological systems are needed to maintain crop yields and soil health. A solution is the Optimized Shrub-intercropping System (OSS) that uses the indigenous shrub, *Guiera senegalensis*, at elevated densities (1200+ ha^{-1}) and incorporates coppiced biomass to soils. Research has shown OSS shifts soil microbial communities that includes organisms with plant growth promoting properties. This manuscript provides further metagenomic and metatranscriptomic data from three experiments: a landscape scale experiment across a rainfall and soil type gradient, a long-term experimental site (+/-OSS), and a mesocosm Simulated Drought experiment, (+/-OSS by +/- organic amendment). 1,180 recovered metagenome-assembled genomes (MAGs) were evaluated for relative enrichment and the microbiome mechanisms that promote millet growth based on encoded metabolisms. These data bases provide a basis for understanding the role of the microbial community in conferring drought resistance in crops of the Sahel.

Background and summary

Agricultural resilience to drought is particularly important for developing countries in semi-arid regions because they have few resources to mitigate the impacts of climate change (IPCC 2018, Heim, 2015, World Food Programme 2023). For example, the Sahelian country Senegal is located in a "climate change hotspot", with change occurring 50% faster than other parts of the world (UN department of Economic and Social Affairs, 2016; Intergovernmental Panel on Climate Change, 2022; ISS Africa 2016). In addition to warming, significant increases in mean aridity and extreme drying are predicted across the West African Sahel in the coming century, due to increasingly erratic rainfall events (IPCC 2018).

Senegal ranks 71st out of 121 countries on the world hunger scale (World Food Programme, 2023), and 36% of its population live below the international poverty line, including 60% of the population are subsistence farming households (World Bank, 2023) who directly consume the on-farm produced food. The United Nations further estimates a nearly 600% increase in population size by the year 2100 (2016). This growing population pressure has caused increased cropping and livestock grazing intensity that has degraded soils in the Sahel (FAO and ITPS, 2015; IPBES, 2018; UNCCD, 2019).

Agroecology is a logical solution for the Sahel to meet these challenges of population, increasing drought with climate change and degraded soils but must be appropriate for the majority, subsistence farmers. Thus a local and biologically-based system is needed (Poppy et al., 2014). Two indigenous shrubs, found throughout the Sahel (Le Houerou, 1980), *G. senegalensis* dominating in northern (drier conditions 200-600 mm annual rainfall) and *P. reticulatum* in southern (wetter 500-1000 mm) offer a basis for addressing these challenges. These shrubs are randomly spaced at low densities

(~130 to 350 ha^{-1}; Lufafa et al., 2008) in farmers' fields and are unmanaged (but have other uses such as fencing, fuel, and medicinal) except that aboveground biomass is coppiced in the spring and unfortunately often burned, depriving soils of much needed organic inputs. These two species are the foundation for the Optimized Shrub-intercropping System (OSS) which increase shrub densities to 1200 to 1500 shrubs ha^{-1} with all coppiced residues are incorporated into soil.

OSS delivers critical ecological and agronomic services including: improved soil quality, carbon (C) sequestration, , nutrient availability, improved water availability, and ultimately increased yields (Figure 1) (Bright et al., 2017, 2021; Kizito et al., 2006). This shrub intercropping system has been found to buffer against low rainfall and in-season drought, producing far higher pearl millet (*Pennisteum glaucum* (L.)R. Br.) yields than sole-cropped millet (Bright et al., 2017, 2021; Dossa et al., 2012, 2013).

This ability of OSS to buffer in-season drought may be due the discovery that these two species perform hydraulic lift (HL) (Kizito et al., 2012). HL happens at night when stomata close and deep taproots move water along a water potential gradient from wet sub-soil above the water table (high water potential) to dry surface soil (low water potential) where water leaks from roots (Kizito et al., 2012). Recently, Bogie et al. (2018) confirmed HL water was transferred from *G. senegalensis* to adjacent millet plants during a simulated in-season drought using labeled water (Bogie et al., 2018). However, the amount of water transferred to inter-cropped millet is relatively low (Bogie et al., 2018). Thus, there are likely other mechanisms for OSS in assisting crops through drought periods. One logical mechanism is the stimulation of a microbiome by OSS that confers drought resistance to crops. Evidence for this is that OSS harbors more diverse microbial

communities and organisms known to have plant growth promoting properties (Debenport et al., 2015; Diedhiou et al., 2021; Mason et al. 2023).

The beneficial microbial community may increase drought resistance in host plants by several mechanisms. Indeed, there is extensive evidence that plant drought tolerance can be induced by rhizobacteria via a variety of mechanisms: (1) production of phytohormones like abscisic acid, gibberellic acid, cytokinins, and indole -3-acetic acid (IAA); (2) ACC deaminase to reduce the level of ACC and thus ethylene production in the plants; (3) increased drought resilience through the production of osmolytes; (4) the production of bacterial exopolysaccharides which improve soil carbon stores and therefore improve water retention (Dimkpa et al. 2009; Timmusk and Nevo 2011; Timmusk et al. 2014), and (5) increasing the plant osmolyte concentration and reducing the host plant's production of reactive oxygen species (Vurukonda et al., 2016).

This manuscript is an overview of data collection, preliminary analyses, and future directions to draw attention to this unique suite of plant-shrub-microbe interactions in an understudied ecosystem. Dynamics of microbial community composition and gene expression were also investigated with emphasis on beneficial organisms that promote plant growth and confer drought resistance to plants. This collection contains the metagenomic and metatranscriptomic data from three nested experimental sites, coupling field and greenhouse method, and represents the culmination of long-term research relationships and expertise, and modern application of cutting-edge metagenomics to solve real-world challenges (Figure 2). Developing an understanding of the mechanisms and interactions of the dynamics between plants and microorganisms in mitigating water stress in crops is important to further develop OSS to reduce the impact of drought that

will increase with climate change and more sustainable agricultural systems for the Sahel and semi-arid regions world-wide.

Methods

Description of Experiments and Methods of Soil Sampling

This study contains data derived from three nested experiments: 1) Landscape Gradient sampling from six field sites along a rainfall and soil type gradient in Senegal, West Africa (Figure 2), 2) long-term field experiment of the Optimized Shrub-intercropping System (OSS), and 3) a Simulated Drought experiment in the Simulated Drought experiment using soils from the OSS experiment (Figure 3).

Field sampling: Landscape, Soil, and Rainfall Gradient Study

Samples were collected from actively farmed fields along a rainfall gradient in the semi-arid Peanut Basin in Senegal. The mean annual precipitation is 540 mm and usually falls between July and September, when millet is grown (Lufafa et al., 2008). Here, the July - September period of frequent precipitation is referred to as the "rainy season," and December-March as the "dry season". Most of the soils (70 - 80%) are sandy Ustipsamments, locally classified as Dior, with less than 1% SOC. The remaining soils are generally the Deck soil classified as Psammentic Haplustalfs, which has a higher quality than the Dior soil and only found in depressional, low landscape positions (McClintock and Diop, 2005). Shrubs and trees are the dominant vegetation in this savanna. *G. senegalensis dominates* in the northern part and *P. reticulatum* dominates the southern part of the Peanut Basin, although *G. senegalensis* shrubs are present in the

southern part as well. Samples were only collected from *G. senegalensis* - associated soils in the 2019 - 2020 sampling season described in this manuscript.

All sites were in fields under the management of separate farmers and have been managed in a peanut (*Arachis hypogea*)–pearl millet (*Pennisetum glaucum*) rotation for over 50 years as reported by collaborating farmers. Shrubs grow freely in farmers' fields at a density of ~ 240 shrubs ha $^{-1}$ and are typically coppiced in May and early June and burned off-site (Lufafa et al., 2008; Diedhiou et al., 2009). Prior to crop planting (~late June for Southern sites to late July in Northern sites) fields receive shallow (0-15 cm) sweep tillage and during the growing season are weeded with an in-row cultivator by animal traction and some hand weeding. Crops are planted with animal drawn small planters with the on-set of the rainy season. Regrowth of shrubs during the growing season is coppiced and laid between cropped rows. Little or no commercial fertilizer is used with small amounts of animal manure applied every few years (Badiane et al., 2000).

The experimental design was a 3 X 2 X 2 X2 factorial with the following treatments: three rainfall/soil type gradient sites; two shrub sampling location treatments (inside and outside the influence of *G. senegalensis*); and two replicates (2 shrubs + associated samples per site). Within each rainfall/soil site, there were two spatially separated landscape-level replications. The three rainfall gradient sampling sites were chosen along a north-south rainfall gradient which were: 1) Louga (Northern - 15.28° N, 15.53° W), 2) Thèis (central - 14.78° N, 16.90° W), and 3) Kaolack (Southern - 14.18° N, 16.25° W). Each region has average annual rainfall of 450, 550, and 750 mm, and the soils are 95, 92, and 86 % sand, respectively.

Per site, 2 shrubs were selected, and the following samples were collected 1) millet rhizosphere within the influence of the *G. senegalensis* ("+shrub", <1 meter from the center of the shrub); 2) millet rhizosphere outside *G. senegalensis* influence ("-shrub", >3 meters from the shrub center, based on Dossa et al. (2010) who reported little or no influence of the shrub at 3 m); 3) +shrub bulk soil; and 4) -shrub bulk soil.

Bulk soil was collected to a depth of 15cm in triplicate using a 5 cm-diameter soil core. +Shrub samples were collected from the base of the shrub, and -shrub samples were collected from either side of the shrub, more than 3m away and in between the rows of millet. -Shrub samples were combined into one sample. Cores were placed in gallon Ziplock bags and homogenized by hand through the bag. Soil was subsampled from each bag with a sterile spatula and placed in a microcentrifuge tube to store for DNA extraction. The remaining soil was used for PLFA extraction and soil chemical analyses.

+Shrub millet rhizosphere samples were collected from plants <1 m from the center of the shrub, and -shrub millet rhizosphere samples were collected from plants 3 - 4 m away from the center of the shrub. Millet plants were selected from within the same row on each side of the shrub. The millet rhizosphere soil was sampled by using a shovel to gently lift intact millet root balls, and shaking millet root balls gently to remove excess soil. For DNA extraction, two roots were selected per plant and rhizosphere soil from all four roots was gently scraped from the roots into one Whirl-Pak bag per sample. Soil remaining on the roots of the two selected plants was collected into one ziplock bag for PLFA extraction and soil chemical analyses.

All samples were transported on ice from field to lab. Samples for DNA extraction were immediately stored at -20°C prior to extraction. Soils for PLFA

extraction and chemical analyses were sieved with a 2mm sieve, and stored at -20℃. Millet plants were harvested at the time of soil sampling, and the height was measured aboveground fresh biomass was weighed and then averaged to give g plant^{-1} biomass.

Samples were first collected in the rainy season (September 2019). The GPS coordinates of each shrub were recorded, and samples were collected from the same locations in the dry season of the following year (March 2020). Samples were collected in identical fashion with the exception of the millet rhizosphere. As millet does not grow in the dry season, samples designated as "rhizosphere" were collected from the row in which the millet plants had grown the previous season via soil core. All soil samples were transported on ice, where they were stored at -20℃. In total, sampling resulted in 96 soil samples (Table 1, Figure 3).

Long-term field experiment of the Optimized Shrub-intercropping System (OSS)

Soils were obtained from long-term OSS experimental plots in Keur Matar, Senegal (near the city of Thies). The experimental site (Keur Matar Arame) is in the northern region of the Peanut Basin (14°45' N, 16°51' W, and 43 m above sea level), with mean annual precipitation of 450 mm and temperatures ranging from 20°C during the rainy season (December–January) to 33°C during the growing season (August - October) (Kizito et al., 2006; Bright et al., 2021). Soil type is a loamy sand known locally as Dior, with a topsoil that is more than 95% sand and <5% clay and a mean pH of 5.5 (Lufafa et al., 2005). It is classified in FAO taxonomy as a Rubric Arenosol (Michéli et al., 2006) and as a Typic Torripsamment in USDA soil taxonomy (Lufafa et al., 2005) Total C and N contents are 0.35% and 0.02% respectively; total P content is

about 95 mg kg^{-1} soil. The soil mainly originates from aeolian deposits and has no distinct horizonation in the top 1m layer (Badiane et al., 2001).

The experimental site was under local farmer management for at least 50 years where it was cropped continuously with a peanut–millet rotation besides 3 fallow years before the start of the experiment in 2003. At this time, *G. senegalensis* was the only woody vegetation in the field (Bright et al., 2021). The main plots were established in the winter (dry season) of 2003 by manually removing existing shrubs from "no shrub" plots (-OSS). The +OSS plots had the existing *G. senegalenis* stand augmented by planting shrub seedlings in the wet season to reach an elevated population of density of 1500 to 1833 shrubs ha^{-1}. The site is 0.5 ha and has a randomized complete block split-plot design. Main plots (46 m by 6 m) have the presence (+OSS) or absence (-OSS) of *G. senegalensis* and subplots (10 m x 6 m) receive fertilizer treatments of 0, 0.5, 1, or 1.5 times the fertilizer recommendations developed by Senegalese Extension for each crop. 1X NPK plots received 22 kg N, 15kg P, and 15 kg K per hectare per year when millet was grown (Bright et al., 2021). There is a 2 m gap between adjacent plots and 3-m gap between blocks (Kizito et al., 2006; Bright et al., 2021).

In early September of 2019 (about 30 days after millet germination) the following samples were collected: 1) -OSS millet rhizosphere soil; 2) -OSS millet roots; 3) -OSS bulk soil; 4) +OSS millet rhizosphere soil; 5) +OSS millet roots; 6) +OSS bulk soil for each level of fertilizer treatment and four replicate plots. Bulk soil samples were obtained in triplicate per plot with 5 cm-diameter core. Cores were homogenized and placed on ice for transport to the lab, where they were subsampled for DNA extraction. Remaining soil was stored for PLFA extraction and chemical analyses. +OSS samples were collected

from the base of three different shrubs within each plot, and -shrub samples were collected between millet rows.

Rhizosphere soil was obtained from two millet plants per plot and removed gently with a shovel so that the root ball remained intact. Excess soil was removed by gently shaking the root ball with the remaining soil adhering to roots designated as “root zone soil”. Immediately after sampling, the intact plant and root ball was placed in a ziplock bag, put on ice in a cooler, and then transported to the lab. Two roots per plant were removed with sterile scissors (n = 4 roots per plot), rhizosphere soil was stripped off with a sterile gloved hand into a Whirl-Pak bag, placed on ice for transport, and immediately stored at -20℃ for DNA extraction. The roots were placed in a 50 mL falcon tube with 15 mL sterile phosphate buffered saline + 1% Triton-X, and stored at 4℃ for surface sterilization within 24 hours of sampling (McPhearson et al ., 2018). Remaining soil was sieved to pass through 2 mm mesh and stored at -20℃ for PLFA extraction and soil chemical analyses. Each plant’s height and fresh biomass was measured and averaged per plot. Sampling was repeated for bulk soil in the same +/- OSS and 0X and 1X NPK plots in a similar fashion in March 2020, with the exception that there were no millet plants growing to sample (n = 16) (Table 2, Figure 3).

Simulated Drought Experiment

Soils were obtained in October of 2019 from the OSS study site from + and -OSS plots where no fertilizer had been applied. See Bright et al. (2021) for detailed description of this field experiment. In brief this was a split-plot experiment with OSS management (+ and -OSS) as the main plot and fertilizer rate as the sub-plot (0, 0.5, 1.0, or 1.5 recommended NPK rate for pearl millet or peanut). This experiment was established in

2004 with each treatment continuously cropped in millet-peanut rotation and managed with local farmer practices of hand labor and animal traction for field operations.

This soil was collected (0-15 cm depth), express-shipped to the Ohio State University where the greenhouse study was conducted, and immediately frozen at -20 ℃. The experimental design of the Simulated Drought experiment was a 2 X 2 X 2 factorial with three replicates and the following treatments: 2 soils (long-term +OSS or -OSS, from 0X fertilizer treatment); 2 soil amendments (no residue or plus *G. senegalensis* residue at realistic, equivalent field rate of 4 Mg ha^{-1} for OSS (Lufafa et al. 2008); and 2 early season drought levels (+/- drought) (Figure 3).

Pots were made from a 4" diameter PVC pipe cut to 50 cm and capped on the bottom to allow for loss of water by drainage and to enable maintain desired water contents. Each received 2.7 kg soil (dry weight) after imposing the soil shrub residue amendment treatment (incorporated to 15 cm as per farmer practice). All +OM treatments received a proportional mix (wt/wt) 60% *G. senegalensis* stems + 40% *G. senegalensis* leaves, consistent with field treatments (Diedhiou et al., 2009). All residues were obtained from the Keur Matar experimental site the previous growing season and air-dried prior to application. 120g of this residue mix was mixed into the top 10 - 15 cm of the pot, consistent with field tillage treatments.

Soil moisture was maintained at 2/3rds water holding capacity (field capacity, ~3.75% gravimetric water content), with pots allowed to stabilize for 10 days before planting millet. Three millet seeds were then planted in each pot at 1 cm depth and thinned to 1 plant per pot. Millet seedlings were grown to the 5-leaf stage, roughly 12 days after emergence (DAE) at field capacity after which water was withheld for 10 days

to mimic the effects of an early growing season drought (Bidinger & Mahalakshmi, 1987). After 10 days of drought, soil was rewetted to field capacity and maintained for a 10-day recovery period, at which point the millet was destructively sampled. Soil moisture was measured during the drought treatment gravimetrically, daily. The control moisture treatment will be maintained at field capacity for the duration of the experiment (Charles et al., 2023a, b).

Soil sampling was performed with a small coring device (10g - 30g per pot) at 4 time points: prior to all treatments' implementation (Phase 0), at beginning of the drought period (Phase I, planting through ~12 DAE), at end of the 10 day drought (Phase II, ~22 DAE), and at millet harvest (Phase III, ~32 DAE) (Figure 2). Soil samples at each time point were split into aliquots for nutrient assays, extracellular enzyme assays, PLFA and DNA/RNA coextraction (Charles et al 2024a, b; Mason et al., 2024a). All samples obtained for metagenomic, metatranscriptomic, and amplicon sequencing were flash frozen on liquid nitrogen and stored at -80 ℃ prior to extraction.

Soil Chemical Analyses

The percent total C and N in samples from all three studies were determined by an elemental analyzer (Carlo Erba CHN EA 1108). Approximately 20 mg of air-dried and homogenized soil was weighed in Sn capsules and combusted under a stream of oxygen at temperatures up to 1800 °C. The evolved CO_2 and nitrogen oxides (NO_x) were passed over copper to remove the excess oxygen and to reduce the NO_x to nitrogen (N_2). The resulting gas mixture was separated and eluted as CO_2 and N_2 using a chromatographic column (porapak PQS). Subsequently, CO_2 and N_2 were detected by a thermal conductivity detector. Acetanilide was used as a calibration standard. Soil pH was

measured using a 1:2 soil slurry with deionized water, and texture was measured via hydrometer. Soil anion and millet biomass nutrient content and stress marker determination methods and results are detailed in Charles et al (2023a; 2023b).

Extracellular Enzyme Activity

Extracellular enzyme assays were performed in triplicate on Simulated Drought experiment samples from phases I and III. β -glucosidase, acid phosphatase, and N-acetyl-β-D-glucosaminidase (NAGase) activities were determined using methods described in Deng and Popova (2011), Acosta-Martínez and Tabatabai (2011), and Tabatabai (1994). Tris (hydroxymethyl) aminomethane (THAM), maleic acid, citric acid, and boric acid dissolved in 0.5 M NaOH and were used as the buffers for these assays. The buffer solvent was then titrated to a pH of 6, 6.5, and 5.8 for each assay respectively using HCl 0.05M. The substrates used to complete each assay's reaction included p-nitrophenyl-β-D-glucoside, p-nitrophenyl phosphate, and p-nitrophenyl-N-Acetyl-β-D glucopyranosides (Sigma N7006; St. Louis, MO). After samples were incubated for 1hr at 37˚C, reactions were stopped, and samples were filtered using a Whatman # 2 filter. The absorbance of the p-nitrophenol product in the filtrate was recorded at a wavelength of 415 nm. Filtrates were diluted with a 1:1 solution of the buffer and THAM as needed. Two analytic replicates and one control were measured for each soil sample. Simulated Drought experiment enzyme assay results can be found in Charles et al 2023b, and previous years Landscape gradient and OSS results can be found in Delay, 2015.

Phospholipid Fatty Acids

For all studies, microbial community biomass was determined by analysis of phospholipid fatty acids (PLFAs) per Frostgard et al 1992 with minor modifications.

Briefly, fatty acids were extracted from 3 g of field moist soil in single phase chloroform-methanol solvent. The extracted lipids were then fractionated into phospholipids, glycolipids, and neutral lipids via silica columns. Phospholipids were then trans-esterified with 6 uL 19:0 internal standard to recover the PLFAs as methyl esters in 200 uL 1:1 Hexane:MTBE.

Biomarkers for microbial groups were designated in Frostegård and Bååth (1996) and have been designated as the following: General Bacterial -14:0, 15:0, 16:0, and 17:0; Actinomycetes - 16:0 10-methyl, 17:0-10-methyl, and 18:0 10-methyl; Gram positive bacteria - 15:0 iso, 15:0 anteiso, 16:0 is0, and 17:0 iso; Gram negative bacteria - 16:1 w7c, 17:0 cyclo, 19:0 cyclo w8c, and 18:1 w7c; arbuscular mycorrhizal fungi 16:1 w5c; Saprophytic fungi - 18:2 w6c and 18:1 w9c; protozoa 20:4 w6c; Stress (17:0 cyc + 19:0 cyc) / (16:1 w7c + 18:1 w7c). An analysis of PLFAs for the Simulated Drought experiment soils can be found in Charles et al 2024b.

DNA Extraction, Library Preparation and Sequencing

Microbial DNA from the millet rhizosphere and bulk soil samples obtained from the Landscape gradient and OSS in the rainy season were extracted via the PowerSoil Pro Total DNA extraction Kit (Qiagen) using 0.25 g. Successful extraction was confirmed via gel electrophoresis and precipitated with sodium acetate for shipment to Ohio State University. Bulk soil samples from the dry season were shipped directly to Ohio State University (due to complications arising from the COVID-19 pandemic), where they underwent identical DNA extraction procedures to the rainy season samples. No millet endophyte or rhizosphere samples were obtained during the dry season, as millet does not grow during that time.

Microbial endophyte DNA was obtained from the millet plant roots in the OSS study. Millet roots were surface sterilized within 24 hours of sampling by first vortexing in a phosphate saline buffer with Triton X. Roots were then placed in another container, washed in 70% ethanol for one minute, 10% bleach + triton X solution for two minutes, 70% ethanol for one minute, and rinsed three times in sterile autoclaved water. Roots were then stored for endophyte extraction (McPhearson et al., 2018). The remaining rhizosphere soil was pelleted and added to the rhizosphere sample collected in the field for extraction via the PowerSoil Pro kit, as described above. Endophyte DNA was extracted from millet roots via the Plant Mini DNA extraction kits (Qiagen) according to manufacturer's instructions, using a bead beater two times for 1 min each to rupture the plant cells. Successful extraction was confirmed via gel electrophoresis and precipitated with sodium acetate for shipment to Ohio State University.

All DNA samples were quantified via Qubit prior to DNA library preparation at the Department of Energy Joint Genome institute. Briefly, 0.2 ng of Genomic DNA was sheared to 300 bp using the Covaris LE220-Plus and size selected with SPRI using TotalPure NGS beads (Omega Bio-tek). The fragments were treated with end-repair, A-tailing, and ligation of Illumina compatible adapters (IDT, Inc) using the KAPA-HyperPrep creation kit (KAPA Biosystems) and 5 cycles of PCR was used to enrich for the final library. Illumina NovaSeq Sequencing was also performed at the DOE/JGI. The prepared libraries were quantified using KAPA Biosystems' next-generation sequencing library qPCR kit and run on a Roche LightCycler 480 real-time PCR instrument. Sequencing of the flowcell was performed on the Illumina NovaSeq sequencer using

NovaSeq XP V1.5 reagent kits, S4 flowcell, following a 2x151 indexed run recipe. This generated 1.3 TB of sequencing, roughly 20 GB per sample.

RNA and DNA were co-extracted from all soil samples obtained from the Simulated Drought experiment using the Zymo RNA/DNA co-extraction kit following manufacturer's instructions with minor modifications. Briefly, nucleic acids were extracted from 0.25 g field moist soil, and cells were lysed using the Powerlyzer for 45 seconds on setting 4. All DNA and RNA samples were checked for concentration and quality using QuBit and BioAnlyzer Tapestation. RNA library preparation was completed by Columbia Genomics Core in Summer 2022 for phases 1 and 2 (start and end of drought only).

DNA libraries prepared for the Simulated Drought experiment were prepared using the Illumina Nextera XT DNA Library Prep kit per manufacturer's instructions with minor modifications. First, all samples with a starting mass of greater than 0.2 ng were prepared using half reactions; samples with a starting mass of < 0.2 ng DNA were prepared using the full reaction. Second, the number of PCR cycles for amplification was dependent on the starting concentration of the sample as well. Samples with a starting mass of greater than 0.8ng were amplified using 15 cycles; 0.5 - 0.8 ng were amplified using 18 cycles; 0.2 - 0.5 ng were amplified using 20 cycles; N/A - 0.2 were amplified using 25 cycles. Fragmentation and tagging were performed in one step at 95C for 3 seconds. Amplification was performed with 15 - 25 cycles (per input mass above) of 95 for 20 seconds, 55 for 30 seconds, and 72 for 30 seconds, followed by the final elongation step at 72 for 5 min and a 10 second hold.

AmPureXP beads (1.8x volume) were used to select for a 300-500 bp insert size. Library concentration was assessed via Qubit, and quality and peak sizes were assessed via Agilent BioAnalyzer TapeStation. Peaks between 300 and 500 bp were determined as adequate for further processing and pooling of the sample. Samples with a large proportion of DNA greater than 1kb underwent a right-hand bead selection following the SPRI select protocol with minor modifications (Beckman Coulter B24965AA). The final pools had average concentrations of 20 ng/uL, 13.2 ng/uL and 12.5 ng/uL and an average size of 434, 480, and 481 base pairs respectively. Pools were shipped overnight on dry ice to the University of Columbia Genomics core. Sequencing was performed on NovaSeqS4 in Summer of 2022. Ten samples failed sequencing due to starting low concentration and were repeated on NexSeq via Applied Microbiome Science Laboratory at the Ohio State University, who both prepared and sequenced the libraries.

Amplicon Sequencing

Soil samples were obtained a from all four experimental phases: at the time of planting (P0), at the five-leaf stage (at the start of the imposed drought) (PI), at the end of the 10-day drought (PII), and at the end of the 10-day recovery period (PIII) (Charles et al., 2024a). Soil microbial (fungal + bacterial/archaeal) DNA was extracted from soil samples using the Zymo RNA/DNA co-extraction kit following manufacturer's instructions with minor modifications. Preparation of samples(n=96) for amplicon sequencing and the sequencing itself were performed at Argonne National Lab in Spring 2022 on Illumina MiSeq 250x250 PE in Spring of 2022. Raw data is stored on NCBI under BioProject PRJNA930014, and methods and results are reported in Mason et al 2024a.

RNA Processing

RNA samples from the start and end of the imposed drought were assessed for extraction quality via Qubit and Agilent Bioanalyzer. Average RIN was found to be 7.3. Library preparation was completed by Columbia Genomics Core in Summer 2022 using RNA RIBOZERO 40M PE100 kit. Briefly, cDNA was obtained from RNA samples after ribosomal depletion to remove rRNAs from total RNA. Sequencing was by the Columbia Genomics core on the ILLUMINA NOVASEQ 4000 instrument. Metatranscriptomes were assessed for quality using FastQC (Andrews, S. 2010), trimmed in Trimmomatic (v.0.3.6, Bolger et al., 2014) , and again assessed for quality in FastQC (Andrews, S. 2010)

Metagenomic Analyses

Raw reads from the OSS and Landscape gradient studies were assessed for quality using FastQC (Andrews, S. 2010), trimmed via BBDuk in BBTools (BBMap – Bushnell B. – sourceforge.net/projects/bbmap/), and then assessed for quality again in FastQC. Raw reads from the Simulated Drought experiment were trimmed in Trimmomatic (v.0.3.6, Bolger et al., 2014) (ILLUMINACLIP: TruSeq3-PE.fa: 2:30:10:2:True SLIDINGWINDOW:4:15 LEADING:3 TRAILING:3 MINLEN:36), and trimmed read quality was assessed again in FastQC. SingleM-v0.13.2 was used to generate de novo OTUs from raw metagenomic and metatranscriptomic reads using alignment to 59 single copy marker genes.

Taxonomic identity of raw metagenomes and metatranscriptomes defined via SingleM v0.13.2-pipe. These data were used to confirm enrichment of individual lineages

via LefSE (Segata et al., 2011). LefSE was also used to confirm enrichment of MAGs by treatment. Further statistical analyses were performed in the Phyloseq package in R 4.0.3 (McMurdie & Holmes, 2013; R Core Team, 2022). Permanova (adonis package) was used to determine statistical differences in community composition with original soil type (+/- shrub), drought, organic matter additions, and phase, using block or replicate as the random effect. Principal Coordinates Analysis (PCoA) was used to visualize these differences. Heatmaps were made using the R package Pheatmap in R 4.0.3. Differences in soil and plant chemistry, plant biomass , and PC category by treatment were evaluated via a wilcoxon signed rank test and a linear mixed effects model.

Metagenomic Assembly

All metagenomic samples were from OSS assembled using Megahit (v1.2.9) with default settings (Li et al., 2015). For OSS assemblies, unmapped reads were indexed via Bowtie2 v2.5.2 (Langmead et al., 2012), assembled via Megahit (v1.2.9), and these assemblies were combined with the original samples and deduplicated as needed via DeDupe (BBtools, Bushnell, n.d.). Trimmed metatranscriptomic reads were assembled in MetaSpades (v3.14.1), and Kraken (v2.1.2) (Wood et al., 2019) was used to verify that very little eukaryotic DNA was present in the assemblies. Quality of all assemblies was assessed using QUAST (v0.4.5) (Mikheenko et al., 2015). Abundance of trimmed reads mapped to assemblies was determined using CoverM (v0.6.1) (Woodcroft, 2022) with --min-covered-fraction 10 and the trimmed mean method as a means to further assess assembly quality. Functional annotations of all ORFs were performed in DRAM (Schaffer et al., 2020), and all proteins from both studies were clustered using the *mcl* Markov Cluster Algorithm (van Dongen, 2008) to produce ~1.6M protein clusters (PCs)

Metagenome Binning

Bins were ultimately obtained from three sources: long-term OSS study with in-house processing by the authors, long-term OSS study reads with processing completed at the Joint Genome Institute, and the Simulated Drought experiment metagenomic reads with in-house processing by the authors. Binning and refinement of OSS metagenomic assemblies was performed in MetaWRAP (Uritskiy et al., 2018) using Maxbin2 (v2.12.1) and Metabat2 (v2.2.7) with a minimum contig length of 500 bp. Bins were also obtained from the OSS metagenomes via the Joint Genome Institute standard metagenome analysis pipeline, using metaSPAdes assembler (v3.13.0) (Nurk et al., 2017) and MetaBat (v0.32.4) with a 3,000 bp minimum contig cutoff and parameter '-superspecific' for maximum specificity. Quality of all bins was evaluated in CheckM (v1.1.6) (Parks et al., 2014) , and bins that were > 70% complete and < 10% contaminated were retained (MIMAG, Bowers et al., 2017) and subsequently dereplicated to 95% ANI using dRep (v2.4.2) (Olm et al., 2017). Taxonomy was assigned to this set of dereplicated medium- and high-quality MAGs (n = 263) via the GTDB-tk v2.3.0 (Chaumeil PA, et al. 2022), and functional annotation of ORFs was performed in DRAM1 (Schaffer et al., 2020).

1180 medium (>70% complete, <10% contaminated, n= 819)and high quality (>90% complete, <5% contaminated, n= 361) MAGs were recovered from OSS assemblies (n=989 using in-house scripts, see Methods, and n=166 from the Joint Genome Institute pipeline), Simulated Drought experiment assemblies (n=25). These 1180 were then dereplicated at 95% ANI to a total 263 MAGs via DRep (Olm et al 2017). 8% of JGI derived MAG and 100% of MAGs derived from the chamber experiment formed their own clusters; i.e. these MAGs were not a subset of the field-

derived MAGs. taxonomy was assigned to this set of dereplicated medium- and high-quality MAGs (n = 263) via the GTDB-tk v2.3.0 (Chaumeil PA, et al. 2022), and functional annotation of ORFs was performed in DRAM (Schaffer et al., 2020). The 263 dereplicated MAGs represented an average of ~30% of the field site microorganisms at the genus level (47% of bacteria and 16% of archaea), and an average of 17% at the species level (25% of bacteria and 13% of archaea). In the Simulated Drought, these 263 MAGs represented an average of 27% (41% of bacteria and 14% of archaea)and 14% (18% of bacteria and 10% of archaea) of the microorganisms at the genus and species levels, respectively.

Viral Analyses

Reads from the OSS study were used to identify viral reads. dsDNA viral sequences are identified in two ways, first by the Virsorter2 using the suggested SOP (Guo et al., 2021; Guo,2020) and second by VIBRANT (Kieft et al., 2019). First, Virsorter2 version 2.2.3 is implemented with options "--keep-original-seq --include-groups dsDNAphage,ssDNA --min-length 5000 --min-score 0.5 all". The resulting predicted viruses are then used as input for CheckV version 0.8.1 and the associated databases (Nayfach et al., 2021) with options "end_to_end" to check for host or contaminating sequences. The curated viruses and proviruses from CheckV are then concatenated and used in a second round with Virsorter2 version 2.2.3 27 and options "--seqname-suffix-off --viral-gene-enrich-off --provirus-off –prep-for-dramv --include-groups dsDNAphage,ssDNA --min-length 5000 --min-score 0.5 all". A custom bash script is then used to implement the Virsoter2 curation SOP (Guo, 2020).

A resulting list of curated dsDNA viral sequences is then used with Seqtk version 1.3 (Li, 2022) and options “subset” to derive the final set of dsDNA viral sequences. Second, dsDNA viruses are also predicted using VIBRANT version 1.2.1 29 and default parameters. All dsDNA viruses predicted from the Virsorter2 SOP are then functionally annotated using DRAM version 1.3 (Schaffer et al., 2020) and DRAM-v.py with options “annotate”. dsDNA viruses predicted from VIBRANT are functionally annotated inherently and are not further annotated.

Curated dsDNA viral sequences from the Virsorter2 SOP, with unique identifiers, are concatenated into a single sequence file and used for population-level clustering with CheckV version 0.8.1 30 and a custom script that leverages BLAST+ (NCBI) with the scripts CheckV anicalc.py and aniclust.py, with options “--min-ani 95 --min-tcov 80”. The resulting dsDNA viral populations are then used as a reference for read recruitment using CoverM version 0.6.1-3 (Woodcroft, 2022) and options “--min-read-percent-identity .95 --min-read-aligned-percent .75 --min-covered-fraction .70 -m trimmed_mean” to derive a per population relative abundance table. dsDNA viral population sequences are then prepared for gene-sharing-network-based taxonomic clustering by first, using prodigal version 2.6.3 (Hyatt et al., 2020) and the options “-p meta” to predict protein-coding sequences. These proteins are then implemented in a custom bash script to prepare the required input file that maps proteins to contigs, for vConTACT2 (Bin Jang et al., 2019). VConTACT2 version 0.11.3 (Bin Jang et al., 2019) is then used to cluster the dsDNA viral populations into roughly genus-level clusters.

Data Records

Raw metagenomic and metatranscriptomic reads and their corresponding assemblies are available from JGI (in the case of the OSS study) and NCBI and are described in Tables 1 - 3. 1180 medium- and high-quality metagenome assembled genomes can be found via NCBI (), and raw reads and OSS viral and eukaryotic scaffolds are available at NCBI under biosample and genome accession numbers detailed in tables 1 - 3 (PRJNA928765: OSS, PRJNA90013 Landscape Gradient Study, PRJNA90014: Simulated Drought Experiment). MAG information (including contamination and completeness scores, taxonomy, and per-treatment enrichment), protein and genome annotations, lineage enrichment, and all data types listed in figure 4 are available at https://zenodo.org/uploads/8384851/.

Technical Validation

Data obtained from field and experimental sites were statistically sound, following a completely randomized block design (OSS) and a factorial design (Landscape Gradient study and Simulated Drought experiment). All DNA and RNA extracts were checked for quantity (via Qubit) and RNA extracts were all checked for quality via Agilent Bioanalyzer Tapestation. Average RIN was 7.3. Read quality was assessed via FastQC before and after trimming in BBDuk and Trimmomatic during which contaminant bases, adapter sequences and short reads were removed before assembly and binning. MAGs were checked for completeness and contamination in CheckM, per MIMAG guidelines, and only high and medium quality MAGs were selected for analysis.

Additionally, basic chemical analyses on soils and ecological analyses on single copy marker genes and PLFAs were performed to assess trends in community composition across studies and compare these trends with previous work at these sites. Soil chemical and microbial ecological trends observed in the three studies highlighted in this manuscript are similar to those observed in previous studies in this system (Supplemental Figures, Table S4).

Usage Notes

Preliminary metagenomic and PLFA results from the Landscape Gradient study, as well as PLFA results from the Long-term OSS experiment, both corroborate previous studies' results and provide opportunities for further hypothesis testing. For example, percent total soil C and N increase along the rainfall gradient and in the presence of shrub and are increased in the presence of shrubs in the north and central sites, but not the south (Fig S1). This follows results reported in Mason et al. (2023). Here, authors also reported a greater shrub impact on soil C and N in the Northern site, which had lower soil C, less annual rainfall, and increased sand content compared with the Central and Southern sites. They found that not only was millet fresh biomass significantly higher in the presence of shrubs at all sites as observed in many previous studies, but that the millet grown in shrub presence was not significantly different across sites at the time of harvest. They hypothesized that this was, in part, because there is a "threshold" of low-C, low-moisture conditions at which the shrub's presence provides an ameliorative effect - one that was not observed at the more moist, higher C soils to the south. However, in samples obtained from the 2019 - 2020 field campaigns, millet height and fresh biomass at time of harvest was not significantly impacted by shrub presence, which is not consistent with

previous findings at these sites (Mason et al., 2023) and results from other intercropping studies in the region (Bright et al., 2017; 2021), prompting further research.

PLFAs were also extracted from millet rootzone and bulk soil from the dry and rainy seasons. Total fungal PLFA abundances were significantly higher in the presence of the shrub ($P< 0.008$), significantly higher at central sites (Central vs Northern, $P< 0.0001$; Central vs Southern, $P< 0.03$) and were significantly higher in millet root zones during the rainy season ($p = 0.00465$) compared with bulk soil. The total bacterial PLFA increase in the presence of shrub ($p=0.0321$), are significantly higher in the dry season than the rainy season ($P< 0.005$), and trended higher in the millet root zone soil than in the bulk soil during the rainy season ($P< 0.06$). Total bacteria were significantly lower in the north sites than the south sites ($p = 0.0130806$) and trended lower in the north site compared with the central sites ($P< 0.08$). Surprisingly, total PLFAs were higher in the dry season ($P< 0.0005$), although there was no significant difference in their abundance by latitude or shrub presence (Figure S2).

Single copy marker gene OTUs were obtained in the rainy and dry season from bulk soil, rhizosphere soil, and from within the rows in which millet had grown as a proxy for the rhizosphere or rooting zone soil during the dry season. Across all sample types and sites, shrub presence and compartment contributed most to the variance in the community ($P< 0.04$ and 0.008, respectively), although the data were highly variable (beta disper by shrub = 0.0240). No differences in Shannon's H diversity, Peilou's J evenness or richness were observed. Unexpectedly, clustering by longitude was also observed overall and in the north and central sites ($p = 0.023$), although this data is also highly variable (beta disper p by longitude = 0.04288). This longitudinal clustering can

be observed at the north sites, where samples significantly cluster by longitude (R^2=0.16, P< 0.001), shrub presence (R2=0.058, P< 0.05), and the interaction between the two (R^2= 0.06, P< 0.04). Longitudinal clustering can be observed in the central sites (R^2= 0.12, P< 0.002), although no clustering was apparent with shrub presence. Longitudinal differences were slight at the south sites (P< 0.09) (Figure S3).

The significant impact of longitude on community composition was surprising, and also seemed to vary with latitude. Shrub presence and latitude significantly impacted community composition in the east sites (R^2 = 0.06, P< 0.01) (R^2=0.10, P< 0.007). However, shrub presence was not a significant driver of community composition variance in the west, although latitude (R^2=0.12, P< 0.004) and sample type were (R^2=0.11, P< 0.02). Across all sites, in the rainy season bulk soil there was an east/ west difference (R^2=0.089, P< 0.05) but not a landscape difference or a difference +/- shrub. In the rainy rhizosphere, there was no difference +/- shrub or by latitude or longitude. In the dry soil and in the millet rhizosphere, the interaction between latitude and longitude was a significant driver of community composition (R^2=0.21, P< 0.002 & R^2= 0.20, P< 0.02), , but there was no difference +/- shrub nor latitude and longitude on their own. East and west sample differences were then calculated by compartment. In the East, no differences in the rhizosphere lineage composition were observed in the rainy season, and in the dry season millet rooting zone, there was a trend towards a significant shrub effect (R^2=0.20, P< 0.09). In the West sites, there was no difference in either the dry or rainy rhizosphere soils (Figure S4).

Mason et al., (2023) reported that the impact of the shrub on millet growth and on the microbial community composition was strongest in the north, and that shrub effect

appeared to diminish along the rainfall and soil type gradient, although differences in method (amplicon sequencing vs single copy marker gene) cannot be disregarded. However, this longitudinal divergence is of particular interest, as it has been previously hypothesized that there is a "threshold" of nutrient status and water availability, below which shrub presence exercises greater control over microbial community composition (Mason et al., 2023). In Senegal, temperatures tend to increase inland (West to East), potentially creating a less favorable environment for millet growth. However, the exact growing-season climatic trends could not be obtained at the granularity necessary to make this comparison. Further research is needed to both confirm the threshold hypothesis and to thoroughly investigate these longitudinal differences as both could have implications for agricultural management.

Preliminary PLFA results from the Long-term OSS study also offer opportunities for future research. In +OSS plots, percent total soil C and N were higher ($P< 0.001$ and $P< 0.03$, respectively), and millet plants were significantly taller and had greater fresh biomass at time of sampling with intercropping ($p<0.01$) (Mason et al., 2024b) (Figure S5). Results are consistent with previous findings (Diedhiou-Sall et al., 2009; Dossa et al., 2012, 2013, Bright et al., 2021) and emphasize the predictable effects of long-term shrub intercropping on millet and soils.

Intercropped soils from the 2019- 2020 sampling season also displayed higher amounts of total PLFAs ($P< 0.01$), consistent with previous findings (Diedhiou-Sall et al, 2009). In the rainy season, millet root zone soil tended to have higher abundances of total PLFAs. Sample type also significantly impacts total PLFA abundances ($P< 0.001$) (Figure S5). This trend is repeated across total bacterial, total fungal, and actinomycetes

markers in the OSS samples from the 2019 -2020 sampling season. However, in contradiction to findings reported in Diedhiou et al., (2009), the Gram+/Gram- ratio tended to be lower in the presence of the shrub. This may indicate that the community supported by the shrub may be actually be less resilient to stress and disturbance than -shrub communities, as Gram+ organisms have been found to be more resilient (de Vries & Shade, 2013; Qiao et al., 2020). This supports previous hypotheses about the -OSS microbial community possibly being composed of a community of 'persisters' composed of fungi and gram+ organisms (Mason et al.,2024a; 2024b).

There were also significantly higher amounts of total PLFAs found in the dry season soils than both the rainy season soil and the millet root zone soils ($P < 0.0001$ and 0.01, respectively). Total bacterial PLFA and total fungal PLFAs follow the same trend, with dry season soils having the highest abundances of PLFA ($P < 0.0001$). This finding contradicts previous research in this field that dry-season soils are less supportive of microbial communities (Deng et al., 2017; Diedhiou-Sall et al., 2021). Further, dry season bulk soil (the soil not underneath the shrub canopy or within the millet rhizosphere zone) displayed the greatest difference in G+/G- ratios between + and -OSS samples, with the -shrub soils containing higher G+/G- ratios. This difference further supports our 'persisters' hypothesis; it is possible that the -shrub community, containing hardy fungi and gram+ bacteria, remains active during times of stress while the +shrub copiotroph community dies off, resulting in relatively higher numbers of PLFAs in the dry season. The increased abundance of total PLFAs in the 2020 dry season may indicate the presence of a persistent microbial community, laying dormant, but alive, during the

dry season. This interesting finding should be further investigated to corroborate these results in other ecosystems.

Taken together, the preliminary results from the 2019 - 2020 field campaigns and the Simulated Drought experiment both corroborate previous results on the OSS and in actively farmed fields of the Landscape Gradient study, provides more in-depth analysis from the meta'omic analyses provided here. Further analyses of this dataset may include, and not limited to, in-depth characterization of important MAGs and their interactions with the surrounding microbial community, the millet plant and the shrub as well as characterizing genes related to C and N cycling. Microbial genes and processes related to C sequestration are also of special interest as soils in this region are sandy and particularly degraded. Soils in the close proximity to shrubs have consistently shown higher quantities of total C and POM, even without the incorporation of shrub organic matter (e.g. Lufafa et al., 2008; Mason et al., 2023; Bright et al., 2021). It is likely that shrub residues play a major role in driving microbe-microbe and microbe-plant interactions. This is especially relevant for the datasets obtained from the Landscape Gradient study, as the preliminary results suggest a "threshold" level of poor nutrient status and water availability that allows for the dramatic results of intercropping (Mason et al 2023).

The physical mechanisms behind millet responses to treatments are also of interest. A curious finding of the Simulated Drought experiment was that the soil in both + and – OSS plots became severely dry and by 12 days after the water was stopped the water potential was -3 MPa, well below the permanent wilting point. Yet somehow the presence. *G. senegalensis* made enough water available to enable the millet to reach

maturity and produce a yield that did not happen with sole millet. This leads to the one of the fundamental questions of this work: “how can such small amounts of HL water be delivered so efficiently that millet is able to keep growing?” It has been hypothesized that the microbial community plays an important role, through antioxidant, exopolysaccharide, and osmolyte production and phytohormone manipulation, as proposed by Mason et al. (2024b). However, other factors may be at play, specifically, the direct transport of water between the shrub and the millet via mycorrhizae. This hypothesis has proven difficult to directly test in this agroecosystem (M.B.H Bright, unpublished data), although Bogie et al (2018) showed that water was indeed directly transferred from the shrub to the crop. Finally, it has been previously observed that fertilization has a great impact on millet growth. The growth rate increases exponentially with fertilizer up to 1.5X recommended NPK used in the OSS (Bright et al., 2021), indicating that studying shrub-crop-microbe-fertilizer is a potential area of future research.

Further ecological studies could include determining the identity and function of the millet endosphere and the viral community, as little work has been done on these topics. This is especially true in terms of the ecological role of the viral community in semi-arid soils. Also, the curious finding that the dry season PLFAs are in higher abundance necessitates further study as it contradicts other research. Finally, although trends +/- shrub are the same across studies, there is limited overlap between their lineage, PC, and MAG composition (Figure S6). Further research is needed to understand why this might be. These discrepancies may derive from differences in sequencing depth (5G/sample in Landscape Gradient and Simulated Drought experiment vs 20G/ sample in

OSS) or limited sample numbers (for example, the 2 replicates in the Landscape Gradient study). It is also possible that these communities are quite different in each study as, is common in the sandy, low biomass soils of the Sahel (Dossa et al., 2012; Bright et al., 2021; Lui et al., 2022)., portions of the community may lay dormant for some time, only to reestablish with, for example, an extra boost of organic matter or watering.

Code Availability

No custom code has been used to generate or process this dataset.

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Author Contributions

Each author’s contribution to the work should be described briefly, on a separate line, in the Author Contributions section.

L.M.Mason:project design, sample collection, MAG generation, data analyses, Simulated Drought experiment design, main author for text

Ibrahima Diedhiou: Program director at ENSA, management of OSS fields

Christine C. Charles: sample collection and processing for Simulated Drought experiment

Afaf Abdelrahim: data analysis

Dylan Cronin: bioinformatics support and guidance

Dean R. Vik: Viral analyses, metagenome assembly, bioinformatics support and guidance

Nicola Lorenz: Laboratory support and guidance

Yueh-Fen Li: Laboratory support and guidance

Richard P.Dick: Direct mentorship of L.M.Mason, project design, lab space, long term project management

Virginia I. Rich: Direct mentorship of L.M.Mason, project design

Competing Interests

The authors report no conflict of interest

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Table 5.1. Sample numbers, locations, and sources collected for the Landscape Gradient Study in August 2019 (rainy season) and March 2020 (dry season)

Table 5.1. Sample numbers, locations, and sources collected for the Latitudinal Gradient Study in September 2019 (rainy season) and March 2020 (dry season)

Season	Shrub	Location	Millet Rhizosphere				Bulk Soil			Millet
			4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	
Rainy	Shrub	North	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		Central	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		South	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
	No Shrub	North	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		Central	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		South	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
Dry	Shrub	North	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		Central	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		South	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
	No Shrub	North	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		Central	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		South	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	8 biomass
		Totals	48 MetaG	48 PLFA	48 C:N	48 MetaG	48 PLFA	48 C:N	96 biomass
		Citation:	2019/2020: PRJNA90014; 10.5281/zenodo.8333016 2012: Mason et al., 2023			2019/2020: PRJNA90014; 10.5281/zenodo.8333016			

Table 5.2. Sample numbers, locations, and sources collected for the OSS Study in September 2019 (rainy season) and March 2020 (dry season)

Season	Shrub	Fertilizer	Millet Rhizosphere			Bulk Soil			Millet Endosphere	Millet plant
			4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N		
Rainy	Shrub	0NPK	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	4 metaG	8 biomass
		1NPK	4 MetaG	4 PLFA	4 C:N	4 MetaG	4 PLFA	4 C:N	4 MetaG	8 biomass
	No Shrub	0NPK	4 metaG	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	4 metaG	8 biomass
		1NPK	4 MetaG	4 PLFA	4 C:N	4 MetaG	4 PLFA	4 C:N	4 MetaG	8 biomass
Dry	Shrub	0NPK	0	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	0	
		1NPK	0	4 PLFA	4 C:N	4 MetaG	4 PLFA	4 C:N	0	
	No Shrub	0NPK	0	4 PLFA	4 C:N	4 metaG	4 PLFA	4 C:N	0	
		1NPK	0	4 PLFA	4 C:N	4 MetaG	4 PLFA	4 C:N	0	
		Totals	16 metaG	32 PLFA	32 C:N	32 metaG	32 PLFA	32 C:N	16 metaG	32 plants
		Citation	Mason et al 2024b, PRJNA928765, 10.5281/zenodo.8332973							

Table 5.3. Sample types and numbers obtained from the Simulated Drought experiment

Sampling Location	Phase				Total samples	Citation
	Planting	Growth	Drought	Recovery		
Millet rhizosphere microbiome	24 16S iTags; 24 ITS iTags;	24 16S iTags; 24 ITS iTags;	24 16S iTags; 24 ITS iTags;	24 16S iTags; 24 ITS iTags	144 16S iTags, 144 ITS iTags	Mason et al, 2024a, PRJNA930013
		24 paired metaG/metaT	24 paired metaG/metaT		48 paired metaG/metaT	Mason et al 2024b, PRJNA930013
	24 PLFA	24 PLFA	24 PLFA	24 PLFA	144 PLFA	Charles et al 2024b, 10.5281/zenodo.8333110
		24 microbial extracellular enzyme activity (EA)		24 EA	48 EA	Charles et al 2024b, 10.5281/zenodo.8333110
		24 short chain fatty acids (SCFA)	24 SCFA		48 SCFA	10.5281/zenodo.8333110
Millet above ground biomass		24 chlorophyll content;	24 chlorophyll content	24 chlorophyll content;	72 Chlorophyll content	Charles et al 2024a, 10.5281/zenodo.8333110
		24 soluble sugar	24 soluble sugar	24 soluble sugar	72 soluble sugar	
		24 Glycine Betaine	24 Glycine Betaine	24 Glycine Betaine	72 Glycine Betaine	
Millet below ground biomass				24 biomass C:N	24 biomass C:N	Charles et al 2024a, 10.5281/zenodo.8333110
				24 root structure scans	24 root structure scans	
Rhizosphere soil nutrient	12 C:N	24 Anions concentration		24 Anions concentration	Anions: 48	Charles et al 2024a, 10.5281/zenodo.8333110
		24 plant available N		24 plant avail-N	Plant avail N: 48	
					C:N 12	

Figure Legends

Figure 5.1. Millet-shrub intercropping induces a significant increase in millet yield and drought resilience. (a) Photograph of millet at the long-term Optimized Shrub-Intercropping System (OSS) study site during the growing season (credit: MBH Bright); non-intercropped plots (-shrub) have reduced biomass and yields compared with intercropped plots (+shrub). Aboveground shrub biomass is not present because in the Optimized shrub-Intercropping System, shrubs are coppiced and tilled into surface soils annually, increasing soil nutrients and C. In typical farmers' fields in the region, coppiced material is burned instead, often off-field. This picture shows millet growth response to OSS in a low rainfall season of 2016 when total rainfall was ~200 mm below the long-term average for this site.(b) Diagram of belowground differences +/-shrub; hydraulic lift (HL; blue arrow) by the shrub exerts a zone of influence on the surrounding soil, supplying a small amount of water to the millet plant and supporting a distinct and active microbiome with greater microbial biomass (cartoon microbial cells indicated). HL occurs in +shrub conditions even when shrubs are coppiced, and here, coppiced material is shown on the soil surface.

Figure 5.2. Experimental datasets examining shrub-crop-microbiome interactions, building on >two decades of soil and agronomic research development and characterizing the Optimized Shrub-Intercropping System. These datasets are the first to include metagenomics (all locations) and metatranscriptomics (Simulated Drought experiment). (a) The location of the seven field sampling sites in the Peanut Basin of the West African country of Senegal. Sites A - F are the on-farm Landscape Gradient study

sites, located in the Louga (North), Fatick (Central), and Kaolack (South) regions, each with a western and eastern site. Site OSS is the long term experimental site (the Optimized Shrub-intercropping System) near Thies. Top inset: location of Senegal and the Sahel region. Bottom inset: GPS coordinates of the sampling locations. Images from Google Maps. (b) Key Questions: The Landscape Gradient, OSS site, and derived Simulated Drought experiment represent 3 nested spatial scales targeting complementary questions about shrub-crop-microbiome interactions.

Figure 5.3. The sampling and experimental designs at each spatial scale, to capture proximity to shrub ("+/- shrub") for two sample types - millet rhizosphere versus bulk soil - with millet endosphere included at the OSS site. Additional details on sample numbers are in Tables 1-3. (a) Landscape Gradient Study sampling. Top: Rainy Season. At each site, 2 shrubs were targeted, and "+shrub" sampling locations were identified <1 m from shrub base, with "-shrub" locations 3 - 4 m from shrub base, outside the influence of the shrub. Bulk soil samples were taken via triplicate cores at each of four locations (shrub 1, +/- shrub, and shrub 2, +/- shrub). Millet rhizosphere/rootzone samples were collected by removing two entire plants for each of four 'treatments' (+/- shrub relative to shrub 1, and +/- shrub relative to shrub 2) and sampled as described in Methods for different uses. Bottom: Dry Season. Samples were collected from the same fields and locations, and the same four treatment variants and two sample types, again at two replicated locations per shrub. As millet is not grown in the dry season, 'millet' cores were taken in the rows where the millet had been grown, and bulk soil samples were collected in between millet rows; the rhizosphere sampling of an entire millet plant was

replaced by combining triplicate cores. Arrows indicate sampling locations.
(b) OSS study site sampling. Top panel: Rainy Season. Samples were collected from +/- OSS plots, from sample types: bulk soil, via triplicate cores, and millet rhizosphere and endosphere in duplicate, by removing the entire plant. This was repeated in each of 4 replicate treatment plots: 4 +OSS, 4 -OSS , as well as 4 of each with 1X fertilizer treatment (not shown) Bottom panel: Dry Season. Samples were collected from +/- OSS plots targeting bulk soil via triplicate cores at the same locations. Arrows indicate sampling location. (c) Simulated Drought Experimental design. +/- OSS soils, and dried shrub residues, were transported from the OSS field site to the Ohio State University for a Simulated Drought experiment, to decouple the impact of the the living shrub from its legacy effect on the soil and microbiome, and the impact of ongoing shrub-derived organic matter input. Three replicates each of four treatments (+OSS soil /+ shrub residue; +OSS soil /- shrub residue; -OSS soil /+ shrub residue; and -OSS soil /- shrub residue) were established and sampled at four time points: planting, growth, end of imposed drought, and recovery).

Figure 5.4. Overview of sample types collected and meta-omic analysis pipeline, across the 3 nested scales of these data. In the field studies, millet was characterized via aboveground height, biomass, and yield, and rhizosphere and bulk soil were characterized via total C & N, phospholipid fatty acid analysis (PLFA), and metagenomics. In the OSS, belowground millet root endosphere microbiota were also metagenomically sequenced. In the Simulated Drought experiment, aboveground millet was characterized more deeply, via height, biomass, and the content of chlorophyll, glycine betaine, and soluble

sugar. Additional information on sample numbers can be found in tables 1 - 3. Belowground millet were characterized by root length, width, biomass, and total C & N. Soil was characterized via total C and N, plant-available N, macro- and micronutrients, short-chain fatty acids (SCFAs), PLFAs, extracellular enzyme analysis (EEAs), amplicon sequencing of the 16S rRNA gene and the ITS2 region, metagenomics, and metatranscriptomics. In the meta-omic analysis pipeline, raw reads were used to identify microbiome composition via SingleM, from which differential abundances by treatment were characterized. Raw reads were also QC'd and assembled. Assemblies of the OSS metagenomes and Simulated Drought experiment metatranscriptomes were used to create protein clusters (PCs) via a Markov Clustering Algorithm. Assemblies of the OSS and Simulated Drought experiment metagenomes were also binned via MetaWrap and the [JGI pipeline], and assessed for contamination and completeness in CheckM. (Choices of which meta-omes to use for which products were made empirically based on dataset performance.) The resulting 1180 metagenome-assembled genomes (MAGs) that were >70% complete and <10% contaminated (per MIMIAG guidance) when then dereplicated to 95% (n= 263). MAG information and all data products listed in this figure are available at https://zenodo.org/uploads/8384851/. Raw metagenomes, metatranscriptomes, and viral and eukaryotic contigs are available via NCBI under the following accessions: PRJNA90014 (Landscape Gradient), PRJNA928765 (OSS), PRJNA90013 (Simulated Drought experiment).

Figure 5.5. Data quantity, quality and validation. (a) Number of post-QC reads per study , +/- OSS. Reads were quality checked in FastQC, and then trimmed via Trimmomatic

(Simulated Drought experiment metagenomes and metatranscriptomes and Landscape Gradient study) or BBDuk (OSS). (b)-(e) Per Sequence Quality metrics for OSS, Landscape Gradient Study, and Simulated Drought experiment metatranscriptomic and metagenomic datasets, respectively. Data were trimmed to remove adapters and low quality sequences via BBDuk and Trimmomatic before QC'd in FastQC. On each plot, the x-axis is the mean Phred score (0 - 35) and the y-axis is the number of sequences.

Figures

Figure 5.1. Millet-shrub intercropping induces a significant increase in millet yield and drought resilience.

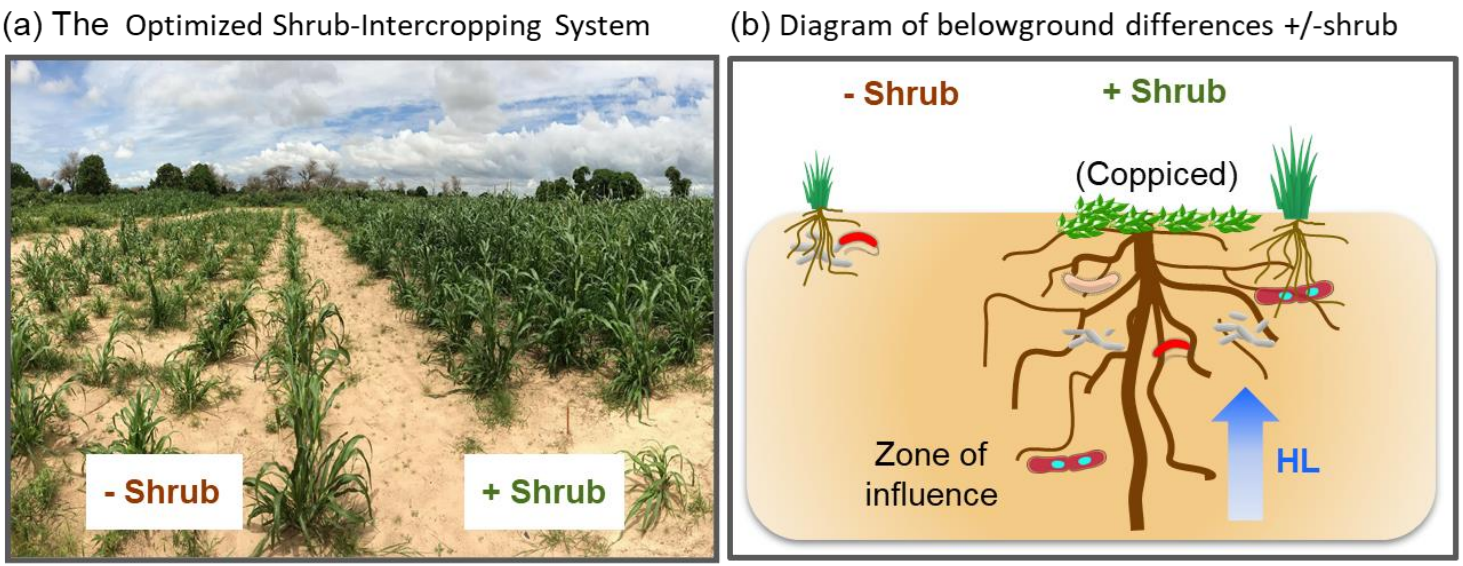


Figure 5.2. Three experimental datasets investigating shrub-crop-microbiome interactions

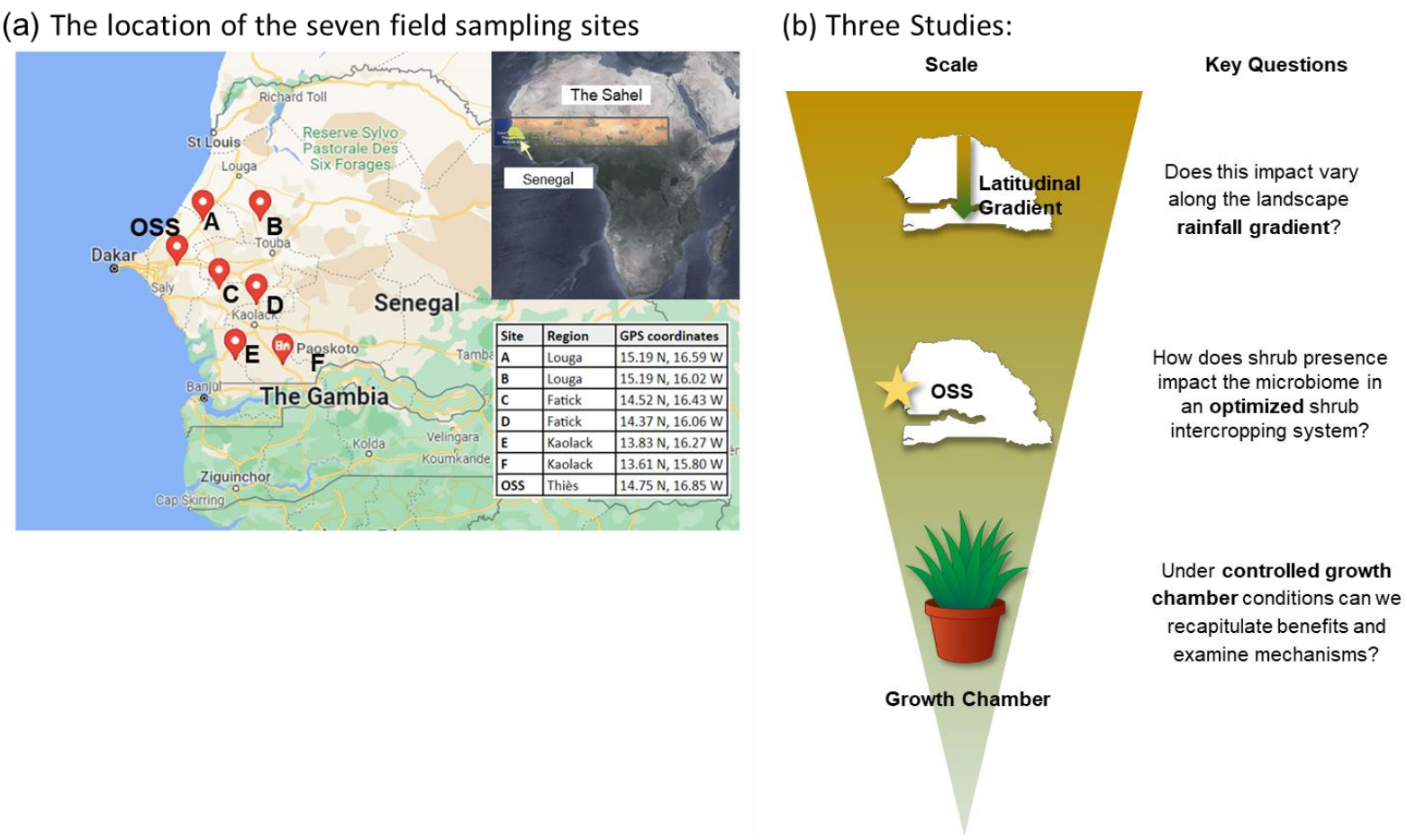


Figure 5.3. Sampling and experimental designs

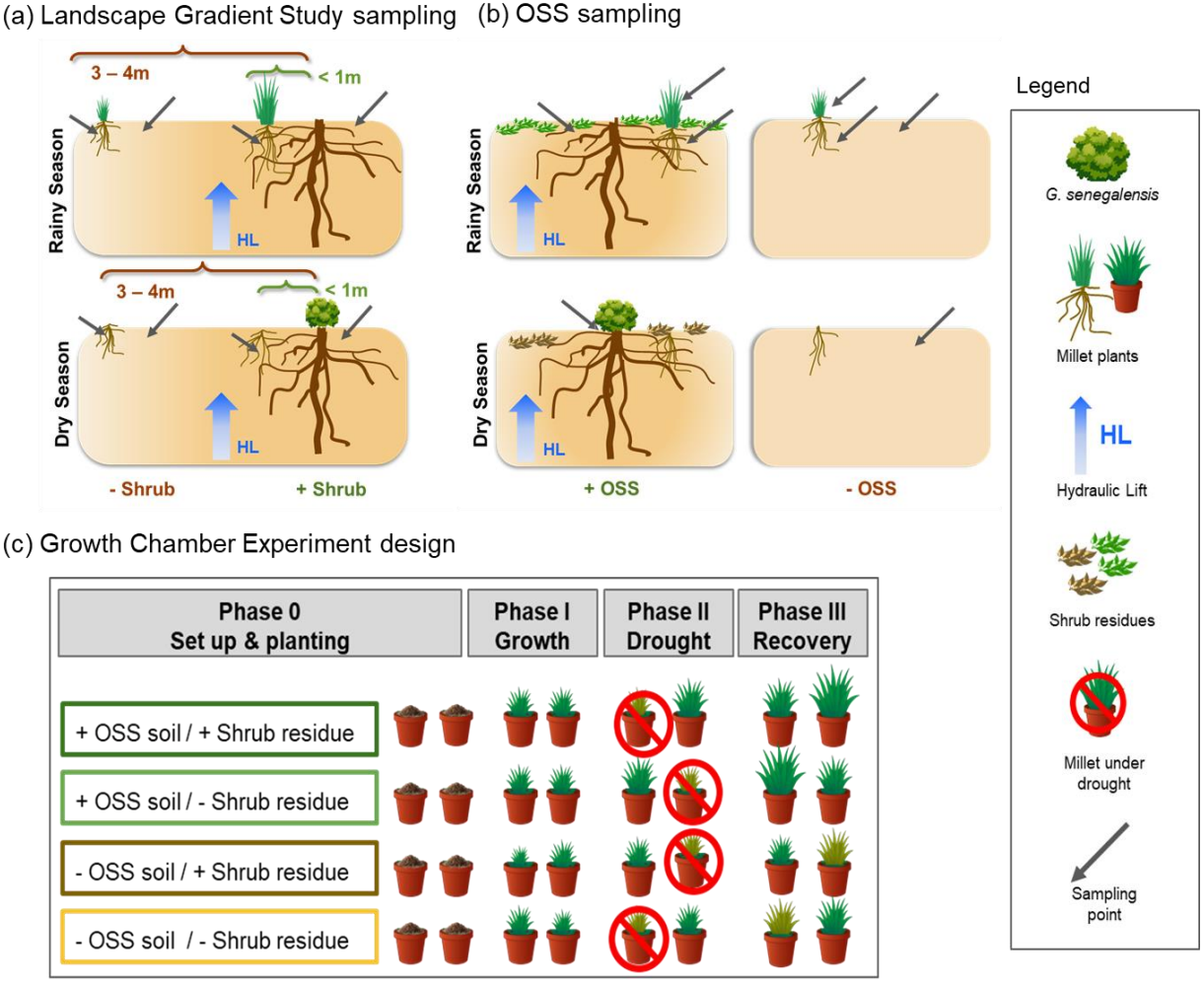


Figure 5.4. Sample types collected and bioinformatics analysis workflow.

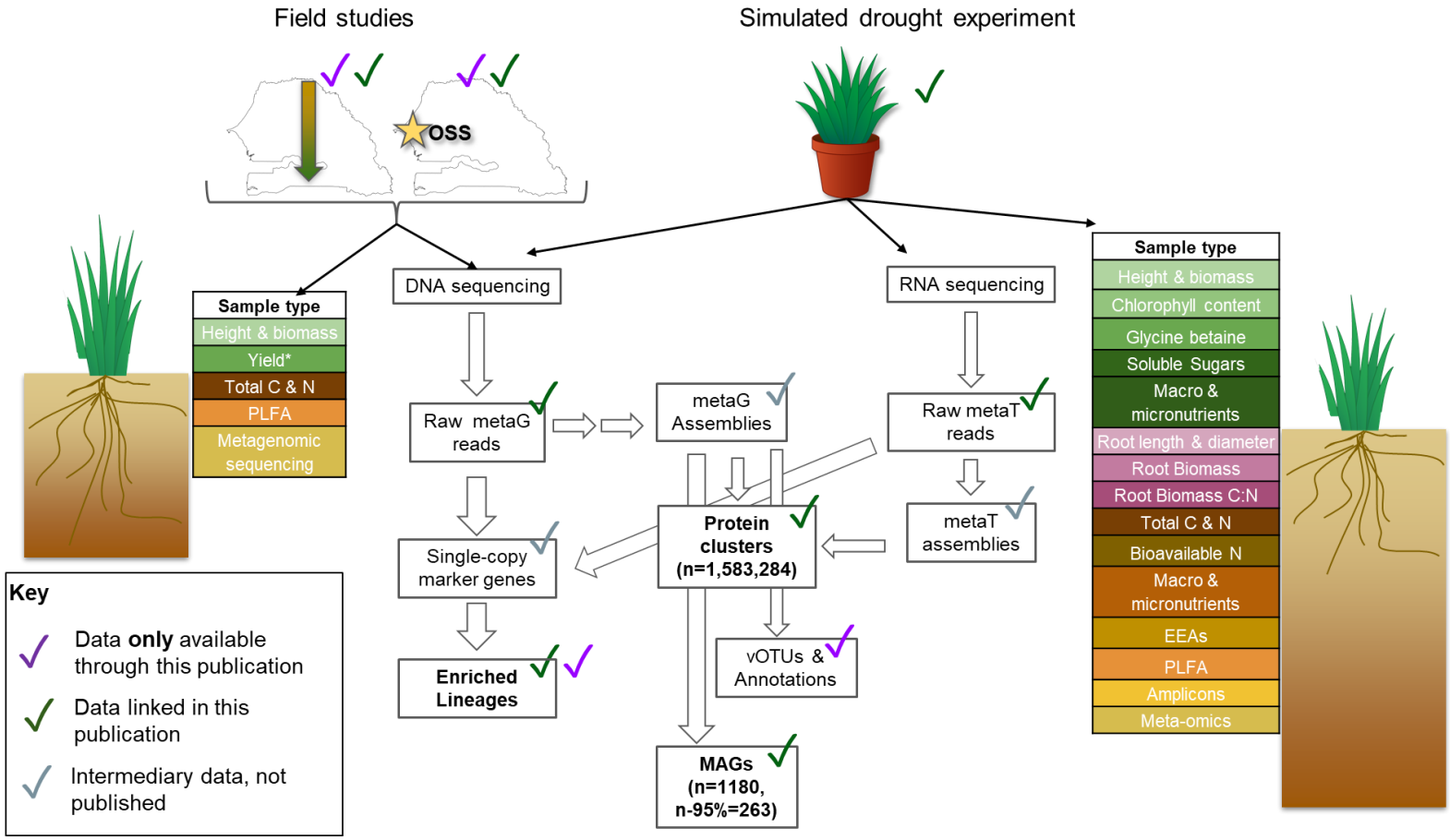
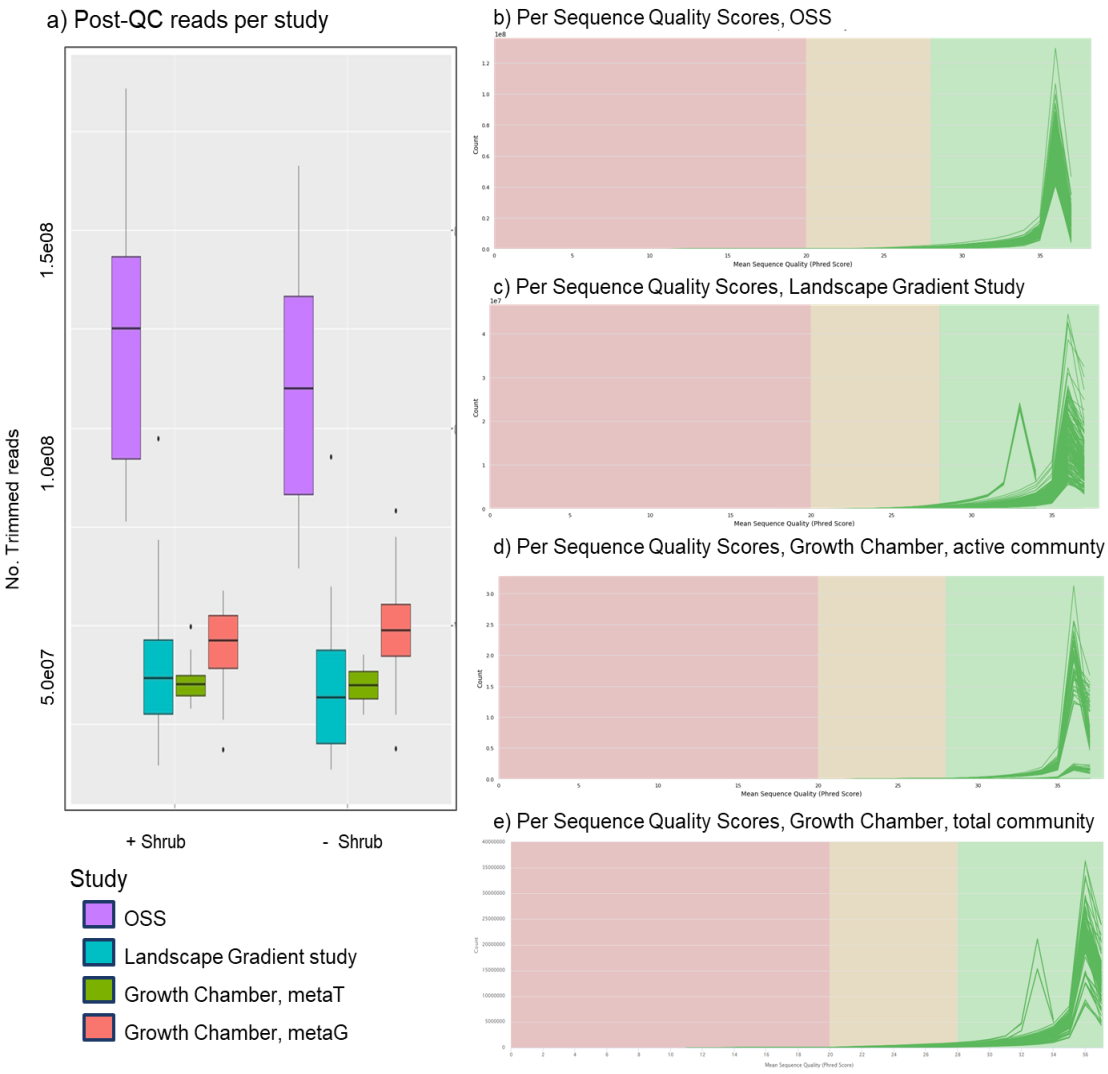


Figure 5.5. Post QC read counts and per sequence quality scores



Supplemental Tables

Table S5.1. Enriched Lineages in the Landscape Gradient Study

Enriched lineages from other studies can be found in Chapter 4 Table S4

Taxonomy	log(mean)	enriched	LDA	mean	site	Sample Type
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales	2.946773	noShrub	2.560645	0.033895	central	dryRhizo
d__Bacteria_p__Gemmatimonadota_c__Gemmatimonadetes_o__Gemmatimonadales	2.551217	noShrub	2.299464	0.020921	central	drySoil
d__Archaea_p__Thermoproteota_c__Nitrososphaeria_o__Nitrososphaerales_f__Nitrososphaeraceae_g__Nitrosocosmicus	2.135725	noShrub	2.016296	0.033895	central	rhizo
d__Archaea_p__Thermoproteota_c__Nitrososphaeria_o__Nitrososphaerales_f__Nitrososphaeraceae_g__Nitrososphaera	3.033652	noShrub	2.598427	0.033895	central	rhizo
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae	2.62968	noShrub	2.245785	0.033895	central	rhizo
d__Bacteria_p__Acidobacteriota_c__Vicinamibacteria_o__Vicinamibacterales	2.610557	noShrub	2.2614	0.033895	central	rhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__GMQP_bins7	2.080822	noShrub	2.019678	0.033895	central	rhizo
d__Bacteria_p__Chloroflexota_c__Chloroflexia_o__Chloroflexales	2.455533	noShrub	2.11871	0.033895	central	rhizo
d__Bacteria_p__Chloroflexota_c__Chloroflexia_o__Chloroflexales_f__Roseiflexaceae_g__JADKFS01	2.387016	noShrub	2.146122	0.019254	central	rhizo
d__Bacteria_p__Chloroflexota_c__UBA6077_o__UBA6077	2.306342	noShrub	2.148002	0.032313	central	rhizo
d__Bacteria_p__Cyanobacteria_c__Cyanobacteriia_o__Cyanobacteriales	2.528984	noShrub	2.216048	0.032313	central	rhizo

d__Bacteria_p__Firmicutes_c__Bacilli_o__Bacillales_B_f__DSM_18226_g__Neobacillus	2.550995	noShrub	2.042147	0.033895	central	rhizo
d__Bacteria_p__Planctomycetota	2.63621	noShrub	2.200253	0.033895	central	rhizo
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Pirellulales	2.224891	noShrub	2.011895	0.033895	central	rhizo
d__Bacteria_p__Chloroflexota_c__Anaerolineae	2.741224	noShrub	2.05147	0.043308	central	soil
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.172792	shrub	2.607503	0.043308	central	drySoil
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Pirellulales	2.227002	shrub	2.002402	0.01796	central	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Jatrophihabitantaceae_g__Jatrophihabitans	2.322174	shrub	2.06424	0.038394	central	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptomycetales_f__Streptomycetaceae_g__Streptomyces	3.05015	shrub	2.338359	0.020921	central	soil
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales	2.862771	shrub	2.5488	0.014306	north	dryRhizo
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__Acidobacteriaceae	2.441398	shrub	2.45484	0.010515	north	dryRhizo
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__SbA1	2.446392	shrub	2.271212	0.013903	north	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__JAFAQI01_g__JAFAQI01	2.700528	shrub	2.447908	0.024947	north	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Jatrophihabitantaceae	2.352138	shrub	2.352894	0.013903	north	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae	3.330328	shrub	2.883302	0.014306	north	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.083118	shrub	2.754713	0.014306	north	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739	3.30246	shrub	2.955385	0.014306	north	dryRhizo
d__Bacteria_p__Chloroflexota_c__Ktedonobacteria_o__Ktedonobacterales_f__Ktedonobacteraceae	2.55613	shrub	2.377879	0.012725	north	dryRhizo

d__Bacteria_p__Myxococcota_c__Myxococcia_o__Myxococcales	2.423005	shrub	2.189239	0.027486	north	dryRhizo
d__Bacteria_p__Proteobacteria	2.724129	shrub	2.434811	0.046251	north	dryRhizo
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Bryobacterales_f__Bryobacteraceae	2.970302	shrub	2.474109	0.020921	north	rhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__70_9	2.643102	shrub	2.07155	0.020921	north	rhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Palsa_465	3.364099	shrub	2.883712	0.043308	north	rhizo
d__Bacteria_p__Patescibacteria	2.484196	shrub	2.056323	0.020165	north	rhizo
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Isosphaerales_f__Isosphaeraceae	2.582533	shrub	2.058399	0.020921	north	rhizo
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__ATCC43930_f__Stellaceae_g__AP_15	2.452045	shrub	2.01453	0.043308	north	rhizo
d__Bacteria_p__Actinobacteriota_c__Acidimicrobiia	2.591734	shrub	2.179469	0.042066	north	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Geodermatophilaceae	2.948319	shrub	2.471562	0.043308	north	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Propionibacteriales	2.533284	shrub	2.124455	0.020165	north	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptomycetales_f__Streptomycetaceae	2.467569	shrub	2.111666	0.020165	north	soil
d__Bacteria_p__Acidobacteriota_c__Acidobacteriae_o__Acidobacteriales_f__Acidobacteriaceae_g__Terracidiphilus	2.467471	shrub	2.174901	0.021947	south	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__Palsa_744	2.605319	shrub	2.235486	0.03895	south	dryRhizo
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Solirubrobacteraceae_g__VAWY01	2.114064	shrub	2.065253	0.017202	south	dryRhizo
d__Bacteria_p__Chloroflexota_c__Anaerolineae	2.655546	shrub	2.221823	0.024481	south	dryRhizo

d__Bacteria_p__Myxococcota_c__Polyangia_o__Palsa_1104_A_f__Fen_1088	2.176149	shrub	2.058186	0.017202	south	dryRhizo
d__Bacteria_p__Acidobacteriota_c__Blastocatellia	2.20124	shrub	2.224667	0.020165	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Microbacteriaceae	2.795331	shrub	2.429149	0.020165	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Micrococcaceae	2.45995	shrub	2.13511	0.042066	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Geodermatophilaceae	2.884539	shrub	2.414922	0.043308	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__JAFAQI01_g__JAFAQI01	2.607614	shrub	2.30727	0.020165	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Mycobacteriaceae	2.494467	shrub	2.188956	0.020921	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Mycobacteriaceae_g__Mycobacterium	3.028083	shrub	2.552218	0.042066	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Mycobacteriales_f__Pseudonocardiaceae_g__Actinomycetospora	1.678621	shrub	2.064179	0.047221	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Propionibacteriales_f__Nocardioidaceae	2.845234	shrub	2.349028	0.043308	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Propionibacteriales_f__Nocardioidaceae_g__Nocardioides	3.307372	shrub	2.826324	0.020921	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Streptosporangiales_f__Streptosporangiaceae	3.181566	shrub	2.656589	0.020921	south	drySoil
d__Bacteria_p__Bacteroidota_c__Bacteroidia_o__Chitinophagales_f__Chitinophagaceae	2.68795	shrub	2.301818	0.020921	south	drySoil
d__Bacteria_p__Firmicutes_c__Bacilli	2.76612	shrub	2.269886	0.020921	south	drySoil
d__Bacteria_p__Firmicutes_c__Bacilli_o__Bacillales_B_f__DSM_18226_g__Neobacillus	2.422917	shrub	2.212943	0.042066	south	drySoil

d__Bacteria_p__Gemmatimonadota_c__Gemmatimonadetes_o__Gemmatimonadales_f__GWC2_71_9	2.499499	shrub	2.172387	0.020165	south	drySoil
d__Bacteria_p__Myxococcota_c__Polyangia_o__Polyangiales	2.304022	shrub	2.08021	0.042066	south	drySoil
d__Bacteria_p__Myxococcota_c__Polyangia_o__Polyangiales_f__Polyangiaceae	2.765981	shrub	2.326223	0.020165	south	drySoil
d__Bacteria_p__Planctomycetota_c__Phycisphaerae	2.392432	shrub	2.162073	0.042066	south	drySoil
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Gemmatales_f__Gemmataceae	3.114613	shrub	2.612638	0.042066	south	drySoil
d__Bacteria_p__Planctomycetota_c__Planctomycetia_o__Isosphaerales_f__Isosphaeraceae	2.808203	shrub	2.329616	0.020921	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Acetobacterales_f__Acetobacteraceae	2.889671	shrub	2.367954	0.020921	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__ATCC43930_f__Stellaceae	2.390462	shrub	2.15023	0.020165	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Caulobacterales_f__Caulobacteraceae	2.39256	shrub	2.201876	0.020165	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Caulobacterales_f__Caulobacteraceae_g__Phenylobacterium	2.198697	shrub	2.144299	0.038394	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Beijerinckiaceae_g__Microvirga	2.810722	shrub	2.408211	0.042066	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Xanthobacteraceae	3.056406	shrub	2.475683	0.020921	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Sphingomonadales_f__Sphingomonadaceae_g__Allosphingosinicella	2.410126	shrub	2.202669	0.020165	south	drySoil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Sphingomonadales_f__Sphingomonadaceae_g__Sphingomicrobium	3.204663	shrub	2.682934	0.043308	south	drySoil

d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae	3.134956	shrub	2.666305	0.043308	south	drySoil
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__Burkholderiaceae_g__Ramlibacter	2.402102	shrub	2.196079	0.020165	south	drySoil
d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Steroidobacterales_f__Steroidobacteraceae	2.492155	shrub	2.298812	0.043308	south	drySoil
d__Bacteria_p__Actinobacteriota_c__Acidimicrobiia_o__Acidimicrobiales_f__Ilumatobacteraceae	2.267641	shrub	2.043917	0.047221	south	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Cellulomonadaceae	2.191057	shrub	2.104256	0.013874	south	soil
d__Bacteria_p__Actinobacteriota_c__Actinomycetia_o__Actinomycetales_f__Dermatophilaceae	2.472245	shrub	2.233229	0.020165	south	soil
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__GMQP_bins7	2.293059	shrub	2.034483	0.013874	south	soil
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__PALSA_600	3.211062	shrub	2.679679	0.020921	south	soil
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Gaiellales_f__Gaiellaceae_g__Palsa_739_s__Palsa_739sp003161615	2.519594	shrub	2.202078	0.01796	south	soil
d__Bacteria_p__Actinobacteriota_c__Thermoleophilia_o__Solirubrobacterales_f__Thermoleophilaceae	2.635039	shrub	2.267008	0.020921	south	soil
d__Bacteria_p__Myxococcota_c__Polyangia_o__Polyangiales_f__Polyangiaceae	2.882384	shrub	2.503311	0.043308	south	soil
d__Bacteria_p__Planctomycetota_c__Phycisphaerae_o__Tepidisphaerales_f__Tepidisphaeraceae	2.472636	shrub	2.25258	0.01796	south	soil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Beijerinckiaceae	2.689555	shrub	2.319729	0.042066	south	soil
d__Bacteria_p__Proteobacteria_c__Alphaproteobacteria_o__Rhizobiales_f__Rhizobiaceae	2.337674	shrub	2.101186	0.01796	south	soil

d__Bacteria_p__Proteobacteria_c__Gammaproteobacteria_o__Burkholderiales_f__SG8_39	2.536274	shrub	2.163037	0.043308	south	soil
d__Bacteria	4.06167	noShrub	3.508169	0.043308	south	soil
d__Bacteria_p__Actinobacteriota	3.469171	noShrub	3.011716	0.043308	south	soil
d__Bacteria_p__Chloroflexota	3.453174	noShrub	2.874075	0.043308	south	soil

Table S5.2. Enriched MAGs in the Landscape Gradient Study

Enriched MAGs from other studies can be found in Chapter 4 Tables S2 and S3

MAG	Taxonomy (GTDB-tk)	enriched	sample type	LDA score
01_2.bin.1	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_;s_	shrub	north	2.347566291
02_2.bin.1	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Niastella;s_	noshrub	central, millet rhizosphere	2.172169299
04_2_bin.2	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Marmoricola;s_			
08_2_bin.3	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_;s_	noShrub, noOM	drought end, watered	2.270406682
13_2.bin.2	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella;s_			
14_2.bin.2	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_			
19_2.bin.2	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_	noshrub, OM shrub,	drought End, watered all lat, soil	2.757346986 2.517436949

		shrub	south	2.59003 1577
2021_COA1R. bin.14	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_ Dictyobacter;s_			
2021_COA1R. bin.15	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g _VBDL01;s_			
2021_COA1R. bin.17	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobactera ceae;g_Dyella_B;s_			
2021_COA1R. bin.18	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Catenulisporaceae;g_Ac tinocrinis;s_			
2021_COA1R. bin.4	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g _CAIMXF01;s_			
2021_COA1R. bin.9	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Niastella;s_	noshrub	central, millet rhizosph ere	2.17216 9299
2021_COA2R. bin.1	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_ Bu33;s_			
2021_COA2R. bin.19	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobactera ceae;g_Dokdonella_A;s_			
2021_COA2R. bin.20	d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_UBA11236;f_UBA11236;g_Chersky-265;s_			
2021_COA2R. bin.5	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_ Mycobacterium;s_			
2021_COA3D. bin.1	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacterace ae;g_Palsa-465;s_			
2021_COA3R. bin.2	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g _;s_	noShru b, noOM	drought end, watered	2.27040 6682
2021_COA4D. bin.2	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north, millet rhizosph ere	2.87385 9838
		shrub	north	2.71056 701

2021_COA4R.bin.7	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
2021_COC1D.bin.14	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_Palsa-688;g_;s_			
2021_COC1D.bin.8	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_;s_			
2021_COC1D.bin.9	d_Bacteria;p_Nitrospirota;c_Nitrospiria;o_Nitrospirales;f_Nitrospiraceae;g_;s_	shrub	south, millet rhizosphere	2.11721958
2021_COC1R.bin.6	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Puia;s_			
2021_COC2D.bin.12	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_;s_			
2021_COC2D.bin.3	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_BOG-931;s_			
2021_COC2D.bin.7	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Sulfotelmatobacter;s_			
2021_COC2D.bin.8	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_	noshrub, OM	drought End, watered	2.757346986
		shrub,	all lat, soil	2.517436949
		shrub	south	2.590031577
2021_COC2R.bin.12	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_			
2021_COC2R.bin.14	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_;s_	shrub	north, millet rhizosphere	2.268498711
2021_COC2R.bin.15	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_			
2021_COC2R.bin.16	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_			

2021_COC3D.bin.1	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
2021_COC3D.bin.5	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_UBA8260;f_UBA8260;g_JAFALX01;s_			
2021_COC4D.bin.15	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_Palsa-504;s_			
2021_COC4D.bin.7	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
2021_COC4R.bin.12	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Marmoricola;s_			
2021_COC4R.bin.15	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Noviherbaspirillum;s_			
2021_COC4R.bin.18	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Sphingod_Bacteriales;f_Sphingod_Bacteriaceae;g_Mucilaginibacter;s_			
2021_COC4R.bin.19	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_Bradymillet rhizospherebium;s_	shrub	south	2.201091806
2021_COC4R.bin.24	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_			
2021_COC4R.bin.7	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales;f_Bryobacteraceae;g_Bog-105;s_			
2021_COC4R.bin.8	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_	shrub	all lat, millet rhizosphere	2.481273888
		shrub	all lat, soil	2.590212951
		shrub	central, dry soil	2.664458151
		shrub	north, millet rhizosphere	2.690655815
		shrub	north	2.552008435

		shrub	south	2.48135213
		shrub	central, drymillet rhizosphere	2.606636411
		shrub	central, millet rhizosphere	2.77942888
2021_COC4S.bin.1	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_			
2021_COC4S.bin.12	d_Archaea;p_Thermoplasmatota;c_SW-10-69-26;o_JACQPN01;f_;g_;s_			
2021_COC4S.bin.15	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Nevskiales;f_Nevskiaceae;g_Nevskia;s_			
2021_COC4S.bin.18	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_UBA10450;g_AV40;s_			
2021_COC4S.bin.19	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_;s_			
2021_COC4S.bin.24	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_			
2021_COC4S.bin.27	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-612;s_			
2021_COC4S.bin.3	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_CF-121;f_CF-121;g_CF-13;s_			
2021_COC4S.bin.30	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
2021_COC4S.bin.7	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
2021_CSC1R.bin.17	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_JAATET01;g_JAATET01;s_			

2021_CSC1R.bin.5	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptacidiphilus_A;s_			
2021_CSC2D.bin.4	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Casimicrobiaceae;g_VBCG01;s_			
2021_CSC2S.bin.11	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_66-474;s_			
2021_CSC2S.bin.8	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Paraburkholderia;s_Paraburkholderia sabiae			
2021_CSC3R.bin.1	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_;g_;s_			
		shrub	all lat, millet rhizosphere	2.481273888
		shrub	all lat, soil	2.590212951
		shrub	central, dry soil	2.664458151
		shrub	north, millet rhizosphere	2.690655815
		shrub	north	2.552008435
		shrub	south	2.48135213
		shrub	central, drymillet rhizosphere	2.606636411
2021_CSC3S.bin.1	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_	shrub	central, millet rhizosphere	2.77942888

2021_CSC3S.bin.11	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_			
2021_CSC3S.bin.17	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Acidothermales;f_;g_;s_			
2021_CSC3S.bin.19	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Ramlibacter;s_	shrub	drought End	2.098674829
		shrub	south, soil	2.236293347
		noShrub	central, millet rhizosphere	2.26693173
2021_CSC3S.bin.20	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_	noshrub, OM	drought End, watered	2.757346986
		shrub,	all lat, soil	2.517436949
		shrub	south	2.590031577
2021_CSC3S.bin.23	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Longimicrobiales;f_Longimicrobiaceae;g_;s_			
2021_CSC3S.bin.8	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_;s_			
2021_CSC4S.bin.15	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Koribacteraceae;g_Bog-257;s_			
2021_CSC4S.bin.7	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_GCA-003244245;s_			
21_2.bin.2	d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacterales;f_Ktedonobacteraceae;g_Bu33;s_			
24_2_bin.1	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_JAFAQI01;g_JAFAQI01;s_			
3300044652_17	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Iso899;s_			

3300044654_37	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_GCA-003244245;s_			
3300044658_31	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_			
3300044667_14	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north, millet rhizosphere	2.873859838
		shrub	north	2.71056701
3300044667_25	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_UBA9676;s_			
3300044667_30	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_;s_			
3300044684_27	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_			
3300044689_1	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_AC-49;s_			
3300044693_2	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Chromod_Bacteriaceae;g_;s_			
3300044694_26	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_;s_	shrub	north, dry millet rhizosphere	2.060237893
		shrub	north, drySoil	2.060237893
3300044694_9	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptomyces;s_	shrub	all lat, drysoil	2.270505878
		shrub	all lat, soil	2.346110061
		shrub	south, all sample types	2.383500286

		shrub	central	2.379608543
3300044705_27	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_			
3300044741_25	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_JAFAHZ01;s_			
3300044842_12	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_			
3300044842_42	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_			
3300044901_10	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Baekduia;s_			
3300045002_7	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
3300045003_14	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Acidobacterium_A;s_			
3300045003_29	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Teracidiphilus;s_			
3300045003_30	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_Bog-793;g_Palsa-601;s_			
3300045003_43	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium;s_	shrub	south, soil	2.142263198
3300045014_30	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_CAINCZ01;g_;s_			
3300045014_31	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_			
3300045049_17	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_			
3300045049_56	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_VBDL01;s_			
3300045838_42	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_			
3300045976_9	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_			

COA1D.bin.4	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_;s_	shrub	north, millet rhizosphere	2.892651693
COA1R.bin.11	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Ramlibacter;s_	shrub	drought End	2.098674829
		shrub	south, soil	2.236293347
		noShrub	central, millet rhizosphere	2.26693173
COA1R.bin.17	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_			
COA1R.bin.2	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_	noshrub, OM	drought End, watered	2.757346986
		shrub,	all lat, soil	2.517436949
		shrub	south	2.590031577
COA1R.bin.9	d_Bacteria;p_Firmicutes;c_Bacilli;o_Paenibacillales;f_NBRC-103111;g_VKM-B-2647;s_			
COA2R.bin.12	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_			
COA2R.bin.13	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Catenulisporaceae;g_Catenulispora;s_			
COA2R.bin.16	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Microbacterium;s_Microbacterium sp902506375			
COA2R.bin.5	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Curtobacterium;s_			
COA2S.bin.11	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
COA2S.bin.12	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_CAINCZ01;g_;s_			

		shrub	all lat, millet rhizosphere	2.481273888
		shrub	all lat, soil	2.590212951
		shrub	central, dry soil	2.664458151
		shrub	north, millet rhizosphere	2.690655815
		shrub	north	2.552008435
		shrub	south	2.48135213
		shrub	central, drymillet rhizosphere	2.606636411
COA2S.bin.13	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_PALSA-600;s_	shrub	central, millet rhizosphere	2.77942888
COA2S.bin.14	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_			
COA2S.bin.18	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_UBA8260;f_UBA8260;g_;s_			
COA2S.bin.3	d_Bacteria;p_Chloroflexota;c_UBA5177;o_UBA5177;f_UBA5177;g_;s_	noShrub, no OM	drought Start	2.41292667
COA2S.bin.5	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_CF-121;f_CF-121;g_CF-13;s_			

COA3D.bin.6	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_			
		shrub	north, millet rhizosphere	2.873859838
COA3S.bin.8	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
COA4D.bin.4	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_			
COA4R.bin.5	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia;s_Burkholderia dolosa			
COC1D.bin.2	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_Dormibacterales;f_Dormibacteraceae;g_40CM-4-65-16;s_			
		shrub	north, millet rhizosphere	2.873859838
COC1D.bin.5	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
COC1R.bin.13	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Deminuibacter;s_			
		shrub	all lat, drysoil	2.270505878
		shrub	all lat, soil	2.346110061
		shrub	south, all sample types	2.383500286
		shrub	central	2.379608543
COC1R.bin.16	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomycetales;f_Streptomycetaceae;g_Streptomyces;s_			
COC1R.bin.9	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Propionid_Bacteriaceae;g_Microlunatus_A;s_			

COC1S.bin.4	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Micropepsales;f_Micropepsaceae;g_CAIYRG01;s_			
COC1S.bin.50	d_Archaea;p_Thermoplasmatota;c_SW-10-69-26;o_JACQPN01;f_;g_;s_			
COC1S.bin.60	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-744;s_			
COC2D.bin.6	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_	shrub	north, soil	2.70674824
		shrub	south, millet rhizosphere	2.462781182
		noShrub	central, millet rhizosphere	2.633624511
COC2D.bin.9	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_			
COC2R.bin.1	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
COC2R.bin.2	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north, millet rhizosphere	2.873859838
		shrub	north	2.71056701
COC2R.bin.22	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_I;s_			
COC2S.bin.3	d_Bacteria;p_Actinobacteriota;c_;o_;f_;g_;s_			
COC2S.bin.5	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_			
COC2S.bin.6	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_			
COC3D.bin.4	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_AC-14;g_;s_			

		shrub	north, millet rhizosphere	2.873859838
COC3R.bin.17	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
COC3R.bin.18	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Beijerinckiaceae;g_Roseiarcus;s_			
COC3R.bin.2	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Chitinophaga;s_			
COC3R.bin.26	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_Kutzneria;s_			
COC3R.bin.27	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Puia;s_			
COC3R.bin.9	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Asticcacaulis;s_			
COC4D.bin.15	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_			
COC4D.bin.17	d_Bacteria;p_CSP1-3;c_CSP1-3;o_CSP1-3;f_NP-7;g_;s_			
COC4D.bin.36	d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_;f_;g_;s_			
COC4D.bin.7	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_QIAW01;g_;s_			
		shrub	north, soil	2.70674824
		shrub	south, millet rhizosphere	2.462781182
COC4R.bin.16	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_;s_	noShrub	central, millet rhizosphere	2.633624511
COC4R.bin.17	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_	noshrub, OM	drought End, watered	2.757346986

		shrub,	all lat, soil	2.51743 6949
		shrub	south	2.59003 1577
COC4S.bin.16	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_			
COC4S.bin.20	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales;f_Bryobacteraceae;g_Bog-105;s_			
COC4S.bin.25	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Acidobacteriaceae;g_Edaphobacter;s_			
COC4S.bin.5	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Steroidobacterales;f_Steroidobacteraceae;g_13-2-20CM-66-19;s_			
CSA1D.bin.22	d_Bacteria;p_Chloroflexota;c_UBA6077;o_UBA6077;f_CF-72;g_;s_			
CSA1D.bin.30	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_JAFAQB01;s_			
CSA2D.bin.1	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_13-2-20CM-68-14;s_			
CSA2D.bin.10	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_;s_			
CSA2D.bin.2	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_UBA10450;g_Udaeobacter;s_			
CSA2D.bin.6	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrosocosmicus;s_			
CSA2D.bin.7	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
CSA2D.bin.8	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_			
CSA2D.bin.9	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Nitrososphaera;s_			
CSA2R.bin.18	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
CSA2R.bin.36	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_JAATET01;g_JAATET01;s_			

CSA2R.bin.38	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Usitatibacteraceae;g_Usitatibacter;s_			
CSA2R.bin.47	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Oxalicibacterium;s_			
CSA2R.bin.49	d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacterales;f_Baltobacteraceae;g_;s_			
CSA2S.bin.33	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
CSA2S.bin.54	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_IMCC26256;f_;g_;s_			
CSA2S.bin.55	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-744;s_			
CSA2S.bin.58	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_JAFAQI01;g_JAFAQI01;s_			
CSA2S.bin.64	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_AG2;s_			
CSA2S.bin.68	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Pseudonocardiaceae;g_Pseudonocardia;s_			
CSA3D.bin.5	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_Acidimicrobiales;f_UBA8190;g_UBA8190;s_			
CSA4R.bin.1	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Nocardioides;s_	shrub	drysoil, central	2.682247741
		shrub	soil, all lat	2.594610417
		shrub	drySoil, south	2.732406188
		shrub	soil, central	2.840962385
		shrub	soil, south	2.735549451
CSA4R.bin.14	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionid_Bacteriales;f_Nocardioidaceae;g_Nocardioides;s_			
CSA4R.bin.17	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_			

		shrub	north, millet rhizosphere	2.873859838
CSA4R.bin.3	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
CSA4R.bin.6	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_			
CSA4S.bin.6	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_SG8-39;g_SCGC-AG-212-J23;s_			
CSC1D.bin.5	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_			
CSC1D.bin.7	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycod_Bacteriaceae;g_Mycobacterium;s_			
CSC1E.bin.1	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia;s_Burkholderia multivorans			
CSC1R.bin.17	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas_I;s_			
		shrub	drymillet rhizosphere	2.836231191
		shrub	north, drymillet rhizosphere	2.921364452
		shrub	north, drySoil	2.921364452
CSC1R.bin.4	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_	shrub	north	2.80009525
CSC1R.bin.6	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Rhodanobacteraceae;g_Dyella_B;s_			
CSC2D.bin.3	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_	shrub	drymillet rhizosphere	2.836231191

		shrub	north, drymillet rhizosphere	2.921364452
		shrub	north, drySoil	2.921364452
		shrub	north	2.80009525
		shrub	north, millet rhizosphere	2.873859838
CSC2D.bin.37	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
CSC2S.bin.1	d_Bacteria;p_Actinobacteriota;c_Acidimicrobiia;o_IMCC26256;f_;g_;s_			
CSC2S.bin.10	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_millet rhizospherebiales;f_Xanthobacteraceae;g_Bradymillet rhizospherebium;s_	shrub	south	2.201091806
CSC2S.bin.12	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA145;s_			
CSC2S.bin.14	d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Microd_Bacteriaceae;g_Humibacter;s_			
CSC2S.bin.3	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_			
CSC2S.bin.5	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_Reyranella;s_			
		shrub	north, millet rhizosphere	2.873859838
CSC3D.bin.5	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_Gaiellaceae;g_Palsa-739;s_	shrub	north	2.71056701
CSC3D.bin.7	d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__Thermoleophilaceae;g__;s__			

CSC3R.bin.11	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Trinickia;s_			
CSC3R.bin.7	d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_Gp1-AA117;g_Gp1-AA17;s_			
CSC3S.bin.44	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales;f_;g_;s_			
CSC3S.bin.66	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_VAYN01;s_			
CSC3S.bin.68	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Longimicrobiales;f_RSA9;g_;s_			
CSC3S.bin.69	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_	shrub	drymillet rhizosphere	2.836231191
		shrub	north, drymillet rhizosphere	2.921364452
		shrub	north, drySoil	2.921364452
		shrub	north	2.80009525
CSC4R.bin.9	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_	shrub	drymillet rhizosphere	2.836231191
		shrub	north, drymillet rhizosphere	2.921364452
		shrub	north, drySoil	2.921364452
		shrub	north	2.80009525
CSC4S.bin.15	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Acetobacterales;f_Acetobacteraceae;g_Acidisphaera;s_			
CSC4S.bin.2	d_Archaea;p_Thermoproteota;c_Nitrososphaeria;o_Nitrososphaerales;f_Nitrososphaeraceae;g_UBA10452;s_UBA10452 sp009898475			

		shrub	drymillet rhizosph ere	2.83623 1191
		shrub	north, drymillet rhizosph ere	2.92136 4452
		shrub	north, drySoil	2.92136 4452
CSC4S.bin.9	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-465;s_	shrub	north	2.80009 525

Table S5.3. MAG quality - contamination and completeness

Bin Id	# genomes	# markers	# marker sets	0	1	2	3	4	5+	Completeness	Contamination	Strain heterogeneity
COC1R.bin.13.fa	364	303	203	0	303	0	0	0	0	100	0	0
2021_COA1R.bin.9.fa	364	302	203	0	298	4	0	0	0	100	0.99	50
COC3R.bin.6.fa	364	302	203	0	295	7	0	0	0	100	1.23	42.86
COA1R.bin.16.fa	364	302	203	0	294	8	0	0	0	100	2.48	62.5
2021_COC1R.bin.2.fa	364	303	203	0	296	7	0	0	0	100	2.98	0
CSC2S.bin.4.fa	334	368	206	0	355	13	0	0	0	100	5.38	0
3300044672_2	55	659	290	1	653	5	0	0	0	99.66	1.02	0
COA3E.bin.1.fa	55	659	290	20	631	8	0	0	0	99.66	1.12	0
3300044658_23	364	303	203	1	302	0	0	0	0	99.51	0	0
2021_COC4R.bin.10.fa	364	302	203	1	297	4	0	0	0	99.51	1.15	0
COC4R.bin.23.fa	364	302	203	1	297	4	0	0	0	99.51	1.15	0
2021_COC4R.bin.20.fa	26	529	308	7	515	7	0	0	0	99.5	1.67	28.57
2021_COC1R.bin.11.fa	193	427	214	10	407	10	0	0	0	99.43	3.13	50
3300044686_6	334	370	206	3	355	11	1	0	0	99.39	3.62	0
2021_COC2D.bin.13.fa	334	370	206	3	354	12	1	0	0	99.39	3.87	6.67
COC2D.bin.3.fa	334	370	206	3	354	12	1	0	0	99.39	3.87	6.67
2021_COA1R.bin.5.fa	26	529	308	2	517	10	0	0	0	99.35	2.16	60
CSC4R.bin.4.fa	63	336	201	2	329	5	0	0	0	99.34	1.91	40
2021_CSC1R.bin.17.fa	88	230	148	1	224	5	0	0	0	99.32	2.42	0
COC3R.bin.9.fa	26	529	308	3	521	5	0	0	0	99.24	1.02	0
COA1R.bin.14.fa	26	529	308	3	518	8	0	0	0	99.24	1.52	37.5
COA3R.bin.7.fa	91	596	218	6	581	9	0	0	0	99.23	2.93	11.11
CSC3S.bin.15.fa	387	330	193	6	305	18	1	0	0	99.22	5.69	9.52
COC4R.bin.18.fa	26	529	308	8	513	8	0	0	0	99.17	1.75	25
3300044667_15	732	200	117	1	195	4	0	0	0	99.15	3.42	0

3300045003_29	2258	187	116	1	184	2	0	0	0	99.14	1.72	0
CSC2E.bin.1.fa	134	1172	336	4	1165	3	0	0	0	99.07	0.38	0
CSC4R.bin.13.fa	26	529	308	3	515	11	0	0	0	99.03	2.22	9.09
2021_COA2R.bin.3.fa	364	303	203	4	298	1	0	0	0	99	0.12	0
3300044683_29	69	400	198	2	391	7	0	0	0	98.99	2.02	28.57
CSA2D.bin.2	88	230	148	2	221	7	0	0	0	98.99	2.93	14.29
CSASD.bin.2.fa	88	230	148	2	221	7	0	0	0	98.99	2.93	14.29
2021_COA3R.bin.13.fa	91	596	218	5	577	14	0	0	0	98.97	2.57	14.29
COC3R.bin.19.fa	120	572	265	6	550	14	2	0	0	98.95	2.63	25
2021_CSC2S.bin.10.fa	455	315	190	7	301	7	0	0	0	98.92	2.46	42.86
2021_CSC3S.bin.23.fa	2993	147	91	1	143	3	0	0	0	98.9	3.3	0
CSC3S.bin.59.fa	2993	147	91	1	141	5	0	0	0	98.9	4.95	40
2021_CSC4S.bin.2.fa	2993	147	91	1	138	8	0	0	0	98.9	6.78	0
CSC4S.bin.6.fa	2993	147	91	1	138	8	0	0	0	98.9	6.78	0
3300044741_33	2993	147	91	1	137	9	0	0	0	98.9	7.33	0
2021_COC1R.bin.14.fa	120	572	265	10	542	19	1	0	0	98.84	3.41	31.82
2021_COC2R.bin.6.fa	26	529	308	7	510	12	0	0	0	98.79	2.75	33.33
COA2R.bin.10.fa	120	572	265	10	548	13	1	0	0	98.75	3	18.75
COC4S.bin.30.fa	268	398	220	6	363	29	0	0	0	98.75	7.03	62.07
COC1R.bin.12.fa	33	350	203	10	326	14	0	0	0	98.59	4.39	35.71
2021_COC4S.bin.12.fa	148	188	125	11	176	1	0	0	0	98.58	0.4	0
COA2R.bin.8.fa	364	303	203	5	296	2	0	0	0	98.51	0.25	50
2021_CSC4R.bin.1.fa	26	529	308	6	512	10	1	0	0	98.51	2.54	15.38
2021_COC1R.bin.13.fa	91	596	218	7	560	29	0	0	0	98.49	6.07	6.9
2021_CSC3S.bin.25.fa	387	330	193	4	302	24	0	0	0	98.39	6.25	16.67
CSA4S.bin.6.fa	223	425	211	4	412	8	1	0	0	98.34	2.83	27.27
3300044652_29	732	199	116	3	195	1	0	0	0	98.28	0.86	0
CSA1S.bin.7.fa	732	199	116	3	194	2	0	0	0	98.28	1.72	0
2021_CSA1S.bin.3.fa	732	199	116	3	193	3	0	0	0	98.28	2.59	0
2021_COC4S.bin.11.fa	2258	187	116	2	177	8	0	0	0	98.28	4.41	37.5
2021_COA4R.bin.2.fa	334	368	206	7	345	15	1	0	0	98.28	4.97	0

2021_COA3R.bin.15.fa	69	400	198	8	386	6	0	0	0	98.27	1.48	50
CSC2S.bin.11.fa	35	495	282	5	478	12	0	0	0	98.23	2.78	0
COC1R.bin.11.fa	91	596	218	20	559	17	0	0	0	98.23	3.9	5.88
2021_COC3D.bin.3.fa	901	171	117	3	162	6	0	0	0	98.21	2.4	83.33
COC1R.bin.1.fa	55	659	290	43	580	34	2	0	0	98.17	5.81	17.5
COA3R.bin.1.fa	193	427	214	29	394	4	0	0	0	98.13	1.87	50
COA1E.bin.1.fa	91	596	218	5	585	6	0	0	0	98.11	1.52	16.67
COC4D.bin.7.fa	2258	188	117	5	183	0	0	0	0	98.09	0	0
2021_COC4D.bin.8.fa	2258	188	117	5	182	1	0	0	0	98.09	0.17	0
CSA2R.bin.37.fa	364	302	203	12	279	11	0	0	0	98.07	3.1	54.55
COA4R.bin.8.fa	120	574	266	21	506	37	10	0	0	98.04	8.98	34.33
3300045049_37	364	302	203	4	293	5	0	0	0	98.03	1.64	20
CSA3R.bin.3.fa	91	596	218	25	563	8	0	0	0	98.03	2.03	12.5
2021_COA2R.bin.9.fa	78	840	354	52	773	15	0	0	0	98	1.51	26.67
COC1R.bin.10.fa	120	572	265	13	546	13	0	0	0	97.99	2.4	7.69
CSC1R.bin.8.fa	108	570	250	42	510	18	0	0	0	97.99	3.6	38.89
2021_COC1R.bin.15.fa	33	350	203	5	330	15	0	0	0	97.98	4.78	33.33
CSA2R.bin.18.fa	120	572	265	19	540	13	0	0	0	97.96	2.07	7.69
2021_COA3R.bin.7.fa	55	659	290	23	612	24	0	0	0	97.94	2.3	33.33
2021_COC1D.bin.6.fa	5449	104	58	2	84	18	0	0	0	97.93	8.93	44.44
2021_COA2R.bin.12.fa	120	574	266	9	544	20	1	0	0	97.89	3.49	26.09
2021_COC4S.bin.6.fa	2258	188	117	3	180	5	0	0	0	97.86	2.79	80
3300044705_27	732	199	116	4	194	1	0	0	0	97.84	0.86	0
CSA1R.bin.5.fa	564	349	230	6	331	12	0	0	0	97.83	2.83	41.67
CSA2S.bin.42.fa	268	398	220	21	363	12	2	0	0	97.82	4.95	27.78
3300044658_14	193	427	214	37	384	6	0	0	0	97.8	1.76	16.67
COA4R.bin.7.fa	334	368	206	8	344	15	1	0	0	97.8	4.97	0
COC4S.bin.10.fa	148	188	125	12	175	1	0	0	0	97.78	0.4	0
COA3E.bin.3.fa	55	659	290	10	640	9	0	0	0	97.73	1.59	11.11
2021_COC4R.bin.24.fa	924	161	108	5	151	5	0	0	0	97.67	1.94	60
COA2R.bin.6.fa	78	840	354	54	776	10	0	0	0	97.65	0.94	40

COC2S.bin.6.fa	901	171	117	9	157	5	0	0	0	97.63	2.56	0
13_2_bin.2	55	659	290	10	630	19	0	0	0	97.55	2.28	31.58
2021_COA3R.bin.14.fa	108	570	250	45	491	33	1	0	0	97.48	4.68	41.67
2021_COA2R.bin.15.fa	91	596	218	12	575	9	0	0	0	97.42	2.52	11.11
2021_COC4S.bin.25.fa	26	529	308	30	472	25	1	0	1	97.38	6.78	18.37
CSC1R.bin.14.fa	88	230	148	4	221	5	0	0	0	97.3	2.7	0
COA3S.bin.3.fa	35	495	282	9	470	16	0	0	0	97.28	3.47	0
COA2D.bin.4.fa	268	398	220	13	373	12	0	0	0	97.24	2.59	66.67
COC2D.bin.8.fa	268	398	220	15	377	6	0	0	0	97.22	1.67	50
2021_COC2D.bin.15.fa	268	398	220	15	376	7	0	0	0	97.22	2.12	42.86
CSA1E.bin.1.fa	108	570	250	50	511	9	0	0	0	97.19	1.19	33.33
2021_COC4D.bin.14.fa	901	171	117	6	157	8	0	0	0	97.15	2.94	25
COA3S.bin.9.fa	901	171	117	6	156	9	0	0	0	97.15	4.56	44.44
COA3R.bin.10.fa	69	400	198	24	369	7	0	0	0	97.14	1.77	28.57
CSC2S.bin.9.fa	455	315	190	12	291	12	0	0	0	97.1	3.18	8.33
3300044658_7	364	302	203	28	263	11	0	0	0	97.09	2.98	54.55
3300044656_21	193	427	214	32	386	7	2	0	0	97.08	2.94	38.46
2021_CSC1R.bin.3.fa	108	570	250	50	498	22	0	0	0	97.07	4.17	27.27
3300045976_37	732	199	116	5	193	1	0	0	0	96.98	0.86	0
2021_CSC4R.bin.13.fa	63	336	201	20	313	3	0	0	0	96.97	1.49	33.33
2021_CSC2D.bin.5.fa	268	398	220	12	382	4	0	0	0	96.96	0.85	75
3300044719_14	88	230	148	5	221	4	0	0	0	96.96	2.03	50
2021_COC2R.bin.7.fa	91	596	218	13	575	8	0	0	0	96.96	2.41	0
2021_CSC1R.bin.16.fa	26	529	308	33	485	10	1	0	0	96.93	3.41	38.46
3300044693_27	37	824	336	42	728	50	4	0	0	96.93	7.21	9.68
CSC2D.bin.12.fa	268	398	220	18	373	6	1	0	0	96.88	1.27	55.56
COA3E.bin.4.fa	64	769	248	48	705	16	0	0	0	96.88	2.2	25
COC1D.bin.10.fa	901	171	117	6	161	4	0	0	0	96.82	2.56	25
02_2_bin.1	364	302	203	9	285	8	0	0	0	96.8	2.08	25
2021_COC1R.bin.5.fa	55	659	290	45	594	20	0	0	0	96.76	3.84	30
COC4S.bin.17.fa	108	570	250	33	522	14	1	0	0	96.74	2.85	52.94

3300044684_12	26	529	308	17	505	7	0	0	0	96.72	1.46	57.14
2021_COC4S.bin.24.fa	108	570	250	46	516	8	0	0	0	96.7	2.15	62.5
CSA1R.bin.4.fa	120	572	265	24	531	17	0	0	0	96.69	2.91	35.29
COA2R.bin.7.fa	91	596	218	29	552	15	0	0	0	96.67	3.75	0
CSC1R.bin.1.fa	26	529	308	38	478	12	1	0	0	96.65	3.75	40
CSC1D.bin.5.fa	2258	188	117	21	163	4	0	0	0	96.58	2.99	0
COA3S.bin.10.fa	732	200	117	4	190	6	0	0	0	96.58	4.7	16.67
COC3R.bin.13.fa	91	596	218	31	551	14	0	0	0	96.57	2.91	0
3300044667_3	732	199	116	5	193	1	0	0	0	96.55	0.86	0
COC4S.bin.29.fa	2258	187	116	4	174	9	0	0	0	96.55	5.52	11.11
COA4R.bin.5.fa	64	769	248	51	709	9	0	0	0	96.54	1.39	66.67
2021_COA4R.bin.4.fa	64	769	248	51	708	10	0	0	0	96.54	1.79	70
2021_COC3D.bin.1.fa	268	398	220	22	374	2	0	0	0	96.53	0.32	50
2021_CSC4R.bin.6.fa	108	570	250	47	507	16	0	0	0	96.52	2.89	37.5
2021_COA3R.bin.12.fa	55	659	290	44	592	23	0	0	0	96.52	4.15	43.48
2021_COA2R.bin.5.fa	268	395	220	25	366	4	0	0	0	96.5	1.02	75
2021_COC1R.bin.6.fa	364	302	203	31	264	7	0	0	0	96.5	2.22	14.29
2021_CSC2S.bin.2.fa	334	368	206	21	337	10	0	0	0	96.5	3.92	0
2021_CSA1R.bin.6.fa	91	596	218	27	552	16	1	0	0	96.5	4.15	0
2021_CSA1R.bin.8.fa	120	572	265	26	532	14	0	0	0	96.42	2.62	35.71
CSC3S.bin.66.fa	732	199	116	7	191	1	0	0	0	96.38	0.43	100
COC2R.bin.7.fa	91	596	218	18	554	23	1	0	0	96.38	6.55	0
2021_COA1R.bin.4.fa	193	427	214	15	407	5	0	0	0	96.32	1.01	0
COC1R.bin.8.fa	364	302	203	8	287	7	0	0	0	96.31	2.22	14.29
COC4D.bin.10.fa	901	171	117	10	155	6	0	0	0	96.3	3.37	16.67
3300045013_13	2258	188	117	7	174	7	0	0	0	96.3	3.85	71.43
CSC4D.bin.5.fa	2258	188	117	10	172	6	0	0	0	96.29	4.7	50
2021_COC4S.bin.4.fa	67	481	276	37	415	26	3	0	0	96.27	7.65	0
2021_CSA1S.bin.5.fa	274	388	214	14	353	21	0	0	0	96.26	4.58	9.52
CSA1S.bin.6.fa	274	388	214	14	353	21	0	0	0	96.26	4.58	9.52
COC1R.bin.4.fa	924	155	106	12	140	3	0	0	0	96.17	2.83	0

2021_COC1R.bin.8.fa	924	155	106	13	138	4	0	0	0	96.17	3.77	0
3300045003_57	268	398	220	14	372	12	0	0	0	96.14	3.14	41.67
CSA1D.bin.30.fa	207	145	103	6	137	2	0	0	0	96.12	1.94	0
COA2R.bin.4.fa	268	398	220	22	365	11	0	0	0	96.1	2.19	45.45
CSA4S.bin.5.fa	732	199	116	12	185	2	0	0	0	96.03	1.01	50
COC2R.bin.17.fa	26	529	308	19	501	9	0	0	0	96.01	1.99	33.33
2021_COA3D.bin.2.fa	2258	188	117	16	162	10	0	0	0	96.01	4.72	20
CSC4R.bin.2.fa	55	659	290	58	581	20	0	0	0	95.96	3.47	55
CSA2R.bin.23.fa	88	230	148	6	213	11	0	0	0	95.95	4.56	36.36
COC4R.bin.1.fa	924	161	108	8	151	2	0	0	0	95.88	1.85	50
2021_COA1R.bin.16.fa	67	481	276	17	439	23	2	0	0	95.87	6.63	13.79
COA1R.bin.18.fa	193	427	214	15	403	6	3	0	0	95.8	2.06	53.33
COC3R.bin.12.fa	193	427	214	17	400	10	0	0	0	95.8	3.04	40
CSC4R.bin.18.fa	108	570	250	57	493	19	1	0	0	95.76	3.69	50
CSC1E.bin.1.fa	64	769	248	55	696	18	0	0	0	95.73	1.34	66.67
COC2D.bin.2.fa	901	171	117	9	159	3	0	0	0	95.73	2.14	0
COA2S.bin.7.fa	2258	188	117	23	161	4	0	0	0	95.72	2.99	0
CSA1R.bin.7.fa	91	596	218	31	549	16	0	0	0	95.71	4.46	18.75
2021_COA2R.bin.1.fa	924	151	101	5	140	6	0	0	0	95.71	5.94	16.67
2021_CSA1R.bin.4.fa	924	151	101	5	140	6	0	0	0	95.71	5.94	16.67
COA2R.bin.14.fa	924	151	101	5	140	6	0	0	0	95.71	5.94	16.67
COA2R.bin.15.fa	67	481	276	17	444	18	2	0	0	95.7	4.2	8.33
COC2R.bin.20.fa	323	387	234	53	313	21	0	0	0	95.7	6.92	19.05
2021_CSC3S.bin.16.fa	732	199	116	11	187	1	0	0	0	95.69	0.86	0
COA1R.bin.9.fa	46	481	186	46	432	3	0	0	0	95.68	0.67	0
2021_COC4S.bin.3.fa	924	161	108	8	148	5	0	0	0	95.63	2.14	0
2021_CSC1R.bin.18.fa	67	481	276	28	434	17	2	0	0	95.62	4.64	13.04
14_2_bin.1	2258	187	116	20	166	1	0	0	0	95.61	0.86	0
2021_CSC4S.bin.13.fa	924	161	108	18	137	6	0	0	0	95.59	4.35	50
3300044684_27	108	570	250	66	500	4	0	0	0	95.58	1.3	25
COA3S.bin.5.fa	732	200	117	7	192	1	0	0	0	95.56	0.85	0

2021_COA3R.bin.10.fa	193	427	214	55	367	5	0	0	0	95.55	1.55	40
COC1S.bin.20.fa	732	199	116	8	179	12	0	0	0	95.55	5.45	33.33
CSC3R.bin.5.fa	732	199	116	8	188	3	0	0	0	95.52	2.16	33.33
2021_CSC3S.bin.19.fa	193	427	214	31	383	13	0	0	0	95.5	2.85	30.77
CSC4R.bin.9.fa	732	200	117	9	185	6	0	0	0	95.47	1.88	0
2021_CSC3R.bin.12.fa	2258	188	117	24	158	6	0	0	0	95.46	2.53	33.33
CSC2D.bin.48.fa	35	495	282	19	453	23	0	0	0	95.45	3.45	39.13
COC4S.bin.5.fa	2231	190	119	40	147	3	0	0	0	95.44	1.43	0
COA2R.bin.12.fa	108	570	250	38	524	8	0	0	0	95.43	1.93	50
2021_CSA1R.bin.9.fa	924	155	106	8	144	3	0	0	0	95.41	1.99	0
2021_COC4S.bin.7.fa	268	398	220	13	373	11	1	0	0	95.41	2.65	42.86
COA2S.bin.17.fa	732	199	116	8	186	5	0	0	0	95.4	2.39	20
COC4S.bin.18.fa	732	199	116	8	181	9	1	0	0	95.4	6.7	8.33
2021_CSA3R.bin.7.fa	91	596	218	26	558	12	0	0	0	95.36	2.66	8.33
3300045001_15	2258	188	117	22	165	1	0	0	0	95.35	0.85	0
COA2R.bin.11.fa	55	659	290	31	603	25	0	0	0	95.35	3.08	0
2021_COA3R.bin.2.fa	193	427	214	51	362	14	0	0	0	95.35	4.41	78.57
2021_CSC4S.bin.14.fa	2258	188	117	13	169	6	0	0	0	95.34	4.44	66.67
CSC1D.bin.1.fa	924	161	108	13	142	6	0	0	0	95.3	4.81	33.33
CSC1R.bin.6.fa	55	659	290	76	567	15	1	0	0	95.29	2.1	50
COA1D.bin.2.fa	901	171	117	12	155	4	0	0	0	95.29	2.99	25
3300044694_26	732	199	116	11	186	2	0	0	0	95.26	1.29	0
CSA3D.bin.4.fa	35	495	282	21	458	16	0	0	0	95.24	3.72	18.75
CSA2S.bin.64.fa	2993	147	91	14	124	9	0	0	0	95.19	3.86	33.33
2021_COC4R.bin.28.fa	67	481	276	18	444	16	3	0	0	95.16	4.31	16
COC4S.bin.3.fa	26	529	308	52	457	18	1	0	1	95.15	5.74	7.14
3300044652_32	387	330	193	22	284	24	0	0	0	95.12	7.85	0
2021_COA2R.bin.11.fa	67	481	276	19	443	17	2	0	0	95.1	4.7	8.7
2021_CSC2D.bin.1.fa	35	495	282	21	447	27	0	0	0	95.09	5.17	33.33
2021_COC4R.bin.15.fa	193	427	214	53	366	7	1	0	0	95.08	2	50
CSC1R.bin.3.fa	67	481	276	31	429	19	2	0	0	95.02	4.36	16

2021_CSC4S.bin.7.fa	35	495	282	21	462	12	0	0	0	95.01	2.33	8.33
CSC4D.bin.13.fa	35	495	282	21	458	16	0	0	0	95.01	3.43	25
2021_COC2R.bin.9.fa	193	427	214	32	368	27	0	0	0	95	7.7	22.22
2021_COA2R.bin.19.fa	55	659	290	53	589	17	0	0	0	94.98	2.26	5.88
COA1R.bin.7.fa	67	481	276	21	433	25	2	0	0	94.94	6.75	19.35
COC4S.bin.9.fa	2258	188	117	21	163	4	0	0	0	94.89	1.82	0
COC3D.bin.4.fa	901	171	117	6	163	2	0	0	0	94.87	0.52	50
2021_COC2D.bin.6.fa	901	171	117	10	158	3	0	0	0	94.87	2.14	0
CSC1R.bin.9.fa	193	427	214	54	362	11	0	0	0	94.86	3.67	18.18
2021_COC2D.bin.9.fa	924	161	108	9	146	6	0	0	0	94.86	3.87	50
COC2D.bin.10.fa	924	161	108	9	146	6	0	0	0	94.86	3.87	50
COC3R.bin.28.fa	67	481	276	21	440	18	2	0	0	94.85	5.06	0
COC4D.bin.36.fa	924	161	108	20	139	2	0	0	0	94.84	1.39	0
CSC4S.bin.14.fa	35	495	282	27	446	22	0	0	0	94.84	4.56	9.09
3300044684_62	5449	104	58	4	81	5	14	0	0	94.83	6.93	17.02
COC4S.bin.15.fa	924	161	108	8	148	5	0	0	0	94.8	2.69	20
2021_COC4R.bin.14.fa	108	570	250	64	470	35	1	0	0	94.73	8.4	57.89
CSA1R.bin.2.fa	924	151	101	6	139	6	0	0	0	94.72	5.94	16.67
2021_CSA1R.bin.3.fa	564	349	230	15	323	11	0	0	0	94.7	3.19	72.73
COC2R.bin.5.fa	193	427	214	36	367	23	1	0	0	94.66	5.34	26.92
CSA4R.bin.12.fa	2258	188	117	24	160	4	0	0	0	94.65	2.05	0
2021_COA3D.bin.1.fa	732	200	117	10	189	1	0	0	0	94.64	0.09	0
CSA2R.bin.54.fa	455	315	190	27	273	15	0	0	0	94.64	5.28	6.67
CSC3R.bin.11.fa	108	570	250	68	494	8	0	0	0	94.6	1.05	50
CSC1R.bin.15.fa	108	570	250	59	489	22	0	0	0	94.6	3.64	50
3300045003_44	67	481	276	34	418	25	4	0	0	94.59	8.78	10.81
COA2S.bin.2.fa	732	200	117	11	187	2	0	0	0	94.56	1.28	50
3300044667_14	732	199	116	9	189	1	0	0	0	94.54	0.86	0
COA1D.bin.4.fa	732	199	116	10	187	2	0	0	0	94.54	1.72	0
COA2D.bin.5.fa	732	199	116	10	180	9	0	0	0	94.54	4.22	44.44
2021_CSC4R.bin.8.fa	35	495	282	25	450	20	0	0	0	94.53	2.68	25

2021_COC4S.bin.28.fa	67	481	276	62	386	31	2	0	0	94.52	6.62	2.7
CSA3R.bin.8.fa	67	481	276	24	431	24	2	0	0	94.5	6.99	26.67
CSA4R.bin.9.fa	2258	188	117	23	156	8	1	0	0	94.49	7.12	9.09
COA2S.bin.14.fa	924	161	108	11	147	3	0	0	0	94.48	2.04	0
CSC4R.bin.8.fa	35	495	282	24	459	12	0	0	0	94.47	2.38	25
2021_COA2R.bin.4.fa	108	570	250	55	500	15	0	0	0	94.45	2.46	46.67
CSA2S.bin.3.fa	732	199	116	10	182	7	0	0	0	94.45	5.17	0
3300045958_27	732	200	117	8	190	2	0	0	0	94.44	0.94	0
CSA2R.bin.39.fa	334	370	206	25	320	24	1	0	0	94.42	7.6	18.52
3300044652_17	274	388	214	16	365	7	0	0	0	94.39	1.67	14.29
2021_CSC1R.bin.8.fa	55	659	290	86	555	18	0	0	0	94.35	2.03	38.89
2021_CSC1R.bin.15.fa	108	570	250	64	492	14	0	0	0	94.34	2.26	64.29
CSC3S.bin.25.fa	193	427	214	42	368	17	0	0	0	94.34	2.7	29.41
2021_COA3R.bin.6.fa	924	155	106	15	135	5	0	0	0	94.34	4.72	40
CSC4S.bin.4.fa	924	161	108	18	134	9	0	0	0	94.34	5.46	33.33
3300044689_21	35	495	282	23	462	9	1	0	0	94.33	2.36	8.33
2021_COC4D.bin.9.fa	35	495	282	38	444	13	0	0	0	94.33	2.79	7.69
CSC3S.bin.40.fa	35	495	282	24	452	19	0	0	0	94.3	3.84	21.05
COC1R.bin.14.fa	193	427	214	51	338	37	1	0	0	94.14	7.51	52.5
COC4R.bin.21.fa	193	427	214	44	367	16	0	0	0	94.13	3.96	56.25
CSA1D.bin.5.fa	88	230	148	11	209	10	0	0	0	94.12	3.44	10
2021_COC4R.bin.21.fa	35	495	282	28	452	15	0	0	0	94.1	3.78	0
COC1S.bin.52.fa	268	398	220	32	355	11	0	0	0	94.06	2.44	27.27
2021_COC4S.bin.20.fa	924	151	101	8	140	3	0	0	0	94.06	2.97	33.33
COA2S.bin.3.fa	924	151	101	11	137	3	0	0	0	94.06	2.97	33.33
2021_CSC4R.bin.15.fa	55	659	290	82	546	31	0	0	0	94.06	4.39	58.06
CSA2R.bin.49.fa	924	161	108	18	138	5	0	0	0	94.03	4.63	40
COA3R.bin.2.fa	924	155	106	13	135	7	0	0	0	94.03	5.77	57.14
3300045049_38	26	529	308	31	489	9	0	0	0	93.98	2.15	44.44
COC1D.bin.2.fa	924	161	108	15	140	6	0	0	0	93.98	2.59	33.33
COA3R.bin.8.fa	120	573	265	38	515	19	1	0	0	93.97	4.13	40.91

CSA4R.bin.2.fa	732	199	116	13	176	10	0	0	0	93.97	4.97	60
2021_CSC2D.bin.6.fa	732	200	117	13	181	6	0	0	0	93.96	3.42	83.33
CSC4D.bin.7.fa	35	495	282	25	457	12	1	0	0	93.94	3.43	13.33
CSA2E.bin.1.fa	108	570	250	30	529	11	0	0	0	93.91	1.96	18.18
CSC3R.bin.6.fa	35	495	282	33	442	20	0	0	0	93.79	4.14	15
CSC3R.bin.7.fa	2258	188	117	27	159	2	0	0	0	93.75	1.14	0
3300045837_22	732	200	117	11	189	0	0	0	0	93.7	0	0
COC3R.bin.11.fa	108	570	250	71	454	43	2	0	0	93.68	9.03	34.69
COC1S.bin.50.fa	148	188	125	10	175	3	0	0	0	93.67	0.98	0
2021_COC4D.bin.11.fa	924	161	108	24	135	2	0	0	0	93.67	1.39	0
COC4D.bin.11.fa	35	495	282	58	415	22	0	0	0	93.67	3.92	0
2021_COC4R.bin.18.fa	350	316	210	16	294	6	0	0	0	93.65	2.62	66.67
COA2R.bin.16.fa	69	400	198	36	352	12	0	0	0	93.63	2.36	8.33
2021_COC1D.bin.15.fa	901	171	117	11	158	2	0	0	0	93.6	1.28	0
COC2S.bin.2.fa	732	200	117	11	182	7	0	0	0	93.59	2.35	14.29
CSC2D.bin.44.fa	732	200	117	27	161	9	2	1	0	93.58	6.3	9.52
2021_CSA3R.bin.1.fa	67	481	276	21	438	20	2	0	0	93.57	5.73	11.54
COA2S.bin.5.fa	924	161	108	7	150	4	0	0	0	93.52	3.24	50
2021_COC1D.bin.1.fa	924	161	108	15	135	3	2	6	0	93.52	3.79	17.78
COC4D.bin.3.fa	924	161	108	23	132	6	0	0	0	93.49	4.81	16.67
CSA2S.bin.68.fa	35	495	282	35	435	24	1	0	0	93.45	5.26	25.93
COC1S.bin.12.fa	924	161	108	9	142	10	0	0	0	93.42	6.48	50
2021_COC4D.bin.2.fa	732	200	117	18	179	3	0	0	0	93.39	1.35	66.67
COC4S.bin.20.fa	5449	104	58	5	83	15	1	0	0	93.39	7.63	27.78
CSA4R.bin.16.fa	732	199	116	19	176	4	0	0	0	93.38	3.02	25
2021_COA3R.bin.8.fa	120	574	266	37	519	18	0	0	0	93.35	3.46	50
2021_COA4R.bin.7.fa	120	574	266	50	499	19	6	0	0	93.35	4.42	27.03
2021_COC4D.bin.6.fa	2258	188	117	14	166	8	0	0	0	93.35	5.25	25
3300045001_23	924	161	108	18	139	4	0	0	0	93.32	2.31	75
08_2_bin.2	488	309	185	20	277	8	3	0	1	93.26	4.53	22.22
CSA4S.bin.7.fa	901	171	117	17	142	11	1	0	0	93.25	8.46	42.86

2021_CSC3R.bin.4.fa	78	840	354	77	734	28	1	0	0	93.19	3.55	9.68
COC4S.bin.13.fa	732	200	117	14	181	5	0	0	0	93.16	2.22	40
24_2_bin.1	488	309	185	20	282	6	0	1	0	93.16	2.69	16.67
CSA2R.bin.9.fa	108	570	250	76	478	16	0	0	0	93.15	2.42	37.5
2021_CSC4R.bin.2.fa	732	200	117	18	173	9	0	0	0	93.08	3.13	11.11
COA3R.bin.4.fa	55	659	290	65	572	22	0	0	0	93.06	3.71	45.45
COC4D.bin.32.fa	901	171	117	17	147	7	0	0	0	92.95	2.42	0
COC3R.bin.26.fa	35	495	282	58	415	20	2	0	0	92.91	5.13	15.38
COC4D.bin.17.fa	924	161	108	13	148	0	0	0	0	92.9	0	0
3300044672_20	55	659	290	50	601	8	0	0	0	92.88	1.88	25
CSA2S.bin.29.fa	732	200	117	12	184	4	0	0	0	92.85	0.76	75
COC4R.bin.8.fa	35	495	282	39	443	13	0	0	0	92.82	2.78	15.38
CSA4R.bin.11.fa	91	596	218	70	511	15	0	0	0	92.64	4.26	40
2021_COC4D.bin.13.fa	924	161	108	8	152	1	0	0	0	92.59	0.46	100
3300045001_5	35	495	282	50	418	26	1	0	0	92.59	5.45	3.45
2021_COA2R.bin.13.fa	69	400	198	58	325	17	0	0	0	92.56	4.25	17.65
3300045003_43	26	529	308	54	460	13	1	0	1	92.55	4.65	9.68
CSA1R.bin.3.fa	924	155	106	13	139	3	0	0	0	92.51	2.83	0
2021_COA2R.bin.7.fa	26	529	308	67	447	15	0	0	0	92.49	4.09	40
COC4S.bin.31.fa	924	161	108	27	124	10	0	0	0	92.49	4.23	50
CSC4S.bin.12.fa	2258	188	117	15	155	17	1	0	0	92.47	8.77	80
2021_COC1D.bin.12.fa	2258	188	117	30	152	6	0	0	0	92.46	3.21	83.33
2021_COC4D.bin.3.fa	924	161	108	26	128	7	0	0	0	92.44	5.86	42.86
2021_CSC3S.bin.17.fa	455	311	187	41	262	8	0	0	0	92.43	2.5	37.5
2021_CSC3R.bin.3.fa	732	199	116	19	177	3	0	0	0	92.41	2.16	0
COA3R.bin.9.fa	108	570	250	76	478	16	0	0	0	92.38	4.06	25
COC1R.bin.3.fa	193	427	214	50	374	3	0	0	0	92.37	1.17	33.33
COC3D.bin.7.fa	268	398	220	36	347	15	0	0	0	92.37	2.41	46.67
COC1D.bin.15.fa	107	485	316	39	426	20	0	0	0	92.37	4.66	50
COA1R.bin.10.fa	193	427	214	62	347	18	0	0	0	92.36	6.31	27.78
3300044654_35	35	495	282	57	422	15	1	0	0	92.34	3.56	22.22

COC4S.bin.6.fa	732	200	117	19	167	14	0	0	0	92.34	3.85	64.29
CSA2S.bin.39.fa	35	495	282	37	440	18	0	0	0	92.33	3.9	22.22
CSC4D.bin.18.fa	732	200	117	9	186	5	0	0	0	92.31	3.42	0
COA2S.bin.10.fa	732	200	117	11	179	10	0	0	0	92.31	4.42	20
2021_COC4S.bin.16.fa	732	200	117	11	180	9	0	0	0	92.31	4.66	66.67
COC3R.bin.18.fa	92	481	319	38	427	15	1	0	0	92.29	3.71	11.11
2021_COC1R.bin.7.fa	55	659	290	65	574	19	1	0	0	92.27	3.57	13.64
CSA4R.bin.4.fa	91	596	218	72	507	17	0	0	0	92.27	3.79	52.94
2021_CSC3S.bin.12.fa	35	495	282	41	437	17	0	0	0	92.17	3.26	11.76
COC4D.bin.40.fa	2258	188	117	18	164	6	0	0	0	92.15	4.33	16.67
CSA3R.bin.4.fa	193	427	214	53	360	13	1	0	0	92.13	3.94	43.75
3300044689_8	732	200	117	19	169	12	0	0	0	92.11	4.42	8.33
CSC3S.bin.62.fa	455	311	187	45	251	15	0	0	0	92.11	4.86	33.33
COC4S.bin.16.fa	67	481	276	54	407	17	2	1	0	92.11	6.59	0
COC4S.bin.27.fa	924	151	101	15	132	4	0	0	0	92.08	3.96	25
CSC4S.bin.1.fa	732	200	117	23	174	3	0	0	0	92.05	1.42	66.67
3300044694_9	60	460	233	79	370	11	0	0	0	92.02	2.21	63.64
2021_CSC1R.bin.12.fa	60	460	233	75	360	25	0	0	0	92	5.83	60
2021_CSC4S.bin.5.fa	732	200	117	23	169	8	0	0	0	91.99	2.99	62.5
2021_COC2D.bin.3.fa	107	485	316	49	425	11	0	0	0	91.98	2.66	54.55
CSC2D.bin.3.fa	732	200	117	14	181	5	0	0	0	91.97	2.56	60
3300044693_2	323	387	234	58	320	9	0	0	0	91.88	2.99	22.22
2021_COC3D.bin.7.fa	107	485	316	42	417	26	0	0	0	91.87	6.14	34.62
CSC3D.bin.7.fa	732	199	116	14	180	5	0	0	0	91.83	1.59	0
3300044654_37	35	495	282	39	446	10	0	0	0	91.81	2.48	20
COA2R.bin.3.fa	55	659	290	79	566	14	0	0	0	91.78	2.78	28.57
CSC3R.bin.8.fa	78	840	354	89	733	18	0	0	0	91.67	2.2	16.67
COA3E.bin.2.fa	91	596	218	59	518	19	0	0	0	91.67	3.41	15.79
2021_COC4R.bin.16.fa	55	659	290	101	524	32	2	0	0	91.65	7.1	31.58
COC1S.bin.10.fa	924	151	101	14	136	1	0	0	0	91.64	0.99	0
CSA1R.bin.1.fa	55	659	290	81	535	43	0	0	0	91.58	6.04	9.3

2021_COC1R.bin.9.fa	364	302	203	58	226	15	3	0	0	91.58	8.78	66.67
CSC4R.bin.14.fa	60	460	233	78	359	23	0	0	0	91.55	4.45	47.83
COC2D.bin.14.fa	107	485	316	55	419	11	0	0	0	91.53	2.66	54.55
COA3S.bin.4.fa	732	199	116	22	174	3	0	0	0	91.49	2.59	0
CSA2S.bin.58.fa	488	309	185	32	267	10	0	0	0	91.47	2.8	0
CSASD.bin.4.fa	35	495	282	52	426	17	0	0	0	91.47	3.58	11.76
2021_COC1D.bin.5.fa	455	311	187	49	248	13	1	0	0	91.46	5.31	43.75
COA2R.bin.1.fa	26	529	308	45	463	20	1	0	0	91.42	5.54	43.48
CSA2R.bin.1.fa	2258	188	117	30	143	14	1	0	0	91.39	9.12	76.47
CSC4R.bin.11.fa	488	309	185	25	268	8	8	0	0	91.38	4.09	31.25
CSA2S.bin.55.fa	732	200	117	20	170	10	0	0	0	91.38	5.01	40
COC4R.bin.7.fa	350	316	210	27	283	6	0	0	0	91.35	2.62	66.67
COA3D.bin.4.fa	732	200	117	23	175	2	0	0	0	91.32	1.14	0
2021_COC4S.bin.15.fa	67	481	276	48	409	23	1	0	0	91.32	6.54	23.08
COC1R.bin.7.fa	55	659	290	94	552	13	0	0	0	91.28	2.11	15.38
2021_CSC3R.bin.6.fa	35	495	282	40	445	10	0	0	0	91.28	2.13	20
2021_CSC2S.bin.5.fa	63	336	201	30	297	9	0	0	0	91.27	2.63	66.67
COC1D.bin.12.fa	2258	188	117	45	138	5	0	0	0	91.27	3.59	40
COC3R.bin.15.fa	55	659	290	92	546	20	1	0	0	91.26	3.49	65.22
COC3R.bin.8.fa	108	570	250	84	456	24	5	1	0	91.16	5.53	53.33
19_2_bin.1	2258	188	117	28	153	7	0	0	0	91.13	4.61	57.14
COC2R.bin.9.fa	119	544	284	76	449	19	0	0	0	91.11	3.51	0
2021_CSA4D.bin.1.fa	2258	188	117	21	157	9	1	0	0	91.11	6.18	75
3300045838_35	732	200	117	25	174	1	0	0	0	91.1	0.85	0
COC2D.bin.11.fa	732	199	116	29	162	8	0	0	0	91.09	3.16	12.5
2021_CSC3S.bin.14.fa	732	200	117	41	149	10	0	0	0	91.09	7.26	0
2021_COC4S.bin.8.fa	732	200	117	23	174	3	0	0	0	91.05	2.14	0
COC3D.bin.2.fa	35	495	282	38	435	22	0	0	0	91.05	3.98	31.82
CSA2S.bin.15.fa	924	161	108	26	127	8	0	0	0	91.05	7.41	25
CSC1R.bin.4.fa	732	200	117	43	156	1	0	0	0	91.04	0.85	100
COA2D.bin.7.fa	35	495	282	39	442	12	2	0	0	91.02	3.34	27.78

CSC1R.bin.16.fa	193	427	214	72	339	14	2	0	0	91	5.2	30
CSC2S.bin.5.fa	63	336	201	23	307	6	0	0	0	90.99	1.9	83.33
2021_COC1R.bin.3.fa	193	427	214	60	341	25	1	0	0	90.99	8.52	35.71
COC1S.bin.57.fa	924	161	108	16	142	3	0	0	0	90.97	2.16	33.33
2021_COC1D.bin.8.fa	455	311	187	50	241	18	2	0	0	90.89	6.09	16.67
2021_COC2R.bin.20.fa	60	460	233	86	347	27	0	0	0	90.88	7.44	40.74
2021_COC3D.bin.8.fa	35	495	282	40	440	15	0	0	0	90.87	3.23	33.33
COA1R.bin.13.fa	35	495	282	70	387	37	1	0	0	90.87	8.76	52.5
2021_COA4R.bin.1.fa	924	155	106	16	135	4	0	0	0	90.83	3.77	0
COC4R.bin.14.fa	119	544	284	82	435	26	1	0	0	90.8	5.07	17.24
2021_CSA1R.bin.5.fa	334	370	206	44	302	22	2	0	0	90.8	7.31	35.71
2021_COC2D.bin.12.fa	207	145	103	11	131	3	0	0	0	90.78	2.91	0
COC2D.bin.4.fa	207	145	103	11	131	3	0	0	0	90.78	2.91	0
CSA1S.bin.8.fa	35	495	282	47	427	20	1	0	0	90.76	4.96	65.22
2021_CSC2S.bin.3.fa	901	171	117	14	147	10	0	0	0	90.74	5.94	50
2021_CSA1R.bin.2.fa	55	659	290	85	541	33	0	0	0	90.71	3.94	3.03
2021_CSC3S.bin.4.fa	732	200	117	22	169	8	1	0	0	90.68	6.84	9.09
3300045836_24	35	495	282	40	438	16	1	0	0	90.61	4.02	42.11
COA2S.bin.9.fa	2258	188	117	30	146	12	0	0	0	90.59	8.17	25
COC2D.bin.12.fa	2258	188	117	21	159	8	0	0	0	90.57	3.86	62.5
2021_COC2R.bin.15.fa	119	544	284	69	457	18	0	0	0	90.56	3.06	0
CSA2R.bin.45.fa	26	529	308	54	456	18	1	0	0	90.54	3.99	14.29
2021_COA1R.bin.8.fa	35	495	282	73	389	32	1	0	0	90.49	9.23	51.43
2021_CSA3R.bin.2.fa	108	570	250	81	466	23	0	0	0	90.48	3.9	60.87
COC1R.bin.5.fa	268	395	220	62	318	15	0	0	0	90.47	3.45	93.33
CSC1D.bin.3.fa	732	199	116	34	158	7	0	0	0	90.45	4.02	28.57
2021_COA1R.bin.2.fa	323	387	234	55	299	33	0	0	0	90.42	8.23	33.33
2021_COA4D.bin.1.fa	2258	188	117	26	153	9	0	0	0	90.41	4.06	66.67
2021_COC4D.bin.10.fa	901	171	117	16	142	13	0	0	0	90.4	9.12	15.38
3300045049_56	193	427	214	53	368	6	0	0	0	90.36	1.79	66.67
2021_COC1D.bin.4.fa	107	485	316	58	408	19	0	0	0	90.35	4.1	57.89

COA1R.bin.8.fa	323	387	234	55	299	32	1	0	0	90.35	8.99	42.86
CSC3D.bin.10.fa	2258	188	117	35	150	3	0	0	0	90.33	1.99	33.33
3300044765_12	55	659	290	68	573	18	0	0	0	90.33	2.15	11.11
04_2_bin.2	387	330	193	22	291	17	0	0	0	90.33	5.57	11.76
COA1R.bin.11.fa	193	427	214	74	331	21	1	0	0	90.32	4.64	33.33
COA3D.bin.2.fa	901	171	117	23	141	7	0	0	0	90.3	4.91	85.71
CSC1R.bin.13.fa	60	460	233	87	359	14	0	0	0	90.28	2.36	57.14
08_2_bin.3	193	427	214	39	365	22	1	0	0	90.23	3.2	36
CSC4R.bin.10.fa	732	200	117	24	168	8	0	0	0	90.23	4.7	0
CSC4D.bin.2.fa	107	485	316	54	415	16	0	0	0	90.21	3.56	31.25
COC4R.bin.5.fa	108	570	250	87	473	10	0	0	0	90.18	2.43	60
CSA3R.bin.5.fa	924	151	101	13	133	5	0	0	0	90.17	4.95	20
3300044656_22	364	302	203	26	273	3	0	0	0	90.16	1.01	100
COA3D.bin.3.fa	2258	188	117	48	132	8	0	0	0	90.15	5.47	25
2021_CSC4S.bin.9.fa	207	145	103	16	123	6	0	0	0	90.13	5.83	0
CSA1R.bin.9.fa	334	370	206	45	314	9	2	0	0	90.12	3.93	26.67
2021_COC4R.bin.2.fa	2993	147	91	12	127	8	0	0	0	90.11	7.51	37.5
2021_COA1R.bin.15.fa	193	427	214	65	359	3	0	0	0	90.06	1.17	0
COC2S.bin.7.fa	2258	188	117	47	135	6	0	0	0	90.06	4.32	16.67
CSC4D.bin.15.fa	107	485	316	55	413	17	0	0	0	90.04	3.69	58.82
COC3R.bin.10.fa	268	395	220	43	349	3	0	0	0	90	0.49	100
COA2S.bin.1.fa	148	188	125	16	168	4	0	0	0	90	2.4	0
COA2D.bin.3.fa	732	200	117	26	158	13	3	0	0	89.99	5.13	27.27
3300045744_21	732	200	117	30	168	2	0	0	0	89.96	1.71	50
COC4S.bin.26.fa	732	200	117	24	162	12	2	0	0	89.94	5.38	72.22
COA1D.bin.3.fa	268	398	220	39	325	33	1	0	0	89.91	7.17	52.78
3300044842_11	60	460	233	65	372	22	1	0	0	89.9	6.33	24
COA4R.bin.6.fa	924	155	106	17	135	3	0	0	0	89.89	2.83	0
3300045003_14	2258	188	117	47	136	5	0	0	0	89.89	3.28	80
2021_COC2R.bin.13.fa	193	427	214	64	339	23	1	0	0	89.88	6.7	50
COC4D.bin.15.fa	732	200	117	25	173	2	0	0	0	89.86	0.5	100

2021_CSC1R.bin.6.fa	268	395	220	62	320	13	0	0	0	89.86	3.35	46.15
2021_CSC1R.bin.7.fa	732	200	117	33	163	4	0	0	0	89.84	2.56	50
3300045014_31	2258	188	117	51	134	3	0	0	0	89.77	1.92	66.67
3300044705_15	732	199	116	41	156	2	0	0	0	89.75	1.03	0
2021_COC1D.bin.16.fa	732	199	116	28	162	9	0	0	0	89.74	5.17	66.67
3300044705_16	223	425	211	45	373	6	1	0	0	89.72	1.78	55.56
CSASD.bin.5.fa	455	315	190	56	254	5	0	0	0	89.69	2.37	20
21_2_bin.3	5449	104	58	9	74	20	1	0	0	89.66	7.41	8.7
CSA2S.bin.33.fa	268	398	220	48	324	25	1	0	0	89.58	5.45	53.57
3300045838_42	2258	188	117	52	133	3	0	0	0	89.54	2.56	0
2021_CSA3R.bin.3.fa	193	427	214	75	339	13	0	0	0	89.54	2.82	53.85
CSA2D.bin.1	732	199	116	34	162	3	0	0	0	89.53	2.16	33.33
CSASD.bin.1.fa	732	199	116	34	162	3	0	0	0	89.53	2.16	33.33
COC4D.bin.28.fa	732	200	117	32	165	3	0	0	0	89.52	2.14	66.67
3300044693_6	60	460	233	81	364	14	1	0	0	89.46	3.82	52.94
CSC4S.bin.10.fa	2258	188	117	26	153	9	0	0	0	89.43	4.99	11.11
2021_COC2D.bin.14.fa	2993	147	91	40	102	5	0	0	0	89.41	4.95	20
2021_CSC3S.bin.28.fa	732	200	117	21	175	4	0	0	0	89.4	3.42	0
2021_COC4R.bin.22.fa	108	570	250	80	463	27	0	0	0	89.37	3.95	51.85
CSA2R.bin.63.fa	26	529	308	75	435	18	1	0	0	89.36	3.99	14.29
3300044667_2	35	495	282	50	425	20	0	0	0	89.35	2.86	45
2021_CSA1S.bin.2.fa	35	495	282	55	419	20	1	0	0	89.34	4.96	65.22
2021_COC2R.bin.21.fa	35	495	282	93	371	31	0	0	0	89.33	6.35	35.48
2021_COC4S.bin.26.fa	732	200	117	19	174	7	0	0	0	89.23	2.71	71.43
2021_COC4D.bin.7.fa	732	200	117	29	163	8	0	0	0	89.21	1.37	50
3300044652_2	334	368	206	54	307	7	0	0	0	89.1	2.91	42.86
3300044685_18	2258	188	117	52	129	7	0	0	0	89.1	4.91	57.14
COA4D.bin.4.fa	2258	188	117	24	155	9	0	0	0	89.07	3.63	77.78
CSA2S.bin.10.fa	732	199	116	29	163	7	0	0	0	88.98	5.6	28.57
COC3D.bin.6.fa	107	485	316	58	409	17	1	0	0	88.97	3.96	25
CSA2S.bin.23.fa	455	311	187	46	252	13	0	0	0	88.94	5.61	38.46

3300044765_30	69	400	198	41	343	16	0	0	0	88.91	4.58	6.25
COA1R.bin.3.fa	193	426	214	86	316	23	1	0	0	88.9	6.8	38.46
COC2S.bin.1.fa	924	161	108	13	136	12	0	0	0	88.89	3.65	25
3300045837_39	35	495	282	57	428	9	1	0	0	88.87	2.54	16.67
2021_COC2D.bin.11.fa	2258	188	117	23	157	8	0	0	0	88.87	3.86	62.5
CSC4D.bin.19.fa	732	199	116	21	167	10	1	0	0	88.83	3.59	53.85
2021_COA1R.bin.6.fa	193	427	214	71	327	28	1	0	0	88.83	7.99	41.94
3300045836_35	63	336	201	54	280	2	0	0	0	88.82	1	50
COC1D.bin.8.fa	455	311	187	51	254	6	0	0	0	88.82	2.32	50
3300044656_32	26	529	308	80	439	10	0	0	0	88.78	2.21	60
CSA4D.bin.2.fa	2258	188	117	26	154	7	1	0	0	88.76	5.27	70
3300044741_25	924	161	108	20	141	0	0	0	0	88.72	0	0
CSC1R.bin.2.fa	55	659	290	116	510	30	2	1	0	88.7	6.24	23.81
COA3R.bin.5.fa	64	769	248	98	653	18	0	0	0	88.69	2.27	61.11
2021_CSC3S.bin.27.fa	732	199	116	27	165	7	0	0	0	88.65	3.76	14.29
CSA4R.bin.14.fa	387	330	193	55	265	9	1	0	0	88.64	4.66	41.67
CSC4S.bin.8.fa	107	485	316	56	406	22	1	0	0	88.63	2.64	40
2021_CSC2D.bin.3.fa	107	485	316	60	406	18	1	0	0	88.63	5.35	61.9
3300044741_8	35	495	282	46	437	12	0	0	0	88.61	1.99	41.67
2021_COC1R.bin.12.fa	268	395	220	59	327	9	0	0	0	88.6	1.96	66.67
3300044688_17	35	495	282	52	431	12	0	0	0	88.55	2.26	33.33
3300044719_30	60	460	233	64	386	10	0	0	0	88.46	2.37	40
COC4S.bin.11.fa	901	171	117	14	151	6	0	0	0	88.46	3.28	0
CSC3S.bin.2.fa	2993	147	91	17	124	6	0	0	0	88.43	6.59	0
2021_CSC1R.bin.5.fa	455	315	190	46	263	6	0	0	0	88.4	2.24	0
2021_CSC3R.bin.2.fa	193	426	214	83	335	8	0	0	0	88.4	2.62	25
2021_CSC2D.bin.10.fa	924	151	101	34	112	5	0	0	0	88.38	4.95	20
2021_CSC2D.bin.7.fa	732	200	117	38	153	7	2	0	0	88.28	2.85	7.69
CSA2R.bin.24.fa	60	460	233	93	352	15	0	0	0	88.27	3.67	33.33
2021_CSA1R.bin.7.fa	732	199	116	29	161	8	1	0	0	88.26	4.22	63.64
04_2_bin.1	924	161	108	26	131	4	0	0	0	88.25	2.62	25

2021_COC4D.bin.5.fa	334	368	206	71	272	22	2	1	0	88.18	9.6	35.29
2021_CSC4R.bin.12.fa	60	460	233	95	355	10	0	0	0	88.16	1.97	30
3300045014_30	2258	188	117	41	145	2	0	0	0	88.11	1.71	50
2021_COA1R.bin.3.fa	55	659	290	83	536	40	0	0	0	88.07	5.01	85
COC2D.bin.7.fa	924	151	101	28	120	3	0	0	0	88.02	2.09	66.67
2021_CSC2S.bin.1.fa	69	400	198	47	344	9	0	0	0	88.02	2.91	77.78
CSA4R.bin.17.fa	274	388	214	55	311	22	0	0	0	88.01	3.74	18.18
COC3R.bin.22.fa	564	345	226	55	276	14	0	0	0	87.97	4.1	21.43
2021_CSC4S.bin.10.fa	107	485	316	61	410	14	0	0	0	87.96	3.22	50
2021_CSC3R.bin.7.fa	564	345	226	67	259	19	0	0	0	87.95	3.99	47.37
3300044690_13	732	200	117	19	181	0	0	0	0	87.89	0	0
2021_COC1D.bin.14.fa	901	171	117	15	151	5	0	0	0	87.89	2.66	60
2021_COA4R.bin.3.fa	91	596	218	99	467	30	0	0	0	87.87	5.32	3.33
2021_COC4R.bin.29.fa	193	427	214	77	325	25	0	0	0	87.8	7.7	20
COC4R.bin.11.fa	924	151	101	37	109	5	0	0	0	87.79	4.95	0
21_2_bin.2	924	151	101	14	127	9	1	0	0	87.79	7.46	8.33
2021_CSC3S.bin.11.fa	274	388	214	51	325	12	0	0	0	87.75	2.52	33.33
3300044667_48	387	330	193	45	276	9	0	0	0	87.74	2.33	11.11
3300044686_5	924	161	108	24	136	1	0	0	0	87.7	0.93	0
2021_COA3D.bin.4.fa	268	398	220	57	304	35	2	0	0	87.69	9.62	21.95
3300044685_11	334	368	206	50	301	17	0	0	0	87.66	6.07	17.65
CSA1D.bin.22.fa	924	151	101	31	116	4	0	0	0	87.64	3.17	0
2021_COC2D.bin.10.fa	732	199	116	33	156	10	0	0	0	87.64	4.89	10
2021_COC2D.bin.1.fa	924	151	101	30	118	3	0	0	0	87.62	2.09	66.67
COC3R.bin.23.fa	924	151	101	22	126	2	1	0	0	87.62	3.47	40
2021_COA1R.bin.1.fa	46	481	186	80	398	3	0	0	0	87.59	0.72	33.33
CSC3D.bin.1.fa	2258	188	117	25	152	10	1	0	0	87.58	5.68	76.92
COA3S.bin.12.fa	732	199	116	33	153	13	0	0	0	87.5	7.26	46.15
2021_CSC3R.bin.11.fa	60	460	233	104	327	29	0	0	0	87.45	7.53	55.17
2021_CSC3R.bin.1.fa	2258	188	117	51	134	3	0	0	0	87.44	1.28	100
COA2S.bin.16.fa	732	199	116	29	162	8	0	0	0	87.43	3.53	50

CSC3S.bin.30.fa	732	199	116	51	147	0	0	1	0	87.39	2.59	16.67
2021_CSA4D.bin.5.fa	732	199	116	29	165	4	1	0	0	87.35	4.45	0
CSA3D.bin.1.fa	732	200	117	30	165	5	0	0	0	87.32	1.54	80
COA2D.bin.6.fa	732	200	117	28	162	5	5	0	0	87.32	3.77	35
COC2R.bin.3.fa	64	769	248	148	595	25	1	0	0	87.29	3.44	57.14
COA2S.bin.13.fa	732	199	116	31	157	11	0	0	0	87.28	2.01	27.27
CSC2D.bin.16.fa	107	485	316	69	404	12	0	0	0	87.21	2.9	58.33
3300044901_10	732	200	117	48	143	8	1	0	0	87.18	4.13	0
COC4D.bin.20.fa	2258	188	117	28	152	8	0	0	0	87.16	5.18	50
COC3R.bin.27.fa	364	302	203	64	221	17	0	0	0	87.14	4.71	64.71
CSC4D.bin.12.fa	732	200	117	28	157	10	5	0	0	87.13	9.02	24
CSC4R.bin.17.fa	193	427	214	85	332	10	0	0	0	87.12	2.1	20
CSC3R.bin.1.fa	564	345	226	74	254	17	0	0	0	87.12	5.09	52.94
2021_CSA3R.bin.4.fa	732	199	116	28	165	6	0	0	0	87.1	3.97	66.67
COC1D.bin.6.fa	901	171	117	17	146	8	0	0	0	87.08	3.68	12.5
COC2R.bin.1.fa	732	200	117	49	147	4	0	0	0	87.07	1.2	25
21_2_bin.1	364	302	203	73	223	6	0	0	0	87.07	2.22	0
3300044842_7	364	302	203	74	222	6	0	0	0	86.94	2.22	50
CSC1R.bin.10.fa	455	315	190	66	242	7	0	0	0	86.93	2.54	0
COC4R.bin.19.fa	55	659	290	109	519	30	1	0	0	86.92	5.7	15.15
2021_COC1D.bin.13.fa	223	425	211	57	355	11	2	0	0	86.91	2.76	5.88
COA3S.bin.7.fa	35	495	282	82	399	13	1	0	0	86.89	4.23	68.75
2021_CSC3S.bin.1.fa	732	199	116	56	141	2	0	0	0	86.87	1.29	0
2021_COC4S.bin.27.fa	732	199	116	36	156	7	0	0	0	86.87	3.16	14.29
3300044684_55	35	495	282	50	435	10	0	0	0	86.84	1.95	20
3300044694_34	35	495	282	86	400	9	0	0	0	86.82	1.6	0
COC2D.bin.1.fa	732	199	116	29	164	6	0	0	0	86.8	3.48	33.33
COA1R.bin.12.fa	924	151	101	14	128	9	0	0	0	86.8	6.53	33.33
CSC2S.bin.3.fa	732	199	116	39	143	17	0	0	0	86.8	8.04	70.59
CSA4R.bin.5.fa	387	330	193	59	256	15	0	0	0	86.79	4.68	40
CSA1R.bin.6.fa	55	659	290	102	527	29	1	0	0	86.77	3.29	12.5

CSC4S.bin.17.fa	924	161	108	23	130	7	1	0	0	86.77	6.29	0
3300044964_18	35	495	282	63	416	16	0	0	0	86.69	3.52	25
CSA2R.bin.60.fa	193	427	214	80	329	18	0	0	0	86.69	5.21	44.44
20_2_bin.2	488	309	185	40	262	6	1	0	0	86.68	4.05	22.22
CSC3R.bin.4.fa	193	427	214	74	347	6	0	0	0	86.65	1.56	50
3300044735_22	924	151	101	34	112	5	0	0	0	86.6	4.95	0
COC4R.bin.6.fa	5449	104	58	12	71	18	3	0	0	86.6	9.8	51.85
2021_CSC3S.bin.22.fa	2993	147	91	51	91	5	0	0	0	86.59	5.49	0
COA2S.bin.18.fa	924	161	108	26	134	1	0	0	0	86.57	0.93	0
COC4R.bin.2.fa	193	427	214	76	327	24	0	0	0	86.57	5.74	37.5
3300045013_40	2258	188	117	60	126	2	0	0	0	86.49	1.71	50
2021_CSA1S.bin.8.fa	387	330	193	81	236	12	1	0	0	86.34	4.32	6.67
COA1R.bin.20.fa	55	659	290	105	531	21	2	0	0	86.33	3.89	66.67
CSC4D.bin.3.fa	488	309	185	50	242	16	1	0	0	86.31	5.41	5.26
2021_COC2D.bin.5.fa	732	199	116	33	160	6	0	0	0	86.3	3.48	33.33
COC2R.bin.18.fa	2993	147	91	14	128	4	1	0	0	86.26	3.58	14.29
CSC3S.bin.68.fa	5449	104	58	42	59	3	0	0	0	86.21	4.31	0
CSA4D.bin.4.fa	732	199	116	33	150	13	3	0	0	86.21	6.15	50
CSC1D.bin.6.fa	268	398	220	66	324	8	0	0	0	86.2	1.87	62.5
2021_CSA3R.bin.8.fa	924	151	101	17	129	5	0	0	0	86.2	4.95	20
2021_COC2R.bin.2.fa	732	200	117	49	148	3	0	0	0	86.15	1.17	66.67
COC3R.bin.25.fa	60	460	233	87	357	15	1	0	0	86.13	2.17	27.78
CSC1D.bin.7.fa	268	398	220	64	322	12	0	0	0	86.13	2.53	75
2021_COC4D.bin.12.fa	2258	188	117	32	147	9	0	0	0	86.12	5.41	77.78
CSC4S.bin.2.fa	207	145	103	21	121	3	0	0	0	86.08	2.91	0
CSC4S.bin.9.fa	732	200	117	32	160	8	0	0	0	85.98	1.45	50
CSA4D.bin.5.fa	732	199	116	32	160	6	1	0	0	85.97	5.32	0
2021_COC4S.bin.22.fa	924	161	108	29	129	3	0	0	0	85.94	1.85	33.33
COA3R.bin.11.fa	108	570	250	92	471	7	0	0	0	85.91	0.97	57.14
CSC2S.bin.1.fa	901	171	117	27	135	9	0	0	0	85.91	4.37	44.44
COC2D.bin.6.fa	2993	147	91	47	96	4	0	0	0	85.86	3.85	0

COC1S.bin.4.fa	564	349	230	61	274	14	0	0	0	85.83	4.39	28.57
CSA1S.bin.4.fa	387	330	193	79	240	11	0	0	0	85.79	3.7	9.09
CSA4D.bin.3.fa	2258	188	117	34	150	4	0	0	0	85.71	2.62	25
2021_CSA4D.bin.2.fa	2258	188	117	34	149	5	0	0	0	85.71	2.9	40
2021_CSC3S.bin.7.fa	2993	147	91	25	117	5	0	0	0	85.66	5.49	0
COA2S.bin.19.fa	2258	188	117	27	146	14	1	0	0	85.65	9.32	5.88
CSC2S.bin.14.fa	69	400	198	53	340	7	0	0	0	85.61	1.89	100
COA3S.bin.8.fa	732	199	116	30	163	6	0	0	0	85.6	3.59	33.33
CSC3S.bin.39.fa	732	199	116	38	144	17	0	0	0	85.6	9.97	41.18
3300044658_13	55	659	290	85	560	14	0	0	0	85.59	2.49	7.14
2021_COA3D.bin.3.fa	901	171	117	34	125	12	0	0	0	85.59	6.92	66.67
2021_COC2R.bin.10.fa	64	769	248	192	517	60	0	0	0	85.49	7.1	23.33
COA2S.bin.4.fa	732	200	117	29	166	5	0	0	0	85.47	2.64	40
COA3R.bin.6.fa	88	230	148	53	165	11	1	0	0	85.47	4.97	14.29
COA3S.bin.13.fa	2258	188	117	28	151	9	0	0	0	85.47	5.73	55.56
2021_CSC1R.bin.9.fa	193	427	214	71	313	37	6	0	0	85.47	9.93	32.73
2021_CSC4R.bin.3.fa	193	427	214	92	326	9	0	0	0	85.31	2.57	22.22
COA2S.bin.15.fa	732	200	117	24	168	8	0	0	0	85.3	5.98	25
2021_COC4D.bin.4.fa	901	171	117	29	141	1	0	0	0	85.19	0.85	0
CSA1R.bin.8.fa	46	481	186	78	395	8	0	0	0	85.19	0.87	12.5
CSA2R.bin.38.fa	1495	261	164	64	190	7	0	0	0	85.06	3.66	71.43
COC1D.bin.7.fa	455	311	187	68	223	20	0	0	0	85.02	7.83	20
COC4R.bin.16.fa	2993	147	91	32	107	8	0	0	0	84.97	4.8	50
3300045976_17	44	1171	324	211	953	7	0	0	0	84.93	0.68	42.86
CSC3S.bin.44.fa	732	199	116	40	157	2	0	0	0	84.91	1.72	0
CSC1R.bin.12.fa	268	395	220	76	309	10	0	0	0	84.89	2.16	20
14_2_bin.3	924	161	108	20	130	11	0	0	0	84.88	6.33	9.09
COA3D.bin.6.fa	901	171	117	35	122	14	0	0	0	84.78	6.45	7.14
COC2R.bin.6.fa	334	368	206	88	261	17	2	0	0	84.77	6.63	26.09
CSA4R.bin.3.fa	732	199	116	52	143	4	0	0	0	84.71	1.94	100
2021_COC4S.bin.9.fa	2258	187	116	41	142	4	0	0	0	84.7	1.77	0

2021_CSC3S.bin.2.fa	35	495	282	74	380	38	3	0	0	84.67	6.48	12.77
COC1D.bin.13.fa	334	370	206	65	282	19	4	0	0	84.63	6.25	38.71
2021_COA3D.bin.6.fa	901	171	117	26	133	11	1	0	0	84.61	9.32	0
COC2D.bin.5.fa	564	345	226	61	268	16	0	0	0	84.6	3.8	56.25
3300044684_41	67	481	276	82	375	24	0	0	0	84.59	5.43	33.33
COC1D.bin.5.fa	732	199	116	42	154	3	0	0	0	84.57	1.9	33.33
2021_CSC3S.bin.15.fa	35	495	282	103	368	23	1	0	0	84.56	6.3	34.62
2021_COC1R.bin.1.fa	334	368	206	71	270	24	3	0	0	84.53	7.3	42.42
COC1R.bin.9.fa	387	330	193	48	271	11	0	0	0	84.52	3.11	36.36
CSA2S.bin.18.fa	2258	188	117	31	153	4	0	0	0	84.51	2.62	75
COA3S.bin.6.fa	924	151	101	24	125	2	0	0	0	84.49	1.1	50
COC1D.bin.1.fa	223	425	211	76	332	16	1	0	0	84.49	2.31	15.79
2021_CSC1R.bin.4.fa	5449	104	58	47	57	0	0	0	0	84.48	0	0
COC4R.bin.24.fa	5449	104	58	47	56	1	0	0	0	84.48	1.72	0
COA4R.bin.3.fa	5449	104	58	47	55	2	0	0	0	84.48	2.59	50
COA3R.bin.12.fa	5449	104	58	47	54	3	0	0	0	84.48	5.17	0
CSA2D.bin.9	207	145	103	28	115	2	0	0	0	84.44	1.94	0
CSASD.bin.9.fa	207	145	103	28	115	2	0	0	0	84.44	1.94	0
2021_COA4R.bin.6.fa	387	330	193	68	234	27	1	0	0	84.44	8.31	6.67
2021_COC4R.bin.25.fa	924	151	101	42	103	6	0	0	0	84.42	5.94	0
CSC2D.bin.22.fa	924	151	101	38	105	8	0	0	0	84.42	7.43	12.5
COA3R.bin.3.fa	387	330	193	73	241	16	0	0	0	84.41	6.39	56.25
2021_CSC4S.bin.8.fa	35	495	282	100	364	28	3	0	0	84.41	6.62	29.73
CSC2S.bin.12.fa	2258	188	117	57	129	2	0	0	0	84.38	1.71	100
CSC2D.bin.47.fa	564	345	226	80	255	10	0	0	0	84.35	3.41	40
CSC4D.bin.6.fa	268	398	220	81	295	22	0	0	0	84.31	6.49	31.82
COC1S.bin.9.fa	2258	188	117	61	112	15	0	0	0	84.28	8.83	20
COA2D.bin.1.fa	924	161	108	19	138	4	0	0	0	84.26	3.7	50
CSC1D.bin.9.fa	732	200	117	28	163	9	0	0	0	84.25	4.74	22.22
2021_CSA1R.bin.11.fa	46	481	186	85	388	8	0	0	0	84.23	0.78	12.5
CSC2D.bin.13.fa	732	199	116	40	148	11	0	0	0	84.21	8.05	45.45

2021_COC4R.bin.17.fa	455	315	190	77	217	21	0	0	0	84.21	8.16	9.52
2021_COA4R.bin.5.fa	55	659	290	119	527	13	0	0	0	84.2	2.19	38.46
3300044741_16	35	495	282	90	369	36	0	0	0	84.2	8.01	27.78
3300045049_17	55	659	290	130	517	12	0	0	0	84.16	1.49	16.67
CSC4R.bin.1.fa	78	840	354	151	655	32	2	0	0	84.16	5.06	10.53
2021_COC2D.bin.8.fa	564	345	226	62	269	14	0	0	0	84.15	3.14	64.29
2021_COC4S.bin.10.fa	2258	188	117	27	158	3	0	0	0	84.13	1.42	33.33
CSC4D.bin.4.fa	732	200	117	28	168	4	0	0	0	84.1	1.62	25
2021_COA2R.bin.20.fa	2993	147	91	19	126	2	0	0	0	84.07	1.2	50
2021_CSC3S.bin.20.fa	564	345	226	68	269	8	0	0	0	84.07	3.1	62.5
COC4R.bin.9.fa	387	330	193	69	256	4	1	0	0	83.97	1.81	57.14
2021_COC4R.bin.9.fa	55	659	290	142	504	13	0	0	0	83.97	2.77	15.38
2021_CSC4R.bin.4.fa	732	200	117	41	150	9	0	0	0	83.93	5.41	11.11
2021_CSC2S.bin.9.fa	2258	188	117	50	136	2	0	0	0	83.91	1.71	50
2021_COA2R.bin.8.fa	55	659	290	158	493	8	0	0	0	83.9	1.09	50
COC4S.bin.8.fa	2258	188	117	47	132	9	0	0	0	83.83	3.13	77.78
2021_CSC3R.bin.13.fa	5449	104	58	45	56	3	0	0	0	83.79	4.31	100
CSC4S.bin.18.fa	732	199	116	47	138	13	1	0	0	83.78	8.13	56.25
2021_COC4S.bin.19.fa	207	145	103	24	120	1	0	0	0	83.74	0.97	0
2021_COA4D.bin.4.fa	732	199	116	37	159	3	0	0	0	83.72	1.85	0
COC3R.bin.21.fa	2258	188	117	39	147	2	0	0	0	83.7	1.71	0
2021_COA3R.bin.5.fa	88	230	148	65	157	7	1	0	0	83.68	4.56	10
3300045836_21	60	460	233	90	362	8	0	0	0	83.66	1.95	37.5
2021_CSC2D.bin.8.fa	564	345	226	84	253	8	0	0	0	83.66	3.32	87.5
COC1R.bin.6.fa	334	368	206	59	277	29	3	0	0	83.62	8.68	23.68
COC4R.bin.17.fa	564	345	226	61	281	3	0	0	0	83.57	0.68	66.67
CSC3S.bin.7.fa	564	345	226	64	271	10	0	0	0	83.52	3.16	80
2021_COA1R.bin.14.fa	924	151	101	20	130	1	0	0	0	83.5	0.99	100
CSA2S.bin.54.fa	488	309	185	67	225	15	0	1	1	83.47	8.78	2.78
CSC1D.bin.10.fa	732	199	116	51	142	6	0	0	0	83.39	3.3	50
3300045001_1	732	200	117	37	160	3	0	0	0	83.35	1.57	100

3300045958_15	35	495	282	77	410	8	0	0	0	83.33	1.51	37.5
2021_COC4S.bin.13.fa	901	171	117	21	143	7	0	0	0	83.33	3.37	14.29
3300045001_10	334	368	206	84	274	10	0	0	0	83.29	3.35	10
CSC3S.bin.27.fa	35	495	282	106	369	19	1	0	0	83.26	5.24	31.82
CSA2S.bin.50.fa	732	199	116	46	144	7	2	0	0	83.23	7.84	69.23
CSC3R.bin.2.fa	2258	188	117	51	127	10	0	0	0	83.22	3.62	40
3300045003_56	35	495	282	85	377	29	4	0	0	83.21	9.37	39.02
COC3R.bin.4.fa	732	200	117	35	163	2	0	0	0	83.16	1.71	0
2021_CSC4S.bin.16.fa	732	200	117	53	136	11	0	0	0	83.16	4.27	81.82
COC4D.bin.30.fa	732	199	116	43	153	3	0	0	0	83.13	2.16	0
CSA2S.bin.32.fa	107	485	316	90	381	13	1	0	0	83.1	3.67	56.25
2021_COC4R.bin.6.fa	92	481	319	89	373	19	0	0	0	83.07	3.43	42.11
CSC3S.bin.17.fa	274	388	214	86	291	8	3	0	0	83.06	3.23	11.76
2021_COC4R.bin.1.fa	334	368	206	98	255	14	1	0	0	82.96	6.15	41.18
2021_CSA1S.bin.7.fa	732	199	116	43	146	10	0	0	0	82.95	5.39	0
3300045838_43	924	161	108	25	133	3	0	0	0	82.93	2.31	66.67
2021_COC4R.bin.26.fa	5449	104	58	48	56	0	0	0	0	82.76	0	0
COC4S.bin.25.fa	2258	187	116	51	134	2	0	0	0	82.76	0.91	0
2021_CSA1R.bin.1.fa	5449	104	58	49	52	3	0	0	0	82.76	3.45	0
COC2S.bin.4.fa	148	188	125	40	146	2	0	0	0	82.75	1.6	0
3300045001_13	732	200	117	47	149	4	0	0	0	82.74	1.71	50
3300044666_8	108	570	250	151	414	5	0	0	0	82.72	0.99	40
3300044654_20	732	200	117	33	153	14	0	0	0	82.69	6.15	71.43
CSC3R.bin.3.fa	924	161	108	40	114	7	0	0	0	82.66	6.48	57.14
CSA1D.bin.14.fa	2258	188	117	54	126	7	1	0	0	82.64	7.12	30
2021_CSA1R.bin.10.fa	193	427	214	79	337	11	0	0	0	82.62	2.43	45.45
2021_CSC4S.bin.4.fa	63	336	201	63	245	28	0	0	0	82.59	7.31	35.71
COA2S.bin.8.fa	88	230	148	33	191	6	0	0	0	82.58	3.08	16.67
2021_COA1R.bin.18.fa	455	315	190	88	217	10	0	0	0	82.55	3.77	60
2021_COC2R.bin.5.fa	2993	147	91	27	114	6	0	0	0	82.55	6.04	16.67
CSC4D.bin.8.fa	732	200	117	38	150	12	0	0	0	82.55	7.46	8.33

2021_CSC4S.bin.15.fa	2258	188	117	42	138	8	0	0	0	82.54	1.23	0
3300044667_30	334	368	206	81	277	10	0	0	0	82.53	3.64	50
COC3R.bin.3.fa	46	481	186	90	385	6	0	0	0	82.51	0.93	50
COC4R.bin.12.fa	924	151	101	46	99	6	0	0	0	82.51	5.94	16.67
3300044654_28	732	200	117	22	177	1	0	0	0	82.48	0.28	100
CSA1R.bin.11.fa	732	199	116	32	159	8	0	0	0	82.47	4.17	62.5
2021_CSC4S.bin.6.fa	924	161	108	33	123	5	0	0	0	82.42	3.32	0
COC2R.bin.8.fa	387	330	193	66	239	23	2	0	0	82.39	8.83	20.69
CSC4D.bin.10.fa	488	310	185	60	230	20	0	0	0	82.38	4.64	5
CSC4D.bin.1.fa	732	199	116	41	155	3	0	0	0	82.37	1.58	33.33
2021_CSC3R.bin.10.fa	63	336	201	54	256	24	2	0	0	82.36	6.36	6.67
3300044842_42	2258	188	117	46	139	3	0	0	0	82.34	1.57	33.33
2021_COC4S.bin.21.fa	2258	188	117	60	122	6	0	0	0	82.34	4.27	50
CSC4S.bin.15.fa	63	336	201	62	244	25	5	0	0	82.28	6.32	15
2021_CSC2S.bin.12.fa	37	824	336	151	613	57	3	0	0	82.27	7.59	42.42
2021_COC4S.bin.1.fa	924	161	108	26	135	0	0	0	0	82.24	0	0
2021_COA3D.bin.5.fa	732	199	116	48	148	3	0	0	0	82.2	1.51	33.33
2021_COC4R.bin.4.fa	564	345	226	64	273	8	0	0	0	82.19	1.77	25
COC2R.bin.13.fa	193	427	214	100	307	20	0	0	0	82.14	3.99	40
COC4R.bin.20.fa	334	368	206	91	256	20	1	0	0	82.09	5.83	26.09
2021_COC3D.bin.2.fa	732	200	117	38	160	2	0	0	0	82.07	0.94	50
2021_CSC3S.bin.3.fa	732	199	116	52	137	10	0	0	0	82.07	4.96	50
2021_COC3D.bin.5.fa	924	161	108	29	129	3	0	0	0	82.05	2.04	0
COA2R.bin.5.fa	69	400	198	91	293	16	0	0	0	81.99	3.54	37.5
COC4S.bin.7.fa	2258	188	117	62	124	2	0	0	0	81.94	1.71	0
CSA4R.bin.15.fa	732	199	116	55	132	12	0	0	0	81.88	6.32	58.33
01_2_bin.1	924	151	101	30	110	11	0	0	0	81.86	6.49	9.09
2021_COC2D.bin.4.fa	901	171	117	29	138	4	0	0	0	81.85	2.21	75
COC3R.bin.24.fa	924	151	101	21	127	3	0	0	0	81.85	2.97	0
CSA1S.bin.1.fa	732	199	116	45	147	7	0	0	0	81.8	4.74	0
COC4R.bin.13.fa	92	481	319	106	351	18	6	0	0	81.8	5.61	19.44

CSA2S.bin.27.fa	732	199	116	57	130	12	0	0	0	81.79	5.1	58.33
2021_CSC1R.bin.2.fa	334	370	206	81	280	8	1	0	0	81.76	1.81	18.18
CSC1R.bin.7.fa	274	388	214	89	287	12	0	0	0	81.76	3.12	33.33
3300044842_30	35	495	282	112	367	16	0	0	0	81.76	3.55	12.5
2021_COC4D.bin.1.fa	732	199	116	67	131	1	0	0	0	81.72	0.86	0
CSA3R.bin.7.fa	274	388	214	69	301	18	0	0	0	81.71	4.88	55.56
CSA2D.bin.7	100	693	300	144	505	44	0	0	0	81.71	5.6	22.73
CSASD.bin.7.fa	100	693	300	144	505	44	0	0	0	81.71	5.6	22.73
CSA4R.bin.6.fa	2258	188	117	71	115	2	0	0	0	81.69	1.07	50
CSC2S.bin.6.fa	455	315	190	85	211	18	0	1	0	81.69	8.51	4.17
2021_COC4R.bin.8.fa	732	199	116	57	132	10	0	0	0	81.68	5.53	10
2021_COC2R.bin.16.fa	274	388	214	86	290	12	0	0	0	81.67	2.65	83.33
CSA4S.bin.4.fa	35	495	282	120	360	14	1	0	0	81.66	3.43	17.65
3300044658_31	193	427	214	106	311	9	1	0	0	81.63	1.8	50
CSC4S.bin.3.fa	35	495	282	98	377	20	0	0	0	81.62	4.2	55
COC1R.bin.16.fa	60	460	233	124	316	20	0	0	0	81.58	4.02	20
COC1R.bin.2.fa	60	460	233	124	316	20	0	0	0	81.58	4.02	20
COC4S.bin.4.fa	207	145	103	30	114	1	0	0	0	81.5	0.97	0
2021_CSC4R.bin.17.fa	268	395	220	93	296	6	0	0	0	81.49	1.38	50
2021_COC2D.bin.16.fa	924	161	108	38	117	6	0	0	0	81.49	4.07	33.33
3300044765_23	924	151	101	39	108	4	0	0	0	81.45	3.96	25
CSA2R.bin.47.fa	107	574	251	113	444	17	0	0	0	81.37	2.81	58.82
CSA2R.bin.36.fa	88	230	148	70	156	2	2	0	0	81.32	3.72	0
2021_CSC4R.bin.10.fa	223	425	211	85	324	15	1	0	0	81.3	4.43	16.67
2021_COC3D.bin.6.fa	924	161	108	43	106	12	0	0	0	81.3	8.7	25
2021_COC4S.bin.23.fa	107	485	316	111	352	22	0	0	0	81.29	4.03	22.73
CSA4R.bin.1.fa	387	330	193	89	227	14	0	0	0	81.28	5.66	21.43
CSC4R.bin.6.fa	1495	261	164	72	173	15	1	0	0	81.28	7.68	27.78
CSC4R.bin.16.fa	732	200	117	43	157	0	0	0	0	81.25	0	0
2021_CSC3S.bin.21.fa	732	200	117	50	147	3	0	0	0	81.24	1.42	33.33
CSA4R.bin.13.fa	2258	188	117	48	136	4	0	0	0	81.2	3.42	50

19_2_bin.2	564	345	226	88	230	26	1	0	0	81.2	8.65	20.69
CSA2D.bin.10	5449	104	58	46	58	0	0	0	0	81.19	0	0
CSASD.bin.10.fa	5449	104	58	46	58	0	0	0	0	81.19	0	0
2021_COA3R.bin.1.fa	387	330	193	73	244	13	0	0	0	81.17	2.5	30.77
COC4R.bin.10.fa	732	199	116	53	142	4	0	0	0	81.11	2.16	25
CSC3D.bin.5.fa	732	199	116	34	161	4	0	0	0	81.06	1.38	100
CSC3D.bin.3.fa	732	199	116	43	154	2	0	0	0	81.06	1.72	0
COC2D.bin.15.fa	901	171	117	30	137	4	0	0	0	81	2.21	75
COC4R.bin.22.fa	455	315	190	84	206	25	0	0	0	80.95	8.93	8
2021_COC4S.bin.2.fa	207	145	103	35	107	3	0	0	0	80.82	2.43	0
14_2_bin.2	55	659	290	144	499	16	0	0	0	80.81	2.29	43.75
2021_COC4S.bin.14.fa	924	161	108	30	130	1	0	0	0	80.8	0.93	100
3300045838_29	924	161	108	26	127	8	0	0	0	80.77	5.56	0
2021_COC4S.bin.32.fa	2258	188	117	47	129	12	0	0	0	80.77	8.4	41.67
CSC3D.bin.2.fa	2258	188	117	61	123	4	0	0	0	80.76	2.28	75
3300044667_53	5449	103	57	51	48	4	0	0	0	80.7	7.02	0
2021_COC2R.bin.14.fa	924	151	101	42	103	5	1	0	0	80.69	5.94	50
2021_COA1R.bin.7.fa	193	427	214	110	302	15	0	0	0	80.64	4.69	46.67
CSC4D.bin.11.fa	2258	188	117	56	131	1	0	0	0	80.61	0.85	0
2021_CSC4R.bin.7.fa	455	315	190	83	225	6	1	0	0	80.6	2.01	11.11
COC1S.bin.41.fa	732	199	116	63	133	3	0	0	0	80.6	2.59	0
CSC2D.bin.65.fa	207	145	103	26	107	12	0	0	0	80.58	6.07	0
CSA2S.bin.6.fa	732	199	116	45	148	6	0	0	0	80.57	4.31	66.67
2021_COC4R.bin.12.fa	387	330	193	67	259	4	0	0	0	80.56	1.08	75
COC3R.bin.2.fa	364	303	203	60	238	5	0	0	0	80.54	1.89	40
COA3S.bin.2.fa	5449	104	58	25	62	17	0	0	0	80.53	6.44	23.53
3300044964_10	2258	188	117	67	111	9	1	0	0	80.5	4.73	41.67
3300045003_30	901	171	117	35	133	3	0	0	0	80.48	1.71	33.33
COC1S.bin.31.fa	901	171	117	32	130	9	0	0	0	80.44	4.71	0
3300044719_6	26	529	308	128	397	4	0	0	0	80.41	0.6	100
3300045837_9	2258	188	117	42	139	7	0	0	0	80.39	4.44	0

CSA1D.bin.11.fa	2258	188	117	66	116	6	0	0	0	80.38	4.33	33.33
CSA2D.bin.6	207	145	103	34	107	3	1	0	0	80.38	4.37	16.67
CSASD.bin.6.fa	207	145	103	34	107	3	1	0	0	80.38	4.37	16.67
CSA3R.bin.1.fa	5449	104	58	47	56	1	0	0	0	80.33	0.86	100
2021_COA4D.bin.2.fa	732	199	116	45	149	5	0	0	0	80.33	2.44	60
2021_COC2R.bin.12.fa	193	427	214	117	298	12	0	0	0	80.27	3.06	41.67
2021_COC4R.bin.11.fa	924	151	101	25	123	3	0	0	0	80.25	2.97	0
CSA4R.bin.10.fa	387	330	193	91	228	10	1	0	0	80.21	5.61	30.77
2021_COA3R.bin.9.fa	5449	104	58	49	53	2	0	0	0	80.17	2.59	100
CSA3D.bin.2.fa	564	345	226	94	232	19	0	0	0	80.11	6.11	52.63
CSA4R.bin.8.fa	274	388	214	92	285	10	1	0	0	80.08	3.79	46.15
2021_COC4S.bin.29.fa	2258	188	117	42	136	10	0	0	0	80.08	5.41	30
COA4D.bin.2.fa	732	199	116	51	145	3	0	0	0	79.96	1.36	66.67
3300045002_7	732	200	117	47	140	13	0	0	0	79.87	6.27	7.69
2021_CSC4R.bin.16.fa	5449	104	58	48	55	1	0	0	0	79.81	0.86	100
2021_CSC1R.bin.13.fa	5449	104	58	50	53	1	0	0	0	79.81	1.72	100
COA1R.bin.5.fa	455	315	190	88	217	10	0	0	0	79.74	3.93	10
COC2R.bin.24.fa	193	427	214	119	270	36	1	1	0	79.7	9.38	15.56
CSC1D.bin.4.fa	564	349	230	100	231	16	2	0	0	79.69	5.94	18.18
COC3R.bin.17.fa	732	199	116	36	152	11	0	0	0	79.54	6.19	36.36
CSA2R.bin.29.fa	732	200	117	47	148	5	0	0	0	79.49	1.72	40
2021_CSC3S.bin.9.fa	2258	188	117	66	118	4	0	0	0	79.49	3.42	50
CSC4D.bin.14.fa	5449	104	58	48	51	4	1	0	0	79.48	6.9	85.71
02_2_bin.2	924	151	101	28	111	11	1	0	0	79.43	7.33	7.14
2021_COA2R.bin.10.fa	69	400	198	121	268	11	0	0	0	79.42	3.31	45.45
COC2S.bin.5.fa	924	161	108	46	102	12	1	0	0	79.38	9.26	33.33
COA1R.bin.19.fa	732	199	116	56	133	10	0	0	0	79.33	2.91	70
COC2S.bin.8.fa	901	171	117	32	133	5	1	0	0	79.3	4.04	0
3300044765_32	364	303	203	63	239	1	0	0	0	79.24	0.12	100
COC2S.bin.10.fa	268	398	220	108	289	1	0	0	0	79.23	0.45	100
COC4S.bin.23.fa	732	200	117	63	132	5	0	0	0	79.23	1.62	20

COA4R.bin.4.fa	732	200	117	63	129	8	0	0	0	79.23	4.99	50
CSA2R.bin.26.fa	78	840	354	191	615	31	3	0	0	79.22	4.28	15
3300044693_29	26	529	308	122	400	7	0	0	0	79.21	1.89	100
COC4S.bin.22.fa	107	485	316	114	344	27	0	0	0	79.16	5.19	55.56
2021_COC2R.bin.19.fa	46	481	186	101	375	5	0	0	0	79.13	0.8	20
3300044719_20	119	544	284	137	384	22	1	0	0	79.13	4.1	28
3300045003_62	924	161	108	44	116	1	0	0	0	79.12	0.93	0
3300044684_49	193	427	214	105	316	6	0	0	0	79.1	1.15	33.33
2021_COA3R.bin.3.fa	5449	104	58	47	55	2	0	0	0	79.09	3.45	100
3300045002_25	35	495	282	97	388	10	0	0	0	79.08	2.28	60
CSA3R.bin.2.fa	732	199	116	54	140	5	0	0	0	79.08	3.16	80
2021_CSC4R.bin.5.fa	78	840	354	204	630	6	0	0	0	79.06	0.79	50
2021_COC3D.bin.4.fa	901	171	117	31	136	3	1	0	0	78.98	4.27	0
COC4S.bin.32.fa	901	171	117	39	123	9	0	0	0	78.96	4.95	55.56
2021_COA2R.bin.17.fa	5449	101	57	47	49	5	0	0	0	78.95	4.53	100
2021_COC4R.bin.27.fa	323	387	234	108	268	11	0	0	0	78.93	3.06	18.18
2021_COA1R.bin.10.fa	924	151	101	27	114	9	1	0	0	78.88	8.51	33.33
2021_CSC1R.bin.14.fa	455	315	190	84	214	17	0	0	0	78.85	3.92	23.53
CSA1D.bin.2.fa	207	145	103	26	118	1	0	0	0	78.8	0.97	0
3300044688_12	732	200	117	42	154	4	0	0	0	78.79	2.85	50
COC3R.bin.7.fa	35	495	282	128	349	18	0	0	0	78.75	4.4	11.11
2021_COC4R.bin.7.fa	2258	185	115	48	126	10	1	0	0	78.71	9.64	15.38
2021_CSC3S.bin.10.fa	455	311	187	93	209	9	0	0	0	78.7	3.65	22.22
COA2R.bin.13.fa	455	315	190	84	217	14	0	0	0	78.66	4.23	21.43
COC2R.bin.2.fa	732	199	116	47	150	2	0	0	0	78.65	0.46	100
2021_COC4R.bin.3.fa	455	315	190	75	211	24	5	0	0	78.62	9.41	41.03
2021_CSC2S.bin.6.fa	455	315	190	87	224	4	0	0	0	78.48	1.58	0
2021_CSC2S.bin.8.fa	64	769	248	183	565	21	0	0	0	78.47	2.56	23.81
CSA1D.bin.7.fa	2258	188	117	50	132	6	0	0	0	78.44	3.42	16.67
2021_CSC3R.bin.5.fa	91	596	218	157	401	36	1	1	0	78.4	5.97	11.11
COA2S.bin.12.fa	2258	188	117	49	129	9	1	0	0	78.34	7.76	50

2021_COC4R.bin.19.fa	5449	104	58	47	56	1	0	0	0	78.33	1.72	100
23_2_bin.1	2258	188	117	44	139	5	0	0	0	78.31	2.26	20
2021_CSC2D.bin.4.fa	235	420	211	102	291	25	2	0	0	78.25	6.58	22.58
CSC1R.bin.17.fa	564	337	221	96	220	20	1	0	0	78.24	8.22	39.13
2021_COC2R.bin.3.fa	108	570	250	154	412	4	0	0	0	78.23	0.63	50
COC4D.bin.8.fa	35	495	282	131	348	14	2	0	0	78.18	3.51	35
CSC1D.bin.8.fa	268	398	220	97	289	11	1	0	0	78.16	3.05	35.71
CSC4S.bin.16.fa	732	199	116	67	121	11	0	0	0	78.16	5.6	9.09
2021_CSA3R.bin.6.fa	732	199	116	63	134	2	0	0	0	78.12	1.29	50
CSC3S.bin.69.fa	732	200	117	44	154	2	0	0	0	78.09	0.28	0
CSA2S.bin.44.fa	901	171	117	40	125	6	0	0	0	77.97	4.7	50
3300044706_15	67	481	276	130	331	20	0	0	0	77.91	4.32	40
CSA2R.bin.25.fa	924	151	101	45	103	3	0	0	0	77.89	2.97	0
COA4R.bin.1.fa	91	596	218	152	430	13	1	0	0	77.86	3.13	6.25
CSC1R.bin.18.fa	91	596	218	143	416	33	4	0	0	77.82	8.29	8.89
3300045001_3	924	161	108	51	108	2	0	0	0	77.72	1.39	0
08_2_bin.4	2258	188	117	51	133	4	0	0	0	77.7	1.82	0
3300044685_21	334	370	206	106	254	9	1	0	0	77.64	3.4	25
3300044658_15	334	368	206	116	237	15	0	0	0	77.64	3.6	26.67
CSC4R.bin.15.fa	274	388	214	96	272	19	1	0	0	77.59	5.57	36.36
COC4R.bin.4.fa	5449	104	58	48	50	6	0	0	0	77.59	9.48	33.33
3300044686_16	35	495	282	133	354	8	0	0	0	77.53	2.07	50
COC1S.bin.37.fa	107	485	316	118	338	29	0	0	0	77.44	5.9	37.93
CSC2D.bin.37.fa	732	199	116	69	127	3	0	0	0	77.36	1.15	100
COC4S.bin.1.fa	2258	188	117	74	105	9	0	0	0	77.28	7.12	33.33
3300044735_1	35	495	282	115	366	14	0	0	0	77.22	2.03	28.57
2021_COA2R.bin.14.fa	35	495	282	120	364	11	0	0	0	77.22	3.04	9.09
2021_COC1R.bin.10.fa	387	330	193	90	233	7	0	0	0	77.15	2.07	28.57
3300045003_27	108	570	250	141	421	8	0	0	0	77.13	0.86	62.5
CSA3R.bin.6.fa	732	199	116	60	136	3	0	0	0	77.11	2.16	33.33
COA2D.bin.2.fa	924	161	108	52	102	7	0	0	0	77.11	6.02	0

2021_CSC4R.bin.18.fa	350	316	210	97	216	3	0	0	0	77.08	1.19	0
CSC3R.bin.9.fa	5449	101	57	48	47	6	0	0	0	77.05	5.99	83.33
CSC3D.bin.11.fa	2258	188	117	71	112	5	0	0	0	77.03	2.74	0
3300044658_32	33	350	203	71	277	2	0	0	0	76.93	0.33	50
COA2S.bin.11.fa	732	200	117	65	133	2	0	0	0	76.91	1.28	50
2021_CSC4R.bin.11.fa	107	485	316	138	321	25	1	0	0	76.9	7.01	25
COC2D.bin.9.fa	2258	188	117	70	112	6	0	0	0	76.87	4.27	16.67
COC1D.bin.16.fa	455	311	187	93	204	14	0	0	0	76.86	4.26	50
3300044965_17	924	151	101	36	109	6	0	0	0	76.85	3.28	33.33
COC2S.bin.3.fa	901	171	117	34	136	1	0	0	0	76.73	0.43	0
3300045976_36	5449	104	58	47	56	1	0	0	0	76.72	1.72	0
3300044667_47	35	495	282	126	319	48	2	0	0	76.72	8.59	11.11
COC2R.bin.19.fa	350	316	210	98	213	5	0	0	0	76.67	2.14	0
CSA2D.bin.8	2258	188	117	65	116	4	3	0	0	76.67	2.65	46.15
CSASD.bin.8.fa	2258	188	117	65	116	4	3	0	0	76.67	2.65	46.15
3300045744_11	901	171	117	42	126	3	0	0	0	76.66	1.8	33.33
3300044705_25	35	495	282	135	341	19	0	0	0	76.6	3.85	26.32
2021_CSC2S.bin.11.fa	55	659	290	176	448	35	0	0	0	76.57	4.78	22.86
CSA1S.bin.9.fa	2258	188	117	69	118	1	0	0	0	76.54	0.85	0
2021_COC4D.bin.15.fa	455	311	187	95	192	18	6	0	0	76.53	8.68	41.67
2021_COC2R.bin.18.fa	268	395	220	92	283	17	3	0	0	76.46	2.83	53.85
13_2_bin.1	193	427	214	130	287	10	0	0	0	76.44	2.76	40
CSA1S.bin.5.fa	2993	147	91	49	91	7	0	0	0	76.41	7.14	42.86
COA3D.bin.5.fa	268	398	220	115	259	24	0	0	0	76.4	7.27	29.17
2021_COC4S.bin.18.fa	88	230	148	57	168	5	0	0	0	76.39	2.2	40
2021_COC2D.bin.7.fa	2258	188	117	73	113	2	0	0	0	76.38	1.71	100
COC2D.bin.13.fa	2258	188	117	73	113	2	0	0	0	76.38	1.71	100
COA4R.bin.2.fa	120	574	266	150	414	10	0	0	0	76.37	1.66	50
2021_COA1R.bin.11.fa	5449	104	58	50	54	0	0	0	0	76.36	0	0
CSC4R.bin.20.fa	5449	104	58	52	52	0	0	0	0	76.36	0	0
CSC4R.bin.12.fa	268	395	220	115	274	6	0	0	0	76.36	1.45	66.67

COC1S.bin.60.fa	732	200	117	44	153	2	1	0	0	76.35	3.42	20
COC2R.bin.4.fa	5449	104	58	50	49	5	0	0	0	76.35	6.9	80
COA2D.bin.8.fa	88	230	148	50	172	7	1	0	0	76.34	4.77	20
COA1R.bin.17.fa	67	481	276	123	319	35	4	0	0	76.34	9.28	23.4
3300044842_12	732	199	116	38	157	4	0	0	0	76.26	3.02	0
2021_COA2R.bin.6.fa	455	315	190	103	198	14	0	0	0	76.23	5	0
CSC3S.bin.47.fa	732	200	117	49	136	15	0	0	0	76.21	8.3	26.67
3300044693_26	2993	147	91	52	91	4	0	0	0	76.19	3.85	0
CSA1D.bin.31.fa	207	145	103	44	89	12	0	0	0	76.13	9.71	58.33
2021_CSC4R.bin.14.fa	274	388	214	115	257	16	0	0	0	76.11	4.76	12.5
CSA2R.bin.16.fa	274	388	214	102	271	13	1	1	0	76.06	3.72	31.82
COC2R.bin.21.fa	274	388	214	112	271	5	0	0	0	76.04	1.4	80
CSC3S.bin.55.fa	732	199	116	60	131	8	0	0	0	76.04	6.12	50
3300044687_19	732	199	116	56	137	6	0	0	0	76.02	4.31	0
CSC3D.bin.6.fa	88	230	148	49	177	4	0	0	0	75.99	2.03	0
COC3D.bin.1.fa	924	161	108	54	99	8	0	0	0	75.88	6.48	25
2021_COA1R.bin.17.fa	5449	104	58	54	49	1	0	0	0	75.86	1.72	100
COA1R.bin.15.fa	5449	104	58	54	47	3	0	0	0	75.86	5.17	66.67
COC2D.bin.16.fa	924	161	108	44	110	6	1	0	0	75.85	5.93	44.44
CSC4R.bin.19.fa	564	345	226	95	228	21	1	0	0	75.83	7.52	45.83
COA1R.bin.2.fa	564	345	226	102	228	15	0	0	0	75.79	3.73	46.67
2021_COC2R.bin.17.fa	193	427	214	119	285	23	0	0	0	75.79	6.08	17.39
CSC4R.bin.3.fa	107	485	316	141	320	21	3	0	0	75.76	5.96	16.67
CSC4R.bin.5.fa	350	316	210	106	207	3	0	0	0	75.68	1.19	0
COC2R.bin.11.fa	5449	104	58	50	50	4	0	0	0	75.64	3.76	75
2021_CSC3S.bin.8.fa	732	199	116	54	132	13	0	0	0	75.62	8.48	0
2021_COC1D.bin.9.fa	2258	181	110	44	131	6	0	0	0	75.59	4.6	0
2021_CSC2D.bin.2.fa	60	460	233	141	302	14	3	0	0	75.59	5.48	13.04
3300044735_9	732	199	116	48	148	3	0	0	0	75.57	1.58	66.67
3300044735_26	924	155	106	37	114	4	0	0	0	75.56	3.3	0
COC1S.bin.7.fa	732	199	116	65	124	9	0	1	0	75.52	6.15	13.33

3300044689_1	732	200	117	46	145	9	0	0	0	75.51	1.07	22.22
COC2R.bin.15.fa	268	395	220	117	264	14	0	0	0	75.51	3	50
COC1D.bin.14.fa	564	345	226	101	238	6	0	0	0	75.5	2.08	66.67
2021_CSC2S.bin.7.fa	334	370	206	104	252	13	1	0	0	75.49	4.17	25
CSC3D.bin.8.fa	2258	188	117	62	122	4	0	0	0	75.46	3.42	75
COA4D.bin.1.fa	732	199	116	57	136	6	0	0	0	75.44	3.45	50
3300044667_25	455	311	187	102	205	4	0	0	0	75.43	1.87	75
3300044719_18	108	570	250	163	394	13	0	0	0	75.43	2.03	69.23
CSA4S.bin.3.fa	732	199	116	57	138	4	0	0	0	75.39	1.9	50
2021_COC4S.bin.30.fa	732	200	117	63	136	1	0	0	0	75.33	0.43	100
3300044685_8	455	311	187	83	210	18	0	0	0	75.29	2.81	0
CSA3D.bin.5.fa	901	171	117	57	111	3	0	0	0	75.22	1.45	0
3300044684_6	364	302	203	95	203	4	0	0	0	75.18	1.15	25
COC4S.bin.14.fa	207	145	103	36	107	2	0	0	0	75.18	1.94	0
2021_CSC2D.bin.9.fa	732	199	116	67	129	2	1	0	0	75.17	3.45	20
COC2R.bin.22.fa	564	337	221	106	208	23	0	0	0	75.11	6.47	52.17
COA2S.bin.6.fa	901	171	117	47	121	3	0	0	0	75.05	2.14	33.33
CSC2S.bin.10.fa	37	824	336	201	601	22	0	0	0	75.02	2.66	50
2021_CSC4R.bin.9.fa	924	151	101	49	100	2	0	0	0	74.92	1.98	0
COA2R.bin.9.fa	35	495	282	129	355	11	0	0	0	74.92	3.22	18.18
CSC1R.bin.5.fa	924	151	101	38	109	4	0	0	0	74.92	3.96	25
3300045837_13	35	495	282	114	369	12	0	0	0	74.89	2.34	50
3300044684_44	2993	147	91	47	97	3	0	0	0	74.87	3.3	100
3300045837_31	732	199	116	61	136	2	0	0	0	74.86	1.72	0
3300044654_10	732	199	116	51	144	4	0	0	0	74.76	2.44	50
COC4S.bin.21.fa	924	161	108	34	116	11	0	0	0	74.73	3.7	18.18
COC4S.bin.28.fa	35	495	282	142	330	22	1	0	0	74.7	6	28
CSC1R.bin.11.fa	35	495	282	130	353	12	0	0	0	74.69	2.2	33.33
COA1R.bin.4.fa	5449	104	58	51	52	1	0	0	0	74.64	0.86	100
2021_COA2R.bin.16.fa	387	330	193	89	225	15	1	0	0	74.64	3.34	61.11
2021_COC2R.bin.22.fa	387	330	193	104	217	9	0	0	0	74.62	2.25	33.33

3300044689_7	268	398	220	120	273	4	1	0	0	74.61	1.45	42.86
2021_CSA1S.bin.10.fa	2258	188	117	63	118	7	0	0	0	74.59	3.51	42.86
CSA1S.bin.2.fa	2258	188	117	63	118	7	0	0	0	74.59	3.51	42.86
2021_CSC3S.bin.24.fa	732	200	117	55	139	6	0	0	0	74.59	4.7	16.67
COC3R.bin.5.fa	5449	103	58	51	50	0	1	1	0	74.57	4.31	0
3300044667_1	455	311	187	101	205	5	0	0	0	74.56	1.96	20
2021_COA3R.bin.11.fa	60	460	233	163	277	20	0	0	0	74.54	5.57	35
CSA2R.bin.58.fa	924	151	101	37	106	6	2	0	0	74.53	8.53	16.67
COC2R.bin.16.fa	46	481	186	103	375	3	0	0	0	74.49	0.85	0
2021_COC4S.bin.34.fa	732	200	117	50	143	7	0	0	0	74.36	2.09	28.57
2021_CSC4S.bin.11.fa	732	199	116	68	128	3	0	0	0	74.31	2.16	33.33
CSA1S.bin.10.fa	732	200	117	51	145	4	0	0	0	74.27	1.78	75
COA1R.bin.1.fa	455	315	190	98	203	14	0	0	0	74.26	5.7	7.14
2021_CSA3R.bin.5.fa	274	388	214	121	259	8	0	0	0	74.17	2.16	25
CSA4S.bin.1.fa	274	388	214	114	254	19	1	0	0	74.16	4.89	36.36
CSA1R.bin.10.fa	5449	104	58	51	53	0	0	0	0	74.14	0	0
3300044667_12	5449	104	58	53	51	0	0	0	0	74.14	0	0
2021_COC2R.bin.1.fa	5449	104	58	53	49	2	0	0	0	74.14	3.45	100
COC1D.bin.3.fa	5449	104	58	16	66	16	6	0	0	74.14	7.78	67.65
COC4D.bin.29.fa	924	161	108	53	104	4	0	0	0	74.13	2.62	0
2021_CSC3S.bin.26.fa	732	200	117	64	136	0	0	0	0	74.07	0	0
3300044654_32	732	199	116	42	155	2	0	0	0	74.07	0.72	100
2021_CSC1R.bin.10.fa	564	337	221	114	204	19	0	0	0	74.07	7.69	57.89
CSC3S.bin.4.fa	455	311	187	95	208	8	0	0	0	74.04	2.27	50
2021_COA2R.bin.18.fa	193	427	214	132	280	15	0	0	0	74.03	4.02	13.33
2021_COA3R.bin.4.fa	268	395	220	114	272	8	1	0	0	74.01	2.99	63.64
CSA4D.bin.1.fa	2258	188	117	66	120	2	0	0	0	74	1.71	0
COC3R.bin.14.fa	108	570	250	193	337	39	0	1	0	74	8.47	66.67
CSC3D.bin.4.fa	88	230	148	52	175	3	0	0	0	73.95	1.35	0
3300044705_7	924	151	101	45	103	2	0	0	1	73.94	5.94	16.67
CSC4R.bin.7.fa	924	151	101	51	98	2	0	0	0	73.93	1.98	0

CSC2D.bin.7.fa	223	425	211	117	286	22	0	0	0	73.93	5.18	31.82
2021_CSC2D.bin.11.fa	207	145	103	36	108	1	0	0	0	73.81	0.97	0
3300044683_14	924	155	106	55	96	4	0	0	0	73.81	3.77	0
COC3R.bin.16.fa	732	200	117	69	129	2	0	0	0	73.77	1.28	50
2021_COC4S.bin.33.fa	334	370	206	114	243	13	0	0	0	73.76	5.34	23.08
3300045836_40	26	529	308	127	396	6	0	0	0	73.75	0.81	50
3300045049_28	35	495	282	156	328	11	0	0	0	73.7	2.01	27.27
CSASD.bin.11.fa	207	145	103	43	99	3	0	0	0	73.62	2.91	66.67
CSA1S.bin.11.fa	5449	104	58	53	47	3	1	0	0	73.62	8.62	0
COA1D.bin.1.fa	732	200	117	64	134	2	0	0	0	73.58	1.28	0
3300044656_14	67	481	276	136	329	15	0	1	0	73.58	3.37	0
COA3D.bin.7.fa	732	199	116	66	127	6	0	0	0	73.54	3.05	33.33
2021_COC4S.bin.5.fa	901	171	117	44	114	13	0	0	0	73.53	7.28	38.46
COC2S.bin.9.fa	2258	188	117	63	124	1	0	0	0	73.5	0.85	0
COA2R.bin.2.fa	2993	147	91	64	81	2	0	0	0	73.5	2.2	0
2021_COC2R.bin.8.fa	350	316	210	110	200	6	0	0	0	73.49	2.62	16.67
CSA3D.bin.3.fa	924	151	101	47	101	3	0	0	0	73.49	2.97	0
2021_CSC2D.bin.13.fa	2258	188	117	55	124	9	0	0	0	73.47	6.84	55.56
2021_COA1R.bin.12.fa	455	315	190	103	184	28	0	0	0	73.47	9.3	25
CSC4S.bin.5.fa	5449	104	58	51	45	8	0	0	0	73.45	9.31	25
2021_COC1D.bin.10.fa	455	311	187	95	206	10	0	0	0	73.44	3.83	40
2021_CSC2D.bin.12.fa	732	199	116	60	126	13	0	0	0	73.41	4.22	84.62
2021_CSA1S.bin.4.fa	107	485	316	136	308	35	4	2	0	73.34	8.41	13.56
3300045014_29	2258	188	117	77	108	3	0	0	0	73.29	1.42	0
3300045002_19	732	199	116	70	127	2	0	0	0	73.28	1.01	50
COC1R.bin.15.fa	5449	104	58	51	49	4	0	0	0	73.28	5.17	50
3300045002_13	268	398	220	120	258	17	3	0	0	73.27	4.7	50
2021_COC2R.bin.11.fa	732	199	116	62	131	6	0	0	0	73.24	3.02	83.33
COC1S.bin.42.fa	901	171	117	45	121	5	0	0	0	73.22	2.99	20
2021_CSC3R.bin.9.fa	274	388	214	130	249	9	0	0	0	73.21	1.9	22.22
COC2R.bin.23.fa	5449	101	57	50	48	3	0	0	0	73.11	4.39	100

2021_CSA1S.bin.9.fa	2993	147	91	53	84	10	0	0	0	73.11	9.34	30
COC2R.bin.12.fa	924	151	101	50	95	6	0	0	0	72.94	5.06	33.33
COA3S.bin.1.fa	732	200	117	75	124	1	0	0	0	72.93	0.85	100
2021_COC2D.bin.2.fa	35	495	282	159	319	16	1	0	0	72.88	2.84	42.11
2021_CSC3S.bin.5.fa	924	151	101	52	95	4	0	0	0	72.88	3.96	0
CSA2S.bin.72.fa	63	336	201	122	203	11	0	0	0	72.8	3.28	45.45
CSA2S.bin.56.fa	732	200	117	59	140	1	0	0	0	72.74	0.85	0
CSC3R.bin.10.fa	274	388	214	117	258	13	0	0	0	72.7	3.58	30.77
2021_CSC3S.bin.18.fa	732	199	116	70	123	6	0	0	0	72.62	2.93	33.33
3300044658_18	924	155	106	48	97	10	0	0	0	72.58	7.76	50
20_2_bin.1	924	161	108	45	108	8	0	0	0	72.57	5.43	37.5
2021_CSA1S.bin.11.fa	732	200	117	59	138	3	0	0	0	72.56	1.35	66.67
CSC4S.bin.11.fa	732	199	116	78	111	10	0	0	0	72.56	6.47	30
08_2_bin.1	564	345	226	112	226	7	0	0	0	72.52	2.01	57.14
COC3R.bin.29.fa	564	337	221	117	212	7	1	0	0	72.48	2.94	60
COC3R.bin.1.fa	564	337	221	117	211	8	1	0	0	72.48	3.39	63.64
2021_CSC2S.bin.4.fa	387	330	193	110	210	10	0	0	0	72.48	3.97	30
2021_CSA4D.bin.4.fa	732	199	116	69	128	2	0	0	0	72.45	0.93	100
3300044686_21	924	151	101	53	95	3	0	0	0	72.44	2.09	66.67
3300044740_4	268	398	220	114	281	3	0	0	0	72.42	0.74	66.67
COC1D.bin.4.fa	2258	181	110	48	128	5	0	0	0	72.41	3.69	0
COC2R.bin.14.fa	924	151	101	56	89	6	0	0	0	72.41	4.18	50
COC1S.bin.24.fa	5449	104	58	52	47	5	0	0	0	72.41	7.76	20
COC4S.bin.12.fa	5449	104	58	56	42	6	0	0	0	72.41	8.62	33.33
CSA4R.bin.7.fa	193	427	214	148	265	14	0	0	0	72.39	4.82	28.57
2021_CSA1S.bin.6.fa	5449	104	58	52	52	0	0	0	0	72.38	0	0
COA3R.bin.14.fa	268	395	220	138	248	9	0	0	0	72.37	3.18	44.44
COC3D.bin.5.fa	732	200	117	54	144	2	0	0	0	72.35	1.07	50
CSC3D.bin.9.fa	732	199	116	72	126	1	0	0	0	72.33	0.86	0
3300045958_6	268	398	220	115	279	4	0	0	0	72.28	0.95	75
3300045698_7	732	199	116	57	129	13	0	0	0	72.2	3.59	7.69

CSC2S.bin.7.fa	5449	104	58	52	51	1	0	0	0	72.19	1.72	0
COC1S.bin.48.fa	732	199	116	74	122	3	0	0	0	72.18	2.59	0
3300045838_36	901	171	117	57	102	12	0	0	0	72.16	9.15	8.33
CSC3S.bin.19.fa	732	199	116	59	125	15	0	0	0	72.13	7.66	13.33
3300045013_19	732	199	116	72	124	3	0	0	0	72.05	2.16	100
2021_CSA1S.bin.12.fa	5449	104	58	50	53	1	0	0	0	71.97	1.72	100
2021_COC1D.bin.3.fa	564	345	226	120	219	6	0	0	0	71.96	1.78	83.33
09_2_bin.1	83	247	155	65	178	2	2	0	0	71.95	3.87	12.5
2021_CSA4D.bin.3.fa	2258	188	117	66	120	2	0	0	0	71.93	1.28	0
CSC2S.bin.8.fa	5449	103	57	41	54	5	3	0	0	71.93	3.35	28.57
3300045001_34	901	171	117	56	112	3	0	0	0	71.91	2.14	33.33
2021_COA1R.bin.13.fa	564	345	226	114	226	4	1	0	0	71.86	2.43	57.14
3300044684_52	924	151	101	50	98	3	0	0	0	71.84	2.97	0
2021_COC4S.bin.17.fa	5449	104	58	24	66	14	0	0	0	71.63	6.9	92.86
3300044687_12	901	171	117	52	116	3	0	0	0	71.59	1.38	0
3300045003_25	2258	188	117	65	122	1	0	0	0	71.55	0.43	100
COC4S.bin.19.fa	5449	104	58	57	46	1	0	0	0	71.55	1.72	100
2021_COC4R.bin.5.fa	5449	104	58	57	42	5	0	0	0	71.55	6.03	100
CSC1D.bin.2.fa	732	200	117	74	125	1	0	0	0	71.51	0.43	100
2021_COC4S.bin.35.fa	564	345	226	92	233	20	0	0	0	71.48	4.93	65
3300044740_38	35	495	282	147	330	18	0	0	0	71.45	3.84	22.22
3300044964_14	100	693	300	208	464	19	2	0	0	71.44	1.55	68
CSA2S.bin.38.fa	732	200	117	76	117	7	0	0	0	71.38	3.87	28.57
2021_COC1D.bin.2.fa	107	485	316	139	317	29	0	0	0	71.35	6.75	31.03
COC1S.bin.17.fa	207	145	103	42	101	2	0	0	0	71.31	0.97	0
COC1D.bin.9.fa	924	163	110	59	94	10	0	0	0	71.3	8.64	50
2021_CSC4S.bin.3.fa	2258	188	117	52	129	7	0	0	0	71.28	4.7	0
CSA4S.bin.2.fa	924	160	109	42	115	3	0	0	0	71.24	1.53	33.33
03_2_bin.1	193	427	214	150	253	24	0	0	0	71.23	6.01	58.33
COA3R.bin.13.fa	5449	104	58	52	47	5	0	0	0	71.21	6.9	20
2021_CSC1R.bin.1.fa	364	302	203	122	177	3	0	0	0	71.15	0.99	33.33

COC3D.bin.3.fa	924	161	108	44	115	2	0	0	0	71.14	1.11	0
2021_COC4S.bin.31.fa	901	171	117	52	117	2	0	0	0	71.12	1.28	0
2021_COC1D.bin.7.fa	732	199	116	71	126	2	0	0	0	71.12	1.72	0
3300045837_46	732	200	117	70	128	2	0	0	0	71.08	1.71	0
COA2R.bin.17.fa	387	330	193	99	222	9	0	0	0	71.07	2.59	44.44
COC3R.bin.20.fa	83	247	155	99	135	11	2	0	0	71.06	7.9	11.76
2021_COA4D.bin.3.fa	732	200	117	68	126	6	0	0	0	71.04	4.13	33.33
COA4R.bin.9.fa	5449	104	58	54	49	1	0	0	0	71.03	0.86	100
2021_COA2R.bin.2.fa	732	199	116	80	117	2	0	0	0	71.03	1.72	0
2021_COC1R.bin.4.fa	5449	104	58	55	48	1	0	0	0	71.03	1.72	0
COA4D.bin.3.fa	268	398	220	119	265	12	2	0	0	71.03	3.19	44.44
2021_COC4R.bin.23.fa	732	199	116	72	121	6	0	0	0	70.95	3.16	33.33
COC1D.bin.11.fa	107	485	316	146	305	29	4	0	1	70.93	7.21	15.69
2021_COC4R.bin.13.fa	455	315	190	121	180	14	0	0	0	70.84	4.35	28.57
COC2R.bin.10.fa	108	570	250	199	364	7	0	0	0	70.82	1.77	28.57
2021_CSC1R.bin.11.fa	5449	104	58	54	45	4	1	0	0	70.8	9.48	14.29
COC4S.bin.24.fa	2258	188	117	58	125	5	0	0	0	70.73	2.71	20
COA3D.bin.1.fa	901	171	117	62	98	9	1	1	0	70.72	6.55	22.22
2021_CSA1S.bin.1.fa	5449	104	58	56	48	0	0	0	0	70.69	0	0
COA3R.bin.15.fa	5449	104	58	56	46	2	0	0	0	70.69	2.59	100
2021_CSC3R.bin.8.fa	5449	104	58	57	41	6	0	0	0	70.69	9.48	50
CSC4D.bin.9.fa	207	145	103	50	87	8	0	0	0	70.67	5.25	12.5
COA3S.bin.11.fa	148	188	125	58	128	2	0	0	0	70.52	1.2	50
COA1R.bin.6.fa	91	596	218	204	383	9	0	0	0	70.43	1.65	22.22
3300044735_13	120	572	265	157	401	13	1	0	0	70.41	2.64	43.75
3300044667_26	274	388	214	111	265	12	0	0	0	70.37	3.47	16.67
2021_COC2R.bin.4.fa	5449	104	58	54	50	0	0	0	0	70.31	0	0
COC4R.bin.15.fa	732	199	116	73	108	18	0	0	0	70.29	6.77	11.11
CSASD.bin.3.fa	732	199	116	75	120	4	0	0	0	70.27	1.64	75
2021_CSC4S.bin.12.fa	732	200	117	53	146	1	0	0	0	70.26	0.85	100
2021_COC1D.bin.11.fa	732	199	116	81	108	10	0	0	0	70.23	5.55	60

CSA1S.bin.3.fa	223	425	211	169	241	14	1	0	0	70.21	4.98	11.76
COC1S.bin.3.fa	901	171	117	53	117	1	0	0	0	70.18	0.43	0
2021_CSC3S.bin.6.fa	586	325	181	97	224	4	0	0	0	70.17	0.68	0
CSC2S.bin.13.fa	55	659	290	236	407	16	0	0	0	70.11	2.85	37.5
2021_CSC4S.bin.1.fa	901	171	117	48	117	6	0	0	0	70.1	1.62	50
CSC4S.bin.13.fa	901	171	117	52	114	5	0	0	0	70.09	3.42	60
COC4S.bin.2.fa	88	230	148	68	159	3	0	0	0	70.06	1.69	66.67
COC4R.bin.3.fa	83	247	155	97	134	14	2	0	0	70.03	9.07	5

Supplemental Figure legends

Figure S1. Percent total C and N, millet height, and fresh biomass by latitude and shrub presence in the Landscape Gradient study. (a) percent total C was significantly higher +shrub than -shrub, and higher in the southern region than the northern or central. (b) Percent total N was significantly higher +shrub than -shrub, and higher in the southern region than the northern or central. Millet height (c) and fresh biomass (d) were not significantly different in the presence of the shrub or along the rainfall gradient, but southern regions tended to have taller plants.

Figure S2 Landscape Gradient PLFAs. Rootzone was collected from the rhizosphere of millet plants in the rainy season. After the excess soil was shaken off, the remaining soil was collected for PLFA and soil chemistry. In the dry season, the millet plant was replaced by triplicate cores. Bulk soil was collected via triplicate core (a) and (b) Total PLFAs across sample types, seasons, and sites. Total PFLFA concentrations in bulk soil from dry and rainy seasons are significantly different, but treatment had no other effect on PLFA concentrations (c) and (d) Total fungal PLFAs across sample types, seasons, and sites. Fungal PLFAs are significantly greater in the presence of shrubs. Dry season rootzone and bulk soil had significantly higher

amounts of fungal PLFAs than their rainy season counterparts, and the rainy season root zone soil had more fungal PLFA than bulk soil. The central region had higher amounts of northern and southern regions. (e) and (f) Total bacterial PLFAs across sample types, seasons, and sites. Bacterial PLFAs are significantly greater in the presence of shrubs. Dry season rootzone and bulk soil had significantly higher amounts of bacterial PLFAs than their rainy season counterparts, and the rainy season root zone soil had more bacterial PLFAs than bulk soil. PLFAs increased significantly north to south ($p < 0.05$).

Figure S3 Landscape Gradient lineages across all sites a) colored by +/- shrub, b) colored by region and c) colored by longitude. Lineages cluster significantly by +/-shrub and sample type ($p < 0.05$). Different color schemes were used to better visualize differences by treatment. Data across all regions and treatments was highly variable, making it difficult to draw conclusions.

Figure S4 Landscape Gradient lineages: East vs West. As lineage composition was, surprisingly, significantly different by longitude, ordinations were performed to better visualize differences by treatment ta) East sites only, colored by +/- shrub, b) East sites only, colored by region. In the East site, lineages cluster significantly by +/- shrub, region, and sample type ($p<0.5$). (c) West sites only, colored by +/-shrub; (d) West sites only, colored by region; In the West sites, lineages cluster only by region, and not +/- shrub ($p <0.05$). However, significant differences were observed in +/-shrub lineage composition in the Central and Northern sites ($p < 0.05$, data not shown). Limited sample numbers prohibit more granular statistical testing.

Figure S5 OSS PLFAs across sample types and seasons. Rootzone soil was collected from the rhizosphere of millet plants in the rainy season. After the excess soil was shaken off, the remaining soil was collected for PLFA and soil chemistry. Bulk soil was collected via triplicate core near the base of the shrub for +OSS and in between millet rows for -OSS (a) Total PLFAs are significantly greater in the presence of shrubs. There were significantly more PLFA in the dry season bulk soil than the rainy season rootzone and the rainy season bulk soil and significantly greater total PLFAs in the rainy season rootzone soil than in the bulk soil. (b) Total fungal PLFAs are significantly greater in the presence of shrubs. There were significantly more PLFA in the dry season bulk soil than the rainy season bulk soil and significantly greater total PLFAs in the rainy season rootzone soil than in the bulk soil. (c) Total bacterial PLFAs are significantly greater in the presence of shrubs. There were significantly more PLFA in the dry season bulk soil than the rainy season bulk soil and significantly greater total PLFAs in the rainy season rootzone soil than in the bulk soil.

Figure S6: PCoAs of lineage, gene, and genome data across all studies (a) Lineages abundances across studies: PCoA of total and active lineages. SingleM was used to define taxonomy across 59 marker genes, which are all included in the ordination. (c) PCs abundances across studies: PCoA of active and total PCs. ~1.6M PCs were created from annotated OSS and active Simulated Drought experiment assemblies and trimmed reads from all studies were mapped to these PCs via CoverM0.6.1 to obtain sample coverage in transcripts per million (TPM). (d) MAG abundances across studies: PCoA of active and total MAGs across all studies. 263 (95% dereplicated) MAGs were recovered from the OSS and Simulated Drought experiment studies. All studies were mapped to these MAGs via CoverM0.6.1 to obtain sample coverage in transcripts per million (TPM).

Supplemental Figures

Figure S5.1. Percent total C and N, millet height, and fresh biomass by latitude and shrub presence in the Landscape gradient study

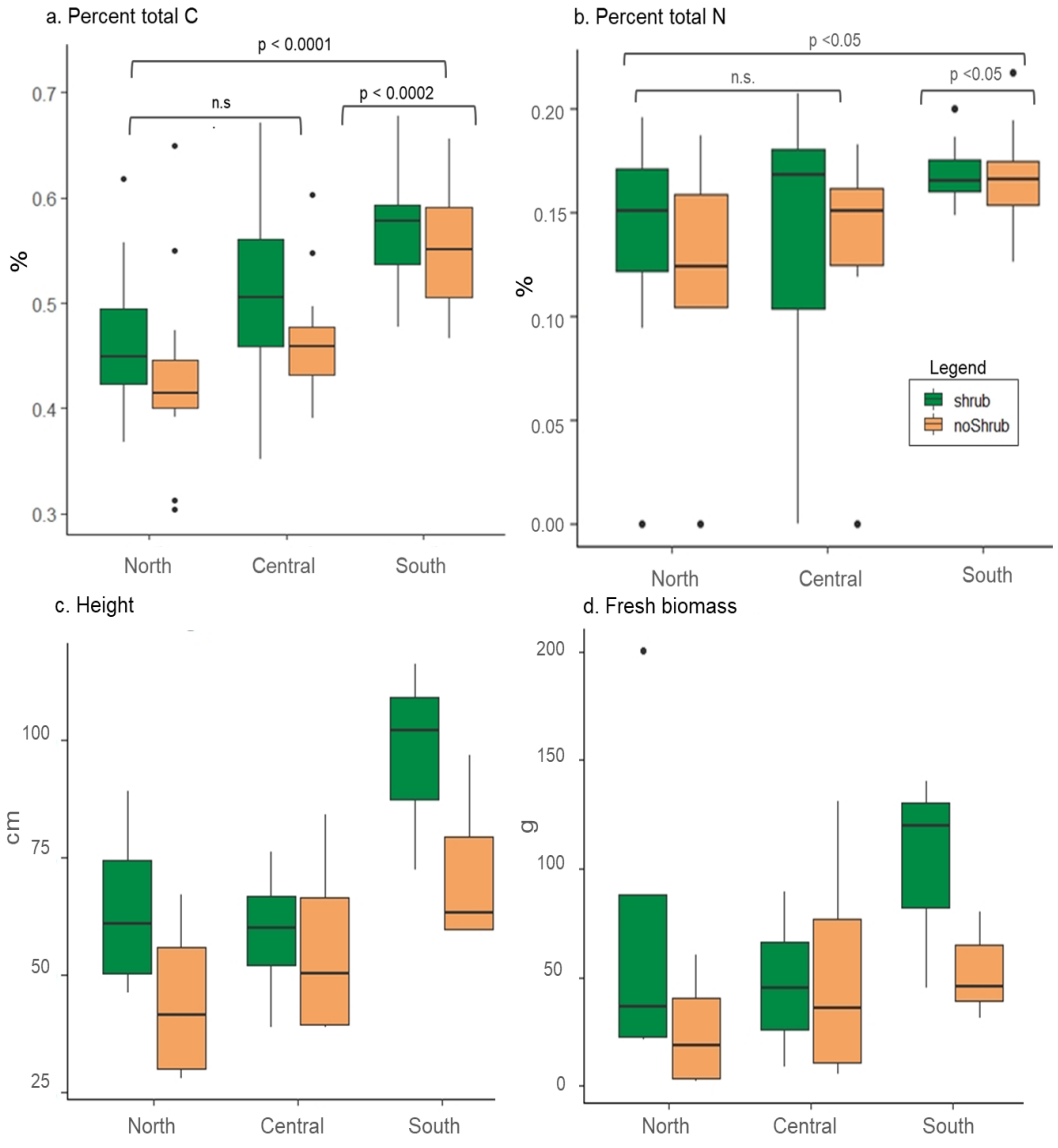


Figure S5.2 PLFA for Landscape Gradient Experiment

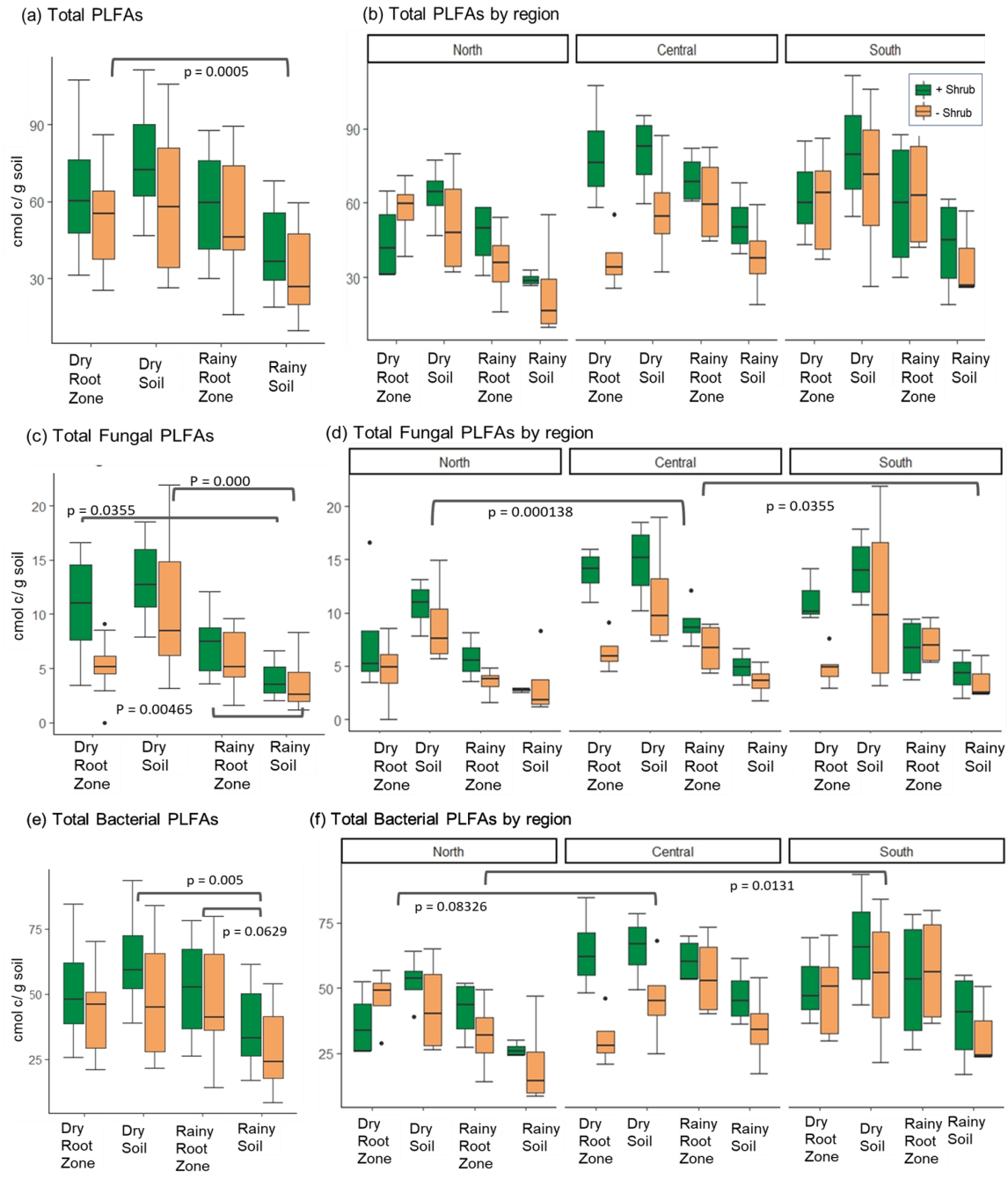
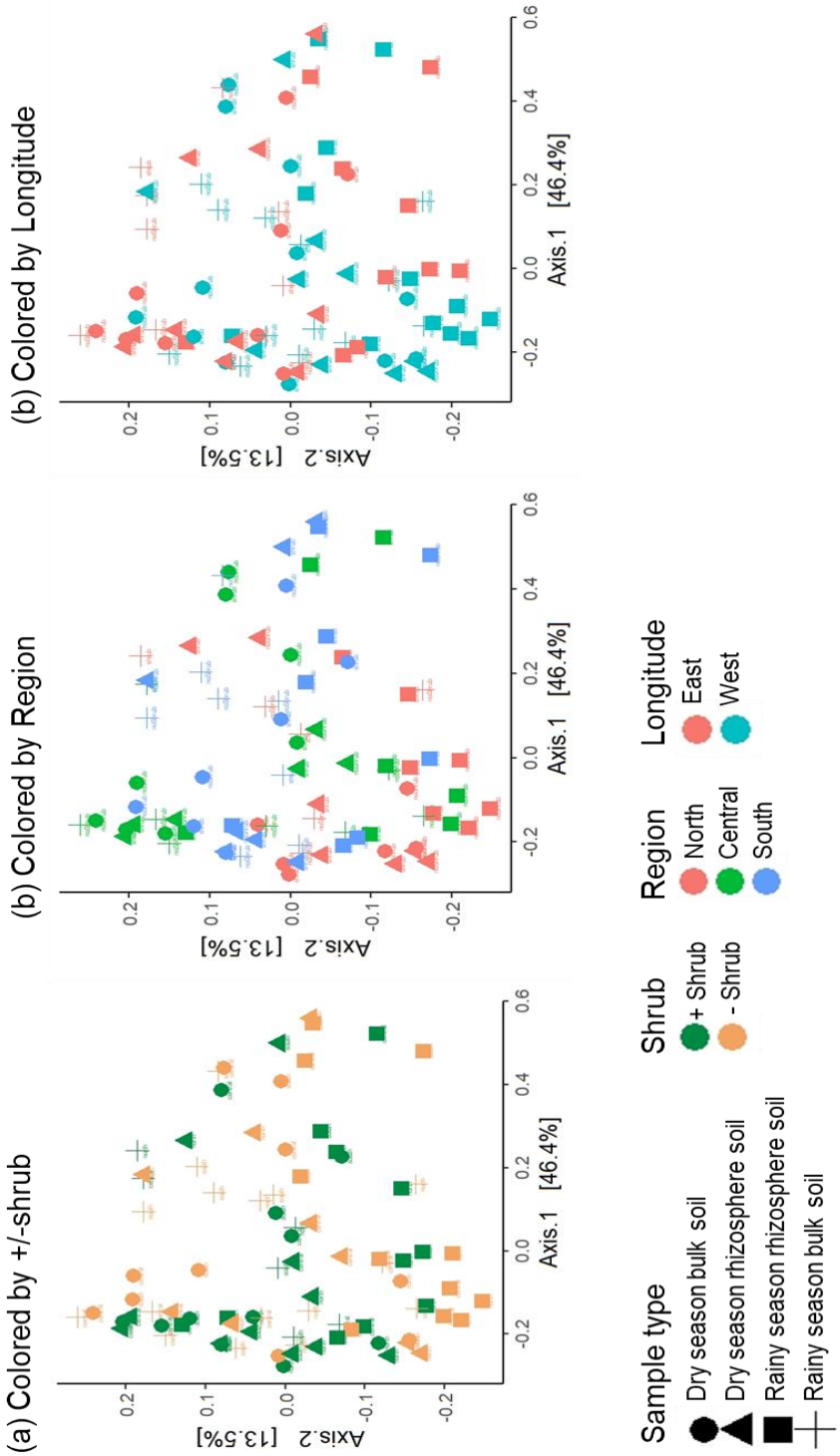


Figure S5.3 Landscape Gradient lineages across all sites.



FigureS5.4 Landscape Gradient lineages: East vs West.

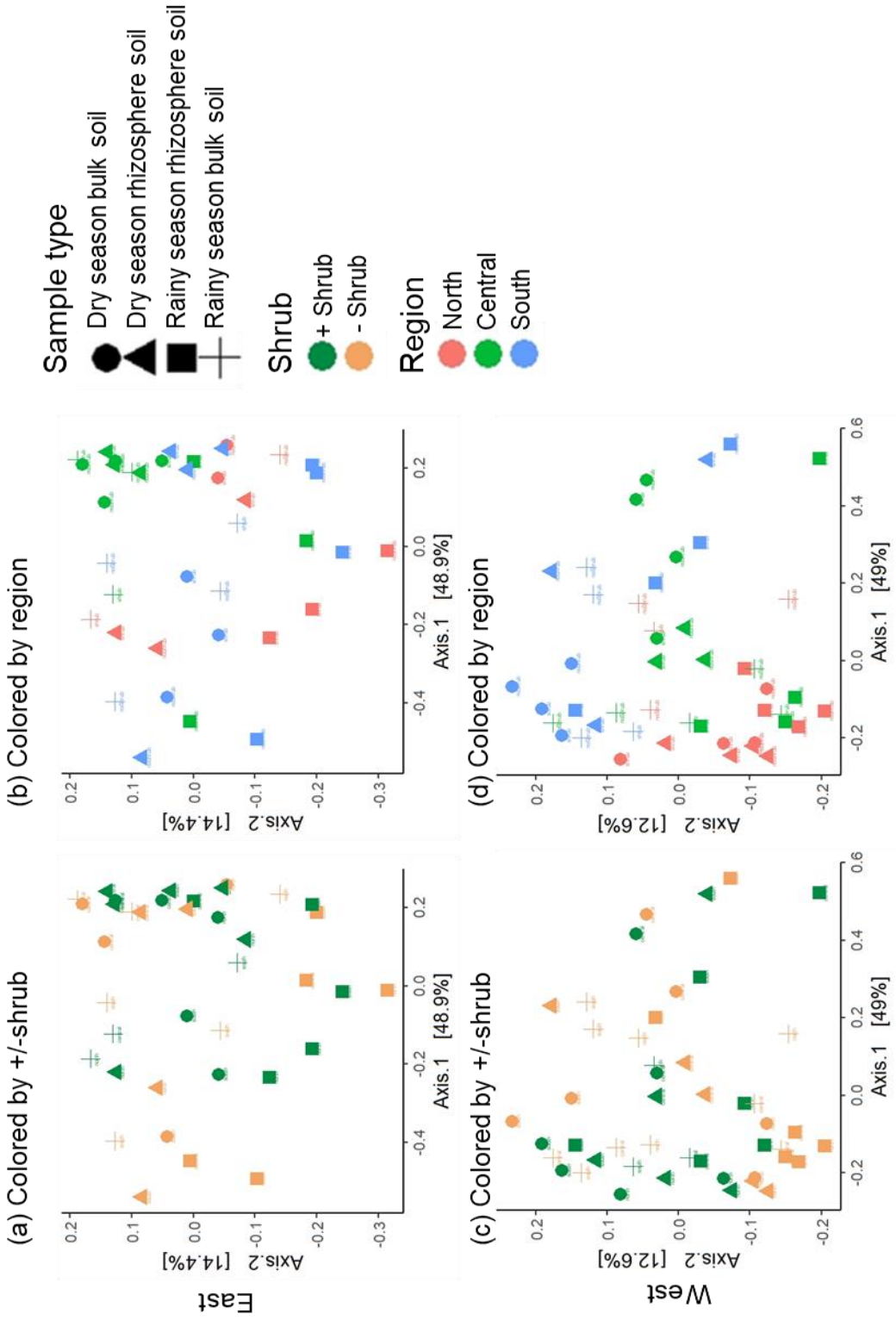


Figure S5.5 PLFAs from Long-term OSS study

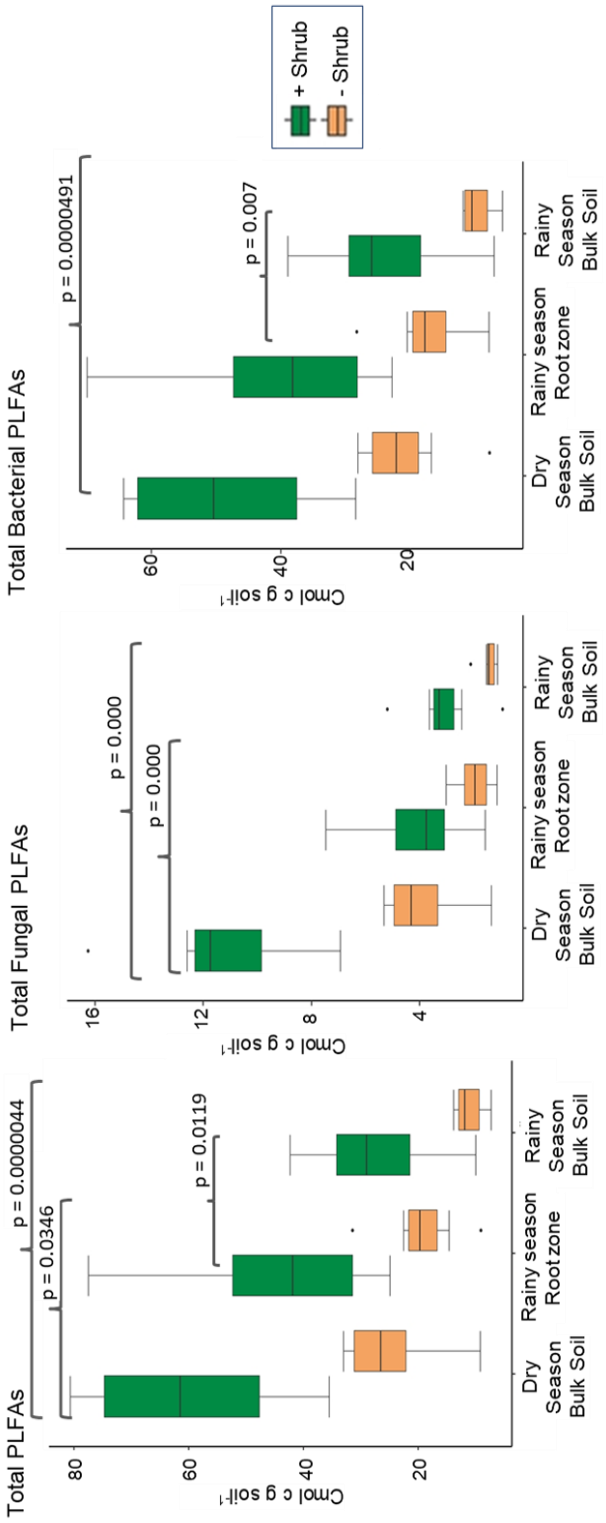
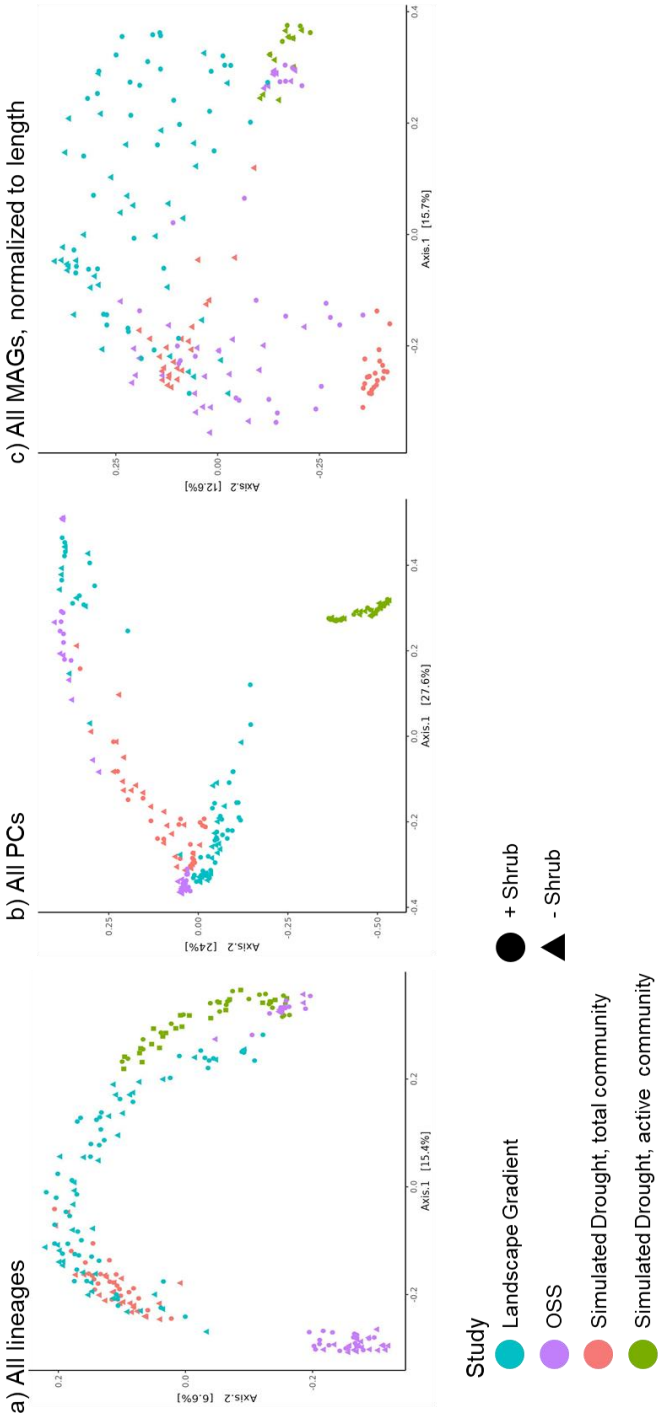


Figure S5.6 PCoAs of lineage, gene, and genome data across all studies



Chapter 6. Synthesis and Conclusions

Chapter 6: Synthesis and Conclusion

Agro-ecosystems of West African Sahel

The West African Sahel is a climatically vulnerable region at the nexus of climate change, soil degradation, and a growing population. The IPCC reported in 2022 that the total rainfall will decrease up to 30% and the number of days over 35°C will increase from 16 to 35 by 2100 (Trios et al., 2022). Summer temperatures are predicted to increase 0.6 - 5°C above pre-industrial levels under mid- and high emission levels. The length of the rainy season is projected to decrease by 4 - 6 days, depending on temperature increases, and this shortening is expected to be most apparent in the delay of its onset or a drought after its start (Trisos, et al., 2022). The 2019 growing season was the most recent example in Senegal of an in-season drought (Laura Mason personal communication, 2023; Senghor et al., 2023). Farmers planted millet in mid-July when the rains began developing good stands of millets. However, after about 20 days the rains stopped with no additional rain for 28 days. Some farmers had to replant their crops while others, where crops survived, had greatly reduced yields. Replanting may require some farmers of the Sahel to go into debt (RTI International, n.d.)

Soil degradation due to loss of soil organic matter (SOM) is another cause of low crop productivity and food insecurity in this region (Lal, 2008; Dai, 2013; World Food Programme, 2023). Soils are generally sandy and have low SOM, and this is further exacerbated by climate change. The increasingly erratic rainfall leads to a loss of

vegetation, and in turn a loss of SOM, and increasing temperatures also accelerate SOM degradation (D'Ordioco et al., 2012). Low levels of SOM also cause a reduction in soil structure, making the soil more susceptible to wind and water erosion (Bationo and Buerkert, 2001; Dossa, 2007). Finally, the traditional agricultural practices to remediate and maintain SOM, such as fallowing, have been greatly reduced to compensate for the population's food needs.

The United Nations further estimates a nearly 6X increase in Senegal's population within the current century (UN Department of Economic and Social Affairs, 2016), putting more pressure on the food system (FAO 2020a). Senegal currently ranks 71st on the world hunger scale (World Food Programme, 2023), and 36% of its population live below the international poverty line, including 60% of people living in rural areas (World Bank, 2023). Further, with global crises such as the Russian invasion of Ukraine and the COVID-19 pandemic, economic growth is slowing while the costs of commodities are rising, key factor in growing poverty in Sub Saharan Africa (World Bank 2023; RTI International, n.d.)

It has been proposed that solutions lie in increasing globalization and the use of Green Revolution technologies, which been successful in improving crop yields in some countries (Pingali, 2012). However, the micronutrient content of the food has not kept pace, leaving people undernourished. The Green Revolution has also contributed heavily to food insecurity and poverty, and its impacts in some underdeveloped countries have been especially limited due to low population density and lack of appropriate infrastructure (Pingali, 2012). The environmental costs of food production might

increase with globalization, for example, because of increased greenhouse gas emissions associated with increased production and food transport (Pretty et al., 2005). Further agricultural intensification has also been linked to a loss of above and belowground biodiversity, reduced plant productivity, loss of SOM, and loss of soil nutrients due to fertilization, (Lambin et al 2014; Lanz et al 2018; Li et al., 2019).

Additionally, most farmers in the Sahel are subsistence farmers, who grow pearl millet and a limited number of other staple crops typically without fertilization or irrigation, and many Green Revolution technologies are not feasible (FAOSTAT, 2015). For example, less than 5% of farmland in Sub-Saharan Africa is currently irrigated (You et al., 2012). Fertilizers are infrequently used for financial reasons and because they decrease in efficiency for crops grown in sandy, poorly structured soils common to the Sahel (Ariga et al., 2019). Subsistence farming also offers benefits such as flexibility and reduced environmental damage caused by agricultural intensification. However, crop yields have remained stagnant for many years, while the population grows rapidly (UN, Department of Economic and Social Affairs, 2016). Therefore, it is crucial to find biologically based and sustainable means of maintaining food security under a changing climate. (Poppy et al., 2014).

A Potential Solution: Agroforestry

Agroforestry is a potential solution for subsistence farmers in the Sahel (Elagib and Al-Saidi, 2020, Ollinaho and Kröger, 2021) to develop practices based on ecological principles for greater sustainability using local, biological resources (Altieri, 2009). The

natural patchiness of the parkland agroforestry landscape in the Sahel creates “islands of fertility” with the shrubs and trees that grow naturally at low densities (Hernandez et al., 2015; Félix et al., 2018). In particular, the indigenous shrubs *Gueira senegalensis* and *Piliostigma reticulatum* found throughout the Sahel (Le Houerou, 1980) and coexist within farmers’ fields offers the foundation for a biologically based management system. Instead of the current situation with low shrub densities in farmers’ field and the burning of coppiced shrub residues; the Optimized Shrub-intercropping System (OSS) increases shrub densities to 1200 to 1500 shrubs ha^{-1} and has all coppiced residues incorporated into soil. OSS has been shown to improve soil quality, carbon (C) sequestration, nutrient availability, improved water availability, and ultimately increased yields (Bright et al., 2017, 2021; Kizito et al., 2006). Notably OSS significantly reduces water stress on crops in low rainfall and in-season drought (Bright et al., 2017, 2021; Dossa et al., 2012, 2013).

The results presented in this dissertation show that OSS strongly impacts the structure and function of the microbial community and this community is able to mediate millet response to drought. Microorganisms benefit plants in direct and indirect ways including the production of antioxidants, exopolysaccharides, osmolytes, and phytohormones, influencing nutrient status of surrounding soils, and increasing soil C content (Rodríguez and Fraga, 1999;Dimkpa et al., 2009;DeForest et al., 2012; Dossa, 2012; Lim and Kim, 2013; Liu et al., 2013; Kang et al., 2014). The overarching goal of this dissertation was to characterize the structure and function of the microbial community at three scales: a landscape gradient study, a long-term field site (the

Optimized Shrub-intercropping System), and in a Simulated Drought experiment, without the presence of *G. senegalensis.*

The first specific objective of this dissertation was to determine microbial community and functional shifts in pearl millet root zone soils with *G senegalensis* intercropping along a rainfall and soil type gradient in the Sahel. This is addressed in Chapter 2, using amplicon sequencing data generated from samples collected during the 2012 rainy season. Chapter 2 reports that the microbial community composition shifts across a soil and rainfall gradient. As climatic conditions become drier and soil has less C, the impact of the shrub on microbial composition and millet growth increases. Outcomes also support the promotion of shrub intercropping for subsistence farmers as a low-cost, local, and highly effective means of increasing crop productivity, remediating degraded soils, and sequestering C in the Sahel.

These sites were soil sampled in 2019 - 2020 and analyzed by and PLFA to determine shifts metagenomic sequencing between wet and dry seasons; and to obtain the first metagenomes along the rainfall and soil type gradient for a more granular analysis of the community and its potential function (Chapter 5). However, results were not totally in line with those described in Chapter 2 (Chapter 2, figure 5) although the percent total C and N followed the same trends (decreasing south to north, but higher in the presence of shrubs, Chapter 5, figure S1). A distinct difference was observed in composition between the eastern and western sites, as well as differences in composition response to treatment between the sites. The community composition from the eastern sites sampled in 2019 – 2020 (Chapter 5, figure S4) followed the same trends as the community composition

results reported in Chapter 2 from the 2012 sampling season; lineages and OTUs clustered by shrub presence and latitude. However, the western sites displayed no +/- shrub difference in community composition except at the northern site. Although this finding does provide support for the "threshold" hypothesis discussed in Chapter 2, it is compelling that the central and southern sites do not display the same trend. Climate projections by the IPCC for this region vary by longitude as well as latitude (Trisos, et al. 2022), and it is therefore imperative to study the effects of shrub intercropping moving west into the country.

Another surprising finding from the 2019- 2020 sampling season is that there was an increase in dry season PLFAs (Chapter 5, figure 2). This contradicts previous PLFA research in the Sahel and in other environments (Diedhiou et al., 2009). This would suggest a more water stressed environment or very low moisture level in the sandy soil of this region increases microbial biomass. Further research is needed to confirm this finding and if it is real, more in-depth research would be justified to determine the mechanisms of this response. Understanding potential functions of microorganisms along the rainfall gradient is limited, which would provide key information on potential function under different climatic and soil health conditions; low rainfall and low C (i.e., the Northern sites) and increased rainfall and slightly increased C (i.e., the Southern sites), as well as reduced shrub densities, compared with the OSS.

Additionally, the metagenomic methods used to characterize the microbial community in the 2019 – 2020 field seasons excluded the fungal community, due to difficulties in DNA extraction and the complexities of eukaryotic genomes (Kuske et al.,

2015; Kumar and Mugunthan, 2018), thus excluding a functionally important microbial group in this investigation of OSS. Fungi play a critical role in SOM degradation, aggregate formation, N dynamics, and may interact with plant hosts as pathogens or beneficials in numerous ways (Zak et al., 2019, Devi et al., 2020; Lehman et al., 2020; Tian et al. 2020). Also, arbuscular mycorrhizal fungi have been hypothesized to directly transport water from shrubs to nearby crops a key function of the intercropping ecosystem and a yet-unanswered question in the OSS (Bogie et al., 2018). Fungi may be more capable of surviving under drought conditions due to their thicker cell walls and being hyphal (Treseder et al., 2018; Liu et al., 2022), and so may maintain their diverse ecological functions during the drought when other organisms are dormant. Therefore, in future work, it is critical to investigate fungal community composition and functions to better understand and predict how the intercropping ecosystem reacts during in-season drought.

The second and third objectives of this dissertation were to a) characterize organisms, community compositional, and shifts in potential functions in an Optimized Shrub-Intercropping System at lineage-, gene-, and genome-level resolutions; and b) characterize organisms, community compositional, and shifts in function of active and total microbial communities in a simulated drought mesocosm study using soils from the OSS long term experimental site, decoupled from the presence of the living shrub and under an imposed early season drought. These objectives were met through work presented in Chapters 3 and 4.

Chapter 4 compares the metagenomes, protein clusters, and metagenome assembled genomes resolved from soils of the Optimized Shrub-intercropping (OSS) Study under +/-OSS management. +OSS has a strong impact on community structure and function (Chapter 4, Figure 2), at all lineage- (both metagenome- and PLFA-derived), gene-, and genome levels of resolution and in both the dry and rainy seasons. There is also a significant increase in the amount of PGPR PCs in the +OSS plots in both seasons (Chapter 4). In the OSS as in the latitudinal gradient study, PLFAs increase during the dry season (Chapter 5, Figure 3). This further highlights the need for researchers to pursue genomic characterization of the fungal community.

The microbial community also shifts over time as part of the Simulated Drought experiment, with significantly different communities present at each of the four phases - planting, the start and end of the simulated drought, and after a 10-day recovery (Chapter 3, Figures 1 & 2). In this experiment there was a synergistic effect on the organic matter amendment treatment by +OSS soil that resulted in maintaining the microbial community composition during the drought treatment. Plants release 50% of the C they fix as exudates into the rhizosphere soil with additional C inputs from litter and fine root turnover, all of which provide substrates for microbial growth (Cavicchioli, et al., 2019). This mechanism is likely important for the responses to +OSS and +OM that was observed in the Simulated Drought experiment. For example, +OSS/-OM enriches for different organisms (Chapter 3, Figure 3) and the composition of PGPR protein clusters differs in the Simulated Drought experiment (Chapter 3).

The impact of the organic matter amendment treatment on community composition in the Simulated Drought experiment increased with time (Chapter 3 Figure 1 & 2, Chapter 4, Figure 4, S7). Also, the OM amendment caused a shift in the composition of actively transcribed target PGPR protein clusters under drought, highlighting the importance of OM amendments in this system. This has important implications for on-farm management, as currently, coppiced shrub residues are burned on-site in the fields. As described in Chapter 4, it is possible that the use of shrub residues may act to mitigate some crop drought stress in the absence of shrubs. Thus, this indicates that fields that have current low shrub densities would benefit by not burning coppiced shrub residues. But additional residues from surrounding fields or uncropped sites should be retrieved and incorporated to get the high rates of shrub inputs to fully obtain the benefits of OSS.

Although organic inputs from coppiced residues is important, Chapter 4 shows the importance of long-term presence of *G. senegalensis* in shifting. Chapter 4 highlights the role of the living shrub by isolating the effect of the microbiome of OSS soil in conferring drought resistance in millet. Here, genomic results from the OSS and the Simulated Drought experiment were directly compared, to see if on-field effects could be replicated without the effect of the living shrub. Similar to the OSS field study, the use of +OSS soil shifted the microbial community composition (Chapters 3& 4) and increased the numbers of target PGPR protein clusters at the start of the drought (Chapter 4), indicating that a substantial portion of the field community was present and functional without the presence of the shrub, at least at the start of the experiment. At the end of the

drought, however, there was no difference +/-OSS or +/-OM in the total counts of PGPR related PCs in either the active or the total community. This indicates that the presence of shrub still plays an important role in the potential for drought stress amelioration by the microbial community. Besides root turnover, it likely is the shrubs' ability to perform hydraulic lift (Kizito et al., 2012; Bogie et al., 2018) that affects the community, as it would support a community that evolves or is maintained by having some moisture year around. This response corresponds to trends in millet drought response reported by Charles et al. (2024a, same experiment). Millet in +OM treatments tended to be taller at the time of harvest, and millet in -OM treatments under drought were significantly shorter than those under +OM (Charles et al., 2024a). Millet in +OSS/+OM also had a reduced chlorophyll A: B ratio, indicating that they were less stressed (Croft et al., 2017; Agathokleous et al., 2020). It is also notable that the results shown in Chapters 2 & 4 represent the first time meta-omics methods were used to study microbial responses to an intercrop system and to drought. Chapter 4 shows the power of meta-omics for developing an understanding the soil microbial composition and specific functions under varying soil management systems.

Conclusions

Semi-arid regions comprise 47% of earth's surface, and around 2 billion people rely on dry land agricultural products currently (FAO, 2020b). This dissertation is the first in-depth microbiome study of the semi-arid agroecosystem in the Sahel, focused on an agroforestry system that is appropriate for the subsistence farming that dominates in

this region. This is important because it is expected that there will be differential microbial responses across ecoregions relative to C cycling and soil sequestration, the spread or range of microbial pathogens, and greenhouse gas emissions climate change (Cavicchioli et al., 2019; Tiedjie et al, 2022; Smith et al., 2023). Furthermore, it is important to focus on soil microbiology relative to agriculture in the Sahel because of the on-going challenge of food insecurity. The United Nations FAO (FAO, 2020a) estimates that there will be more than 100 million undernourished people in West Africa by 2030, with 60.2 million people currently, severely food insecure.

Optimized Shrub-intercropping System (OSS), a type of agroforestry, was investigated for its role in driving microbiome dynamics in relation to in-season drought and buffering crops during water stress. The results have implications for other semi-arid regions as a foundation for manipulating the microbial community to mitigate the expected increase in drought of semi-arid cropping regions. The results presented in this dissertation add to this body of knowledge by determining the roles shrub presence and shrub residue incorporation on the microbial community based on studies that included: a rainfall and soil type gradient study, at the long-term OSS experiment, and in growth chamber simulated drought experiment using meta-omics and traditional soil science methods.

Chapter 2 investigated the relationship between shrubs and the composition of the microbial community along a rainfall and soil type gradient in actively farmed fields. The results showed that *G. senegalensis* had a more significant effect on community composition and millet growth in drier and lower soil C conditions of the northern over

southern cropping region of Senegal, which is consistent with Debenport et al. (2015). Results presented in Chapters 3 and 4 highlight the importance of the living shrub and the of shrub residues to influence community composition and function under a simulated drought. It was observed that the residue amendments influenced transcription of PGPR genes at the end of the drought, and that the influence of OM amendments increased throughout the duration of the experiment. OSS or the history of OSS in the case of the simulated drought experiment, played a major role in determining community composition and function at all stages of the experiment. Chapter 4 also presents the first metagenomic and metatranscriptomic results, including 263 metagenome assembled genomes. These analyses provide insights into the functional response to drought, shrub presence, and shrub residue amendment. Finally, Chapter 5 assembled and summarized all the data collected in this dissertation. This will allow other scientists to access this metagenomic and metatranscriptomic data to answer other questions using bioinformatics. Suggestions are provided that included determining the influence of *G. senegalensis* along a soil type and landscape gradient on the microbial community composition and functions during the dry season or under drought.

In summary, the above findings combined with previous research (Diedhiou et al., 2021; Debenport et al., 2015) indicate that the root system along with litter input of *G. senegalensis* is acting as a repository for a more diverse microbial community that "inoculates" adjacent millet rhizosphere and root zone soil. Importantly, this includes plant growth promoting, as well as drought resisting organisms, some of which are greatly increased in abundance and others only found beneath this shrub. In contrast,

there is some evidence that the absence of shrubs enables the establishment of deleterious microorganisms. Although further, in-depth research is needed, if this is real, it would change the paradigm of why yields are so low in the Sahel. Thus the degraded soil may not only affect crops due to poor nutrient availability and structure (loss of aggregation) but because it harbors microorganisms that inhibit crop growth and yield due to non-pathogenic, deleterious mechanisms (Turco et al., 1989; De Luna et al., 2005).

This dissertation developed fundamental information on the microbial mechanisms for enhanced crop productivity in general and under low rainfall or in-season drought that previous research has shown for OSS under field conditions (Bright et al, 2017, 2021; Dossa et al, 2012, 2013). The results provide justification for pilot testing and scaling projects of OSS. Such investments for subsistence agriculture have great potential to reduce poverty and increase food security in vulnerable environments (Pingali, 2012; Raj et al. 2022).

At the same time further research questions continue to evolve that could produce outcomes useful for modifying or enhancing OSS. Research is needed on whether degraded soils of the Sahel harbor deleterious organisms. Beneficial organisms harbored by shrubs should be isolated in pure cultures and tested for a battery of plant growth promoting rhizobacteria (PGPR) properties. In turn could inoculating soil beneath shrub canopies enhance the abundance of PGPR that are found on adjacent crop rhizospheres and root endospheres? Investigations are needed to determine if there are strains of *G. senegalensis* or *P. reticulatum* that are better suited for intercropping. Agronomic studies are needed to determine: optimal spacing and densities of crops when grown in the OSS

and crop varieties best suited for OSS. Nutrient budgets of shrubs need to be developed to determine the degree to which shrubs are "mining" the subsoil for nutrients that are then deposited at the soil surface through litter inputs and root turnover. This is important for assessing the potential need for supplemental fertilizers for long-term OSS management with subsistence farmers.

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