

Soil microbial diversity in organic and non-organic pasture systems

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Abbreviations: C, Carbon; N, Nitrogen; Al, Aluminum; As, Arsenic; B, Boron; Ca, Calcium; Cd, Cadmium; Co, Cobalt; Cr, Chromium; Cu, Copper; Fe, Iron; K, Potassium; Mg, Magnesium; Mn, Manganese; Mo, Molybdenum; Na, Sodium; Ni, Nickel; P, Phosphorus; Pb, lead; S, Sulfur; Se, Selenium; Ti, Titanium; and Zn, Zinc; DNA, Deoxyribonucleic acid; rRNA, Ribosomal ribonucleic acid; OUT, Operational taxonomic unit, ANOVA, Analysis of variance; PERMANOVA, Permutational multivariate analysis of variance; PCoA, Principle coordinate analysis; LDA, Linear discriminant analysis; and LEfSe, Linear discriminant analysis effect size

Abstract

Understanding the effects of organic pasture management on the soil microbiome is important for sustainable forage production since soil microbiome diversity contributes to improved nutrient cycling, soil structure, plant growth, and environmental resiliency; however, the soil microbiome response to pasture management is largely unknown. This study assessed the soil microbial diversity, richness, and community structure following 10 years of pasture management (organic or non-organic) using Illumina 16S rRNA gene amplicons. Soil samples were collected from 0-15 cm in July and August from 2017-2018. Total soil organic C, N, minerals, and pH were determined. Overall, greater soil bacterial species richness ($P \leq 0.05$) occurred in organic relative to non-organic (conventional) systems. Management affected bacterial species richness (Chao1), with greater richness occurring in organic pasture soils and less richness occurring in non-organic systems ($P \leq 0.05$). Similarly, management ~~effected~~ affected bacterial evenness (Simpson's index), with a more diverse community occurring in organically managed soils relative to non-organic pastures ($P \leq 0.05$). Linear discriminant analysis effect size analysis showed statistically significant and biologically consistent differences in bacterial taxa in organic compared with non-organic soils. Therefore, there was a shift in bacterial community structure in organic relative to non-organic soils ($P \leq 0.05$). Consequently, pasture management affected soil microbial diversity, with greater diversity occurring in organic than non-organic systems, likely owing to applications of organic poultry litter in organic systems compared to non-organic management (use of inorganic-fertilizers and herbicides). Results indicate that when pastures are converted to organic production systems, soil microbial richness and diversity may increase, thereby resulting in enhanced soil microbiome function in the largest agricultural land use category in the US.

Introduction

Soils contain highly diverse microorganisms, with ~~as many as~~ 10⁹ to 10¹⁰ microorganisms per gram (Gans et al., 2005). Soil bacterial species and diversity are important as they are major decomposers of soil organic matter and ~~thus~~ can influence carbon and nitrogen turnover rates (Hättenschwiler et al., 2005), which provides substrates to microbes and nutrients to plants. Nitrogen mineralization in the soil also depends on the abundance and diversity of bacterial taxa (De Ruiter et al., 1993). Higher bacterial diversity is crucial for the breakdown of organic matter that involves complex processes such as chitin degradation (Beier & Bertilsson, 2013). Human activity in soils, including increased use of chemical fertilizers, pesticides, and tillage, has led to a decrease in global soil biodiversity (Hirsch, 2010). Other negative anthropogenic environmental impacts include soil degradation, pesticide accumulation, reduced water availability, and increased greenhouse gas emission, collectively hampering biodiversity (Foley et al., 2005). Organic production practices reduce the use of chemical fertilizers and pesticides and increase sustainable production practices (Gomiero et al., 2011). However, there are still incomplete understandings ~~on~~ of the effects of organic production practices on soil biodiversity (Wu & Sardo, 2010; Tschamtkke et al., 2012; Bünemann et al., 2006). Although, DNA sequencing technologies have made it possible to identify soil bacterial abundance and diversity (Soliman et al., 2017).

Over ~~one-one~~ quarter of the Earth's total land area is used for livestock grazing (Herrero et al., 2013). Grazing directly or indirectly impacts soil microbial communities and C and N availability because livestock feeds on aboveground plants and returns half of ~~the~~ grazed forage to the soil as feces, which may promote bacterial growth (Lovell et al., 1995; Manzano & N  var, 2000; Le Roux et al., 2008; Yang et al., 2013; Tardy et al., 2015). Earlier studies also demonstrated grazing pressure impacts soil microbial communities, with positive associations occurring for soil productivity and microbial α -diversity, and the suppression of bacterial communities in overgrazed soils (Xun et al., 2018). However, limited studies are available on the impacts of organic pasture management on soil microbial communities. Therefore, this study aims to compare long-term (10 years) soil microbiome diversity under organic versus conventionally managed (non-organic) pasture management.

Materials and methods

Study management history

The research was conducted at the USDA-ARS Dale Bumpers Small Farms Research Center in Booneville, Arkansas (35.08  N, 93.98  W), where plots with different management, i.e., organic and non-organic, were established and consistently managed since 2007. Thirty-~~two~~ hectare plots utilized for sheep were managed organically since 2007 and certified organic in 2012 (Nature's International Certification Services, Viroqua, WI). Forage type was predominantly tall fescue (*Festuca arundinacea*). Non-organic sheep pastures were utilized by sheep for more than

30 years and were predominantly bermudagrass (*Cynodon dactylon*). Both forage types have limitations for sheep production and provide little pollinator habitat. Before plots were established, sheep grazed at approximately ~10 sheep ha⁻¹ according to forage availability, which was seasonal and dependent on forage species present (*Eremopyrum triticeum*, *Lolium perenne*, and other voluntary forbs and grasses). Details regarding the soil types of the area are available in (Thomas et al., 2008). Daily rainfall and temperature (NOAA, 2017, and 2018) for 3 days before sample collection is provided in the Table 1.

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Pasture plot preparation for non-organic forage plots

Two 0.16-ha non-organic plots were used for the non-organic treatment in this study. Non-organic plots were sprayed with Roundup [N-(phosphonomethyl)glycine] (41% glyphosate, 4.67 l ha⁻¹) in June, July, September, and October of 2016 and January of 2017, and with Outrider [N-[[[4,6-dimethoxy-2-pyrimidinyl]amino]carbonyl]-2-(ethylsulfonyl)imidazo[1,2-a]pyridine-3-sulfonamide; {Sulfosulfuron}] (Monsanto, St. Louis, MO; 0.096 l ha⁻¹) in September 2016 using a Continental Belton cluster nozzle sprayer (Continental Belton McAlester, SR: A44117, Oklahoma city, OK). Non-organic plots were tilled (Maschio Gaspardo North America Inc., SC 300, Des Moines, IA), and rolled using 12' Big Guy Roller (Grahl Manufacturing, St. Louis, MO) in October 2016. Long-term (15 years) applications of inorganic nitrogen (ammonium nitrate) ~~was~~ were applied to pastures at recommended rates (<https://www.uaex.edu/publications/PDF/FSA-2153.pdf>). The seed-mixes were Buck's Hangout (Hamilton Native outpost, Elk creek, MO; www.hamiltonnativeoutpost.com/14.5 kg ha⁻¹) used in half of each 0.16 ha plot, and other Tallgrass Inexpensive or Tallgrass Exposed Clay subsoil mix (Prairie Moon, Winona, MN; www.prairiemoon.com; 13.44 kg ha⁻¹ and 26.8 kg ha⁻¹, respectively according to commercial nursery recommendations) in the other half of each 0.16 ha plot, planted ~~in-on~~ February 7, 2017, and again same time in 2018 (species percentage per seed mixes are available in the aforementioned websites).

Organic pasture plot preparation

Plots were controlled burned using forestry drip torch after establishing a firebreak around the plots. ~~Cover-A cover~~ crop of oats (*Avena sativa*) was planted ~~in~~ the winter before spring planting native seed mixes. One, 0.4 ha organic plot was seeded ~~in-on~~ February 3, 2017, with "Butterfly and Hummingbird" Mix from Hamilton Native outpost (Elk Creek, MO; www.hamiltonnativeoutpost.com/; at 8.5 kg ha⁻¹; species composition and percentage of each species are available in the above website). The other organic plot was 0.8 ha planted with Tall Grass Inexpensive (Prairie Moon Nursery; 13.4 kg ha⁻¹). ~~Seed-The seed~~ was drilled onto a prepared seed-bed using a Brillion planter (Brillion Farm Equipment, Sure Stand Model SSP-8, Brillion, WI) at a 1.25 cm depth. Soil fertility was adjusted using poultry litter (4.4 Mg ha⁻¹; fresh weight basis) ~~in accordance with following~~ the University of Arkansas soil test recommendation (<https://www.uaex.edu/publications/PDF/FSA-2153.pdf>).

Sheep grazing

Plots were multifunctional for pollinator habitat and sheep forage. Sheep grazed plots if they became weedy (including *Chenopodium album* and *Ambrosia artemisiifolia*), or stubble height reached 1 m. Grazing of the conventional plots occurred to remove excess forage and weeds, but not to the detriment of the native plant species. ~~Stocking~~The stocking rate of each plot was different based on visual assessment of forage availability, which included plant height, the density of unwanted, and desired plants.

Soil sample collection

Soil samples were collected in July and August of 2017 and repeated again in 2018. Soil samples were collected from 0-15 cm, and soil probes were sterilized between plots with 70% ethanol. Samples were packed in sterile whirl-pack bags and stored at -20° C until analysis. Soil sample collection sites were georeferenced using a Global Positioning System unit. For the analysis, 32 independent samples were taken (2 per pasture system × 2 sub-samples per treatment × 2 replications × 2 sample dates per year × 2 years).

Soil physiochemical analyses

Soil samples were dried at 70 °C for 48 h and then ground with mortar and pestle to pass through a 2 mm sieve. Mehlich-3 extractable nutrients (i.e., Al, As, B, Ca, Cd, Co, Cr, Cu, Fe, K, Mg, Mn, Mo, Na, Ni, P, Pb, S, Se, Ti, and Zn) were determined using 1:10 soil volume: extractant solution volume ratio (Tucker, 1992) and analyzed by inductively coupled argon-plasma spectrometry using a 7300 IPC-OES DV (Perlin-Elmer, Waltham, MA). Total C and N were analyzed via dry combustion using a Vario Max CN combustion analyzer (Elementar Americas Inc., Mt. Laurel, NJ). Soil pH was determined on 1:1 soil: distilled water suspension using a symphony B30PCI probe (VWR International, Atlanta, GA).

DNA extraction, PCR amplification, and sequencing

DNA was extracted from each soil sample using the extraction kit of MpBio Fast DNA Spin Kit for Soil (MpBio Laboratories, SKU 116560200-CF) according to the manufacturer's directions. Extracted DNA was quantified using Quant-It™ PicoGreen® (Invitrogen) dsDNA quantitation assay and stored at -20 °C. Bacterial community composition was determined using Illumina Miseq sequencing of 16S rRNA gene amplicons. Extracted DNA was sent to the University of Tennessee Genomic Services Laboratory, where the V4 region of the 16S rRNA gene was amplified with barcoded primers 515F and 806R (Caporaso et al., 2011). Amplicon libraries were pooled, and 291 base-paired end sequences were obtained on the Illumina MiSeq platform, resulting in a total of 3,531,936 sequence reads. Reads were processed using the open-source bioinformatics software Mothur V 1.40.0 following the Miseq SOP protocol (Kozich et al., 2013). Sequences that did not match the primers were eliminated from demultiplexed sequence reads. These ambiguous base sequences with a length of less than 100 bp were deleted, and chimeric sequences were removed using the UCHIME

algorithm implemented in Mothur. After the quality control pipeline, 2,906,534 sequence reads remained using a 97% similarity threshold to define ribotypes in Mothur (21.52% were deleted).

Data analysis and statistics

The green genes database was used to classify the OTU at the genus level using the Bayesian method (Cole et al., 2009), ~~thereafter after that~~ relative abundance of all OTUs ~~were~~ was summed within phylum and analyzed for the relative abundance of OTUs at the phylum level. Based on this subsampled dataset, richness was calculated using the Chao index, and diversity was calculated using the inverse of Simpson using Mothur, and differences by treatments were analyzed using ANOVA in the statistical software R 3.5.1 (Team, 2013) and JMP R 12 (Institute, 2015). Beta-diversity was measured by using Bray-Curtis index, weighted and unweighted UniFrac distance metrics. Principle coordinate analysis plots were generated based on weighted and unweighted UniFrac distance metrics using Microbiome Analyst (Dhariwal et al., 2017). Bacterial community structure was quantified in a matrix of Bray-Curtis similarities, which was then analyzed in a permutational analysis of variance (PERMANOVA) to compare bacterial communities at the phylum OTU level in PRIMER-E (Clark & Gorley, 2006). Linear Discriminant Analysis Effect Size measurement was used to identify taxa differences between treatments with Galaxy (Segata et al., 2011).

Spearman correlation was used to find correlation among soil pH, C, N, C: N ratio, soil mineral (Al, As, B, Ca, Cd, Co, Cr, Cu, Fe, K, Mg, Mn, Mo, Na, Ni, P, Pb, S, Se, Ti, Zn) and number of OTU of most dominant bacteria phyla per treatment (organic and non-organic system). Management (organic or non-organic) and time of sample collection (July or August) was used as the fixed effect and year and replications as the random effect. Principal component analysis was used to determine relationship among variables using R software. Proportion of variance was done to find variance explained by each PCs. Three PCs that explained most variance were selected for further analysis. The eigenvectors were used to show directional orientation (positive or negative) of all variates with respect to the centroid both in numbers and in figures using PCA biplots.

Results

Bacterial community composition based on treatment, year, and sampling period

There were differences in soil bacterial communities at the phyla level between sampling years (2017 and 2018; $P \leq 0.05$); however, there were no differences in bacterial communities between non-organic and organic treatments and sampling period [July and August ($P \geq 0.05$); Table 2]. The following top ten phyla dominated soil bacterial communities: Proteobacteria (mean relative abundance of all libraries was 33.13% in 2017 vs. 32.63% in 2018), Bacteroidetes (6.43% in 2017 vs. 33.44% in 2018), Acidobacteria (23.00% in 2017 vs. 6.86% in 2018), Actinobacteria (8.75% in 2017 vs. 7.07% in 2018), Verrucomicrobia (6.78% in 2017 vs. 8.51% in 2018), Chloroflexi (5.75% in 2017 vs. 3.64% in 2018), Firmicutes (5.95% in 2017 vs. 3.29%

in 2018), Planctomycetes (5.90% in 2017 vs. 1.74% in 2018), Gemmatimonadetes (3.26% in 2017 vs. 0.55% in 2018), and Saccharibacteria (1.06% in 2017 vs. 2.28% in 2018; Fig. 1A). The top 20 soil bacterial communities at the OTU level are presented in Fig. 1B.

Bacterial community alpha diversity is influenced by treatment, sampling years, and sampling period

Alpha diversity was influenced by treatment (organic vs. non-organic), year, and sampling period, as estimated by three different algorithms (Chao1, Shannon, and Simpson's index). Specifically, management affected bacterial species richness (Chao1), with greater richness found in organic pasture soils and fewer species richness occurring in non-organic soils ($P \leq 0.05$) (Table 3). Species richness also varied by years, with greater richness occurring in 2017 compared to 2018 ($P \leq 0.05$). Richness differences between July and August were at the margin of statistical significance ($P = 0.056$). There were richness differences for treatment $\times$ year ($P \leq 0.05$). The Simpson's index was used to calculate the evenness of soil bacterial community and indicated treatments affected bacterial evenness, with a more diverse community occurring in organically managed soils, relative to non-organic soils ($P \leq 0.05$). Year also influenced bacterial community evenness, with greater evenness found in 2018 compared to 2017 ($P \leq 0.05$). However, the sampling period did not result in evenness differences ($P \geq 0.05$). The treatment $\times$ year interaction affected bacterial community evenness ($P \leq 0.05$). The Shannon index was used to measure the community diversity, including both richness and evenness, and there were no treatment or sampling period differences ($P \geq 0.05$). The treatment $\times$ year interaction affected bacterial community diversity ($P \leq 0.05$). Fig. 2A illustrates the influence of treatment and sampling period on soil bacterial richness using Chao1, with Fig. 2B showing bacterial evenness (calculated by using Simpson index), and Fig. 2C presenting the bacterial community diversity (via Shannon index).

Bacterial community structure following treatments and sampling periods

Community structures across treatments and sampling periods were compared to determine if treatments (non-organic and organic) and sampling periods (July and August) impacted the bacterial community structure. Pairwise distances were calculated from all samples using the Bray-Curtis distance metric. These distances were visualized by PCoA, which showed an overlap between bacterial communities from treatments and sampling periods. Significant shifts in community structure from non-organic and organic soils were observed in PCoA plots based on Bray-curtis (PERMANOVA $R = 0.183$, $P \leq 0.05$; Fig. 3). Non-organic samples were distinct from organic samples; however, samples collected from July and August were similar, especially in non-organic systems.

The linear discriminant analysis effect size was used to identify bacterial features represented between non-organic and organic soils and between July and August. The log LDA score cutoff was set at 2 (as an absolute value). Both the negative and positive values for the cutoff can be considered to determine significant features when the score is lower than 2. LEfSe analysis confirmed two features (OTU38 and OTU44), showing statistically significant and

biologically consistent differences in non-organic soil samples collected from August. The other two significant features (OTU11 and OTU56) were found in organic soil samples collected in July (Fig. 4). These identified bacterial species reflected distinct abundance in soil samples. LEfSe also detected 11 bacterial species showing statistically significant differences in organic soil samples collected from August. However, no significant feature can be found in samples collected from non-organic soil in July (Fig. 4).

Soil chemical property relationship with bacterial community structure

The first three PCs were selected (Table 4) for further analysis based on their cumulative variability accounting for 65.80% of the total variation. Principal component 1 explained 37.42% of overall variance, while PC2 and PC3 contributed an additional 16.12% and 12.26%, respectively. Principal component 1, was most strongly affected by soil N, C, and S contents, which are correlated in Fig. 5, as well as in the biplot (Fig. 6a,b). All these factors are positive eigenvectors in PC1, which is shown numerically in Table 5, as well as in Fig. 6a and 6b (as all these vectors were directed toward a positive direction with respect to the centroid). Principal component 2 was most strongly associated with soil pH, Ca, and P contents. These factors are negative eigenvectors in PC2, which is shown in Table 5, as well as in Fig. 6a and Fig. 6c as these vectors were directed toward the negative side. Likewise, PC3 was closely related to soil Zn content, Gemmatimonadetes, and Acidobacteria, which are seen in Table 5 and Fig. 6 (b and c).

Soil pH was negatively correlated with Actinobacteria ($R^2 = -0.61$), Acidobacteria ($R^2 = -0.50$), Chloroflexi ($R^2 = -0.45$), and Planctomycetes ($R^2 = -0.48$). Nitrogen and C were positively correlated with Gemmatimonadetes (N, $R^2 = 0.63$; C, $R^2 = 0.67$), Planctomycetes (N, $R^2 = 0.78$; C, $R^2 = 0.81$), Firmicutes (N, $R^2 = 0.69$; C, $R^2 = 0.71$), Chloroflexi (N, $R^2 = 0.45$; C, $R^2 = 0.45$), Actinobacteria (N, $R^2 = 0.60$; C, $R^2 = 0.57$) and Acidobacteria (N, $R^2 = 0.68$; C, $R^2 = 0.72$). The significant correlation between OTUs of dominant bacterial phyla and soil minerals is given in Table 6. Likewise, relationship between soil pH, C, N, C:N ratio, minerals (Al, As, B, Ca, Cd, Co, Cr, Cu, Fe, K, Mg, Mn, Mo, Na, Ni, P, Pb, S, Se, Ti, Zn) and number of OTU of most dominant bacteria phyla can be seen in Fig. 5 and Fig. 6 a-c.

Discussion

Soil microbial diversity in long-term organic vs non-organic pastures

The study was conducted to assess the microbial diversity, richness and community structure using 16S rRNA sequencing between soil samples taken from organic and non-organic pasture plots. Using Illumina Miseq sequencing, this study found that greater bacterial species richness, evenness, and diversity occurred in organic soils relative to non-organic soils. All of the bacterial communities were dominated by a few major phyla including: Proteobacteria, Bacteroidetes, Acidobacteria, Actinobacteria, Verrucomicrobia, Chloroflexi, Firmicutes, Planctomycetes, Gemmatimonadetes, and Saccharibacteria. The relative abundance of the most dominant

bacterial taxa in this study ~~are~~^{is} similar to that reported by (Lupatini et al., 2017). Although, soil samples were taken to compare differences in bacterial taxa between organic and non-organic pastures with different management systems, it is important to recognize that most dominant bacteria taxa were largely the same in both treatments and months, with some differences only in their relative abundance.

The greater microbial diversity in organically managed soil in the current study is consistent with earlier reports (Hartmann et al., 2015; Mäder et al., 2002). Higher diversity of microbial communities in organically managed pastures is likely related to the restricted use of chemical fertilizers and pesticides and with applications of organically raised poultry litter, which provides essential macronutrients for microbial growth and function (Sun et al., 2004; Chaudhry et al., 2012; Ashworth et al., 2017; Yang et al., 2019). Increases in microbial diversity cause ^a more heterogeneous distribution of bacterial species, ~~thus~~ leading to healthier plant-soil associations and ecosystems benefits for improved sustainability (Brussaard et al., 2007; Crowder et al., 2010). In non-organic pastures, herbicides and chemical fertilizers are regularly applied, causing long-term stress to microbial populations leading to less diverse microorganisms, in part, because these chemicals potentially inhibit or eliminate certain groups of bacteria and selects ^a few bacterial phyla that could thrive in non-organic management systems (El Fantroussi et al., 1999; Stagnari et al., 2014).

Forage pastures in the current study were grazed by organically raised lambs in organic pastures and conventionally raised lambs in non-organic pastures. Our study revealed that pasture management affects soil microbial diversity, suggesting that organically produced poultry litter, less herbicide use, and less antibiotic use in organic production systems (poultry and lamb) bequests greater diversity than conventional lamb pasture-based systems. This study also suggests that soil nutrients via applications of organically raised poultry litter, forage species diversity, and fewer synthetic compounds favors more diverse soil microbial communities resulting in increased alpha diversity.

Relationship between soil pH, C, N, soil C: N ratio and soil minerals on most dominant bacteria phyla

Although bacteria varied temporally and spatially, overall bacterial diversity was largely predicted by soil pH (Lauber et al., 2009). The effect of pH on bacterial community was evident at the phyla level where there was a high relative abundance of Gemmatimonadetes, Planctomycetes, Actinobacteria, Acidobacteria, and Chloroflexi, changing in a consistent manner across the soil pH gradient as depicted both by Spearman correlation as well as PCA biplots. Though some bacterial taxa are correlated with soil pH, pH may not be considered the universal predictor of microbial diversity. The effect of pH on bacterial community structure and diversity in the current study has been supported by various studies where different sequencing methods were used (Blagodatskaya & Anderson, 1998; Bååth & Anderson, 2003; Cookson et al., 2007). Specifically, relative abundance of Acidobacteria, Actinobacteria, Planctomycetes, and Chloroflexi were correlated with soil pH, similar to that in the current study (Sait et al., 2006;

Eichorst et al., 2007). It is notable that soil pH and bacterial community structure were correlated; however, it is hard to identify specific mechanisms that cause these relationships. There are two general explanations that may explain why soil pH was the predictor of bacterial community composition. First, most bacterial taxa have intracellular pH close to neutral (Madigan & Martinko, 2005) and are unable to survive if soil pH falls outside the narrow range of tolerance, i.e., pH of 6.5-7.5). Lower soil pH or acidification inhibits bacterial enzyme activity and overall cell mechanics (Beales, 2004), but some microorganisms can survive in acidic environments (Beales, 2004). Second, pH acts as an integrating factor for a number of several soil variables, e.g., soil organic C, N, P, ion sorption, and salinity, and poultry litter applications are known to increase pH due to its liming effect; (Brady & Weil, 1999).

Soil microbial communities affect C and N turnover with complex interactions involving vegetation types and various soil properties (Bailey et al., 2002; Deng et al., 2016). Therefore, soil microbial community abundance and diversity has have significant correlations with soil total N and C (Liu et al., 2012). In the current study, a strong positive correlation with bacteria phyla (Gemmatimonadetes, Planctomycetes, Firmicutes, Chloroflexi, Actinobacteria, and Acidobacteria) and N and C was observed (both Spearman correlation and PCA biplots). This is important to understand the relationship of soil microbes and for sequestration and stability of N and C in grassland soils.

Close contact of soil minerals and soil microorganisms is essential for biogeochemical cycling and transformation of plant nutrients, and by acquiring necessary enzyme cofactors through minerals (Jansson, 1987; Bennett et al., 2001; Semrau et al., 2010; Ahmed & Holmström, 2014; Jones & Bennett, 2014). Yet, very limited studies have found a relationship between soil microorganisms and minerals. In the current study, some relationships between dominant soil microbiomes and minerals were observed. Correlations existed between some soil minerals and dominant bacterial taxa. However, there are other factors such as pH which could have masked the effect and thus other factors such as pH could have masked the effect, and thus, a future controlled study may be needed to confirm this relationship.

Effect of moisture on soil bacteria

Precipitation drives bacterial abundance (Clarholm & Rosswall, 1980); therefore, rainfall data for three days before the sample collection are presented (Table 1). In the current study, Firmicutes and Actinobacteria (both gram-positive bacteria) were able to maintain their relative percentages even in a comparatively drier 2018 compared to 2017. It is because their gram-positive cell wall structure allows these organisms to withstand drier conditions (Schimel et al., 2007; Lennon et al., 2012; Moreno-Espíndola et al., 2018). There are other factors such as the presence of soil organic C and ability of bacteria to produce biofilms that also helps to Other factors, such as the presence of soil organic C and bacteria's ability to produce biofilms, also help increase or decrease the abundance of gram-negative bacteria (Malik et al., 2018; Moreno-Espíndola et al., 2018).

Soil microorganisms depend on organic C for their growth. Plants provide C to rhizosphere microorganisms in the form of exudates, secretions, lysates, and dead cells (Singh et al., 2004). ~~During drought however, the quantity and quality of C available to soil microbes.~~ However, during drought, the quantity and quality of C available to soil microbes negatively impacts gram-negative bacteria as these are more tightly connected to freshly assimilated plant C (Denef et al., 2009). Drastic decreases of Acidobacteria, Planctomycetes, and Gemmatimonadetes in 2018 could be due to their gram-negative bacterial structure, making them vulnerable to dry soil (Denef et al., 2009). However, ~~there are some gram-negative bacteria that some gram-negative bacteria~~ increased, which could be due to biofilms. Though gram-negative by structure, Proteobacteria, Chloroflexi, and Saccharibacteria were able to maintain similar percentages during 2018 compared with 2017, likely due to their ability to produce biofilms, thus helping them to withstand drought (Or et al., 2007).

Conclusions

The current study was performed to assess soil microbial diversity, richness, and community structure in organic and non-organic livestock pastures using 16S rRNA sequencing. Most of the dominant bacterial taxa were similar in both management systems with some differences in their relative abundance; however, greater soil microbial diversity was observed in organic livestock pastures. More heterogeneous distribution of bacterial species leads to healthier associations at the soil-plant-animal nexus and ultimately improves sustainable agriculture production. Though pH was correlated with the most dominant bacterial phyla, soil properties such as C and N were more strongly correlated. Additionally, we observed a correlation between several soil minerals (Fe, Mg, Ni, S, Al, K, Cd, and Cu) and bacterial phyla (Gemmatimonadetes, Planctomycetes, Firmicutes, Chloroflexi, Actinobacteria, and Acidobacteria). Limited studies are available that outline the relationship between soil minerals and bacterial phyla. However, soil minerals are essential for enzymatic reactions, biochemical cycling, production of chelating agents, and catalyzing reactions. Overall, greater soil microbial diversity in the organic system, suggests organically produced poultry litter, less herbicide and antibiotic use (during poultry and lamb production) resulted in greater soil microbial diversity than the conventional lamb system. Further studies are needed to ascertain driving soil factors for microbial abundance in order to optimize soil function in the largest land-use category in the US, or grasslands.

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