Received: 22 December 2020 | Accepted: 14 October 2021 | Published online: 3 January 2022

DOI: 10.1002/jeq2.20307

Journal of Environmental Quality

TECHNICAL REPORTS

Environmental Microbiology

Soil bacterial community response to rhizoma peanut incorporation into Florida pastures

Victor A. Guerra[1] | **Lukas Beule**[2] | **Cheryl L. Mackowiak**[1] | **Jose C. B. Dubeux Jr.**[3] | **Ann R. S. Blount**[1] | **Xiao-Bo Wang**[4] | **Diane L. Rowland**[5,6] | **Hui-Ling Liao**[1]

[1] North Florida Research and Education Center, Univ. of Florida, 155 Research Road, Quincy, FL 32351, USA

[2] Julius Kühn Institute (JKI)—Federal Research Centre for Cultivated Plants, Institute for Ecological Chemistry, Plant Analysis and Stored Product Protection, Königin-Luise-Strasse 19, Berlin 14195, Germany

[3] North Florida Research and Education Center, Univ. of Florida, 3925 Highway 71, Marianna, FL 32446, USA

[4] State Key Laboratory of Grassland Agroecosystems, Center for Grassland Microbiome, and College of Pastoral, Agriculture Science and Technology, Lanzhou Univ., Lanzhou 730020, PR China

[5] Agronomy Dep., Univ. of Florida, Gainesville, FL 32611, USA

[6] Current address: College of Natural Sciences Forestry, and Agriculture, Univ. of Maine, Orono, ME 04469, USA

Correspondence
Victor A. Guerra, North Florida Research and Education Center, Univ. of Florida, 155 Research Rd., Quincy, FL 32351, USA.
Email: v.savas61@gmail.com

Assigned to Associate Editor Célia Manaia.

Abstract

Incorporating legumes is one option for improving pasture fertility, sustainability, and biodiversity. Diazotrophic microorganisms, including rhizobia that form symbioses with legumes, represent a small fraction of the total soil microbial community. Yet, they can offset nitrogen (N) fertilizer inputs through their ability to convert atmospheric N_2 into plant-usable N via biological N_2 fixation (BNF). This study used amplicon sequencing of 16S rRNA genes to investigate soil bacterial community composition and diversity in grazed 'Argentine' bahiagrass (*Paspalum notatum* Flügge) pastures where N fertilizer was supplanted with legume-derived N from BNF in some treatments. Treatments consisted of bahiagrass fertilized with (a) mineral N (224 kg N ha^{-1} yr^{-1}), (b) combination mineral N (34 kg N ha^{-1} yr^{-1}) and legume-derived N via cool-season clover (CSC) (*Trifolium* spp.) mix, or (c) combination mineral N (34 kg N ha^{-1} yr^{-1}) and legume-derived N via CSC mix and strips of Ecoturf rhizoma peanut (*Arachis glabrata* Benth.). *Bradyrhizobium* spp. relative abundance was 44% greater in the mixed pasture. Other bacterial genera with BNF or denitrification potentials were greater in pastures with legumes, whereas sequences assigned to genera associated with high litter turnover were greater in bahiagrass pastures receiving only mineral N. Soil bacteria alpha diversity was greater in pastures receiving 34 kg ha^{-1} yr^{-1} N fertilizer application and the CSC mix than in pastures with the CSC mix and rhizoma peanut strips. Our results demonstrate soil microbial community shifts that may affect soil C and N cycling in pastures common to the southeastern United States.

1 | INTRODUCTION

Soil N strongly influences soil bacterial community composition in grasslands (Fierer et al., 2012; Leff et al., 2015; Zeng et al., 2016). Additionally, plant species may selectively shape soil microbial communities through root exudates (Berg & Smalla, 2009; Lundberg et al., 2012; Millard & Singh, 2010). Zhou et al. (2017) reported greater soil bacterial diversity and variation in bacterial community composition across legume species than across grass species, concluding that legume species were more influential upon soil bacterial communities than grass species. For example, symbiotically associated rhizobia that provide biological N_2 fixation (BNF) can supply over 20% of N used by grass species when grown with

Abbreviations: ASV, amplicon sequence variant; BNF, biological N_2 fixation; CSC, cool-season clover; SRS, scaling with ranked subsampling.

legumes and support greater herbage productivity as well as legume persistence over time (Jaramillo et al., 2018; Santos et al., 2018; van der Heijden et al., 2006, 2008).

Relatively little has been reported on grassland soil bacterial diversity and composition dynamics that include perennial legumes. In comparison, there are several reports addressing the soil microbiome of temperate, upland grasslands (e.g., McCaig et al., 1999; Millard & Singh, 2010) and even a few on subtropical, perennial grasslands, including bahiagrass (*Paspalum notatum* Flügge) (e.g., Beule et al., 2019; Zhou et al., 2019). Bahiagrass is of particular interest because it dominates Florida pastures.

In North Florida, bahiagrass pasture management is often represented by mineral N fertilizer applications in the summer and overseeding with cool-season annual forages during the dormant winter months. However, N fertilizer losses from Florida pastures through leaching and subsurface runoff can contribute to Florida groundwater pollution (Silveira & Kohmann, 2020). Although bahiagrass tolerates low N fertilizer management (56 kg N ha^{-1} yr^{-1}), greater herbage accumulation is attained at higher (180 kg N ha^{-1}) annual application rates (Mylavarapu et al., 2009; Silveira et al., 2015; Vendramini et al., 2013). A more sustainable balance between economic and environmental benefits might be realized in grass pastures with inclusion of a greater proportion of legume-derived N (Muir et al., 2011; Rouquette & Smith, 2010; Silveira et al., 2014).

Legumes added to bahiagrass pastures through overseeding cool-season cover crop mixes, including clover (*Trifolium* spp.), contribute N to the system and maintain pasture productivity until bahiagrass summer growth resumes (Dubeux et al., 2019). Additionally, incorporating a warm-season perennial legume, such as rhizoma peanut (*Arachis glabrata* Benth.), into bahiagrass pastures minimizes the need for mineral N applications and improves forage nutritional value (Dubeux et al., 2017; McCormick et al., 2014; Mullenix et al., 2016; Santos et al., 2018).

Soil microbial communities associated with monocultures of either rhizoma peanut or bahiagrass share some of the same bacterial genera (Beule et al., 2019; Wang et al., 2019). For example, *Bradyrhizobium* was the dominant bacterial genera in the soil of both plant species grown as monocultures (Beule et al., 2019; Wang et al., 2019). In mixed perennial ryegrass (*Lolium perenne* L.)–white clover (*Trifolium repens* L.) stands, soil bacteria community–level physiological profiles indicated a community composition shift, whereby the capacity to utilize different carbon sources was diminished relative to clover monocultures receiving no N fertilizer or grass monocultures receiving N fertilizer (van Eekeren et al., 2009). Using 16S ribosomal RNA (rRNA) sequence analysis, McCaig et al. (1999) observed no differences in total soil bacterial diversity but greater diversity within the Alphaproteobacteria class in an unfertilized perennial pasture dominated by *Agrostis capillaris* L. and *Festuca ovina* L. compared with improved pastures consisting of an N-, P-, and K-fertilized *L. perene* and *T. repens* mix. Many sequences within the Alphaproteobacteria class were closely related to *Bradyrhizobium* and *Rhizobium* spp. The presence of legumes in grasslands favors an increased proportion of the soil bacterial community being represented by rhizobia performing BNF, yet the effects of legume incorporation on soil bacterial community diversity are less clear. Changes within the soil bacterial community in response to N management and plant species may also have implications for litter turnover and nutrient cycling in perennial pastures.

Core Ideas

- Soil bacterial community composition in bahiagrass pastures was altered by N management.
- Legume incorporation promoted relative abundance of N-cycling bacteria.
- Soil bacteria alpha diversity did not coincide with vegetation diversity.

In this study, we compared bahiagrass pastures under different N fertilization management, where annual mineral N fertilizer applications were offset with proportionately more BNF-N from legumes, in order to determine potential impacts on soil microbial community diversity and composition. An amplicon sequencing based account of bacterial community response to treatments at this site will help identify biological linkages to soil C and N cycling in warm-season, perennial pastures and contribute to the emerging understanding of interactions among plants, soil, and microbes. We hypothesized there would be greater soil bacterial diversity as well as a greater abundance of N cycling bacteria, including rhizobia, in treatments with BNF legumes. The objectives of this study were (a) to determine if changes occurred in soil bacterial diversity among treatments and (b) to identify which bacterial taxa were either enriched or depleted with changes in pasture N management.

2 | MATERIALS AND METHODS

2.1 | Study site and experimental design

The study site was located at North Florida Research and Education Center (NFREC), Mariana, FL (30°52′ N, 85°11′ W; 35 m asl). Soils were Orangeburg loamy sand (fine-loamy, kaolinitic, thermic Typic Kandiudults) (Soil Survey Staff, 2019). Long-term (1987–2017) average precipitation

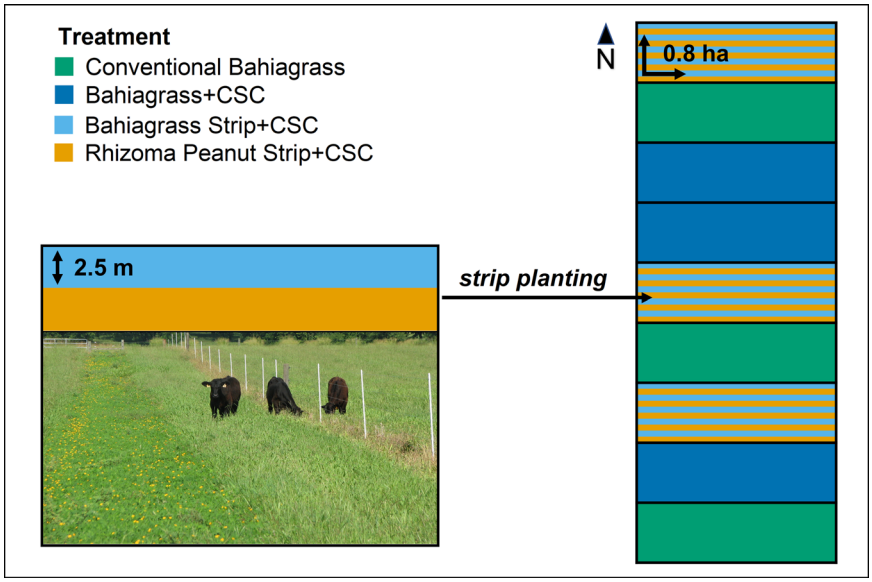

FIGURE 1 Experimental layout of replicated pastures. Treatments consisted of different N management: Conventional Bahiagrass (224 kg N ha^{-1} yr^{-1}), bahiagrass + cool-season clover (CSC) mixture (34 kg N ha^{-1} yr^{-1}), and strip planting consisting of 2.5-m-wide alternating strips of bahiagrass (Bahiagrass Strip+CSC) and rhizoma peanut (Rhizoma Peanut Strip+CSC) (34 kg N ha^{-1} yr^{-1})

was 1,361 mm yr^{-1} (Vose et al., 2014). Total precipitation during our sampling year (2017) was 1,272 mm.

'Argentine' bahiagrass (*Paspalum notatum* Flügge) pastures (0.85 ha) were established June 2014, and each received one of three different N management treatments arranged in a randomized complete block design with three replicates (Figure 1). The first treatment consisted of conventional bahiagrass N management (Conventional Bahiagrass), receiving 224 kg N ha^{-1} yr^{-1}, with 56 kg N ha^{-1} in May and again in July (warm-season), 34 kg N ha^{-1} in December, and 78 kg N ha^{-1} in January (cool-season). In December 2017, the Conventional Bahiagrass treatment was overseeded with 'FL401' rye (*Secale cereale* L.) and 'RAM' oat (*Avena sativa* L.) at 56 kg ha^{-1} of each seed type using a no-till drill. The second treatment consisted of bahiagrass managed under low mineral N fertilizer (34 kg N ha^{-1} applied in December) and included a cool-season clover (CSC) and grass mix (Bahiagrass+CSC) at a 1:2:5 ratio of 'Grazer's Select' ball (*Trifolium nigrescens* Viv.), 'Southern Belle' red (*Trifolium pratense* L.), and 'Dixie' crimson (*Trifolium incarnatum* L.) clovers at 22 kg ha^{-1} total seed mass. This was combined with a 1:1 mix of rye and oat (88 kg ha^{-1} total seed mass) and sowed at 110 kg seed ha^{-1} using a no-till drill in December 2017. Two additional treatments were located in a mixed pasture of bahiagrass (Bahiagrass Strip+CSC treatment) and Ecoturf germplasm, rhizoma peanut (*Arachis glabrata* Benth.), established as alternating strips that were ~2.5 m wide (Rhizoma Peanut Strip+CSC treatment). These two treatments received 34 kg N ha^{-1} in December as part of total pasture fertilization, and the same CSC/grass mix was used in the fall. Imazapic (291 ml ha^{-1}) was applied in May, July, and August only to rhizoma peanut strips. All fertilizer N applications were as a 50:50 mix of uncoated and polymer coated urea (ESN, Agrium Advance Technologies). Along with the fall N application, all pastures received 19 kg P_2O_5 47 kg K_2O and 13.4 kg S ha^{-1}. In spring (April 2017), all pastures were fertilized with 2.24 kg B, 93 kg K_2O, 27 kg Mg, and 12.1 kg S ha^{-1}. A treatment and management summary is given in Table 1. A conceptual representation of

TABLE 1 Botanical composition and mineral N fertilization comprising treatments assigned to replicated ($n = 3$) pastures at the experiment site in Marianna, FL

Treatment	Botanical composition	Mineral N fertilization	
		Warm season	Cool season
		kg ha^{-1}	
Conventional bahiagrass	*Paspalum notatum*	112	112
	Secale cereale		
	Avena sativa		
Bahiagrass + CSC[a]	*Paspalum notatum*	0	34
	Secale cereale		
	Avena sativa		
	Trifolium spp.		
Bahiagrass strip + CSC	*Paspalum notatum*	0	34
	Secale cereale		
	Avena sativa		
	Trifolium spp.		
Rhizoma peanut strip + CSC	*Arachis glabrata*	0	34
	Secale cereale		
	Avena sativa		
	Trifolium spp.		

[a]CSC, cool-season clover.

treatment arrangement is shown in Figure 1, and a detailed description of experimental site, management, and treatment was provided by Jaramillo, Dubeux, Sollenberger, Vendramini, et al. (2021).

2.2 | Grazing management

Grazing management across treatment pastures was similar, where two tester Angus crossbreed steers (*Bos* spp.) grazed each pasture throughout the season. Put-and-take cattle of similar breed, weight, and age were assigned to pastures as needed based on target herbage allowances of 1 kg dry matter kg^{-1} body weight during the cool season and 1.5 kg dry matter kg^{-1} body weight during the warm season. A detailed description of grazing management in this study is provided by Jaramillo, Dubeux, Sollenberger, Vendramini, et al. (2021).

2.3 | Soil sampling, DNA extraction, and library preparation

In April 2017, five soil cores (diameter, 2.54 cm; depth, 10 cm) were collected from five locations within each replicated treatment. In pastures under the strip-planted treatment, five cores were collected from bahiagrass strips and five from rhizoma peanut strips. Independent soil cores were placed in sealable plastic bags and stored at 4 ˚C while in the field. Upon return to the laboratory within the same day, soil samples were immediately passed through a 2-mm sieve to remove large roots and debris and stored at −20 ˚C. Soil DNA extraction was performed using a commercial DNA isolation kit (PowerSoil, Mobio Laboratories Inc.) using 0.45 g soil. The V4 region of bacterial 16S rRNA genes was targeted in a three-step polymerase chain reaction using the primer pair 515F (5′-GTGC CAGC MGCC GCGG TAA-3′) and 806R (5′-GACT ACHV GGGT WTCT AAT-3′) (Caporaso et al., 2011) as described previously (Chen et al., 2018). Amplicons were indexed using 10-bp-long barcodes and zero to five frameshifting nucleotides to ensure nucleotide diversity during sequencing. Indexed polymerase chain reaction products were pooled equimolar and sequenced in one multiplexed Illumina run using the MiSeq Reagent Kit v2 (2 × 250 bp) (Illumina Inc.) at Duke Center for Genomic and Computational Biology.

2.4 | Bioinformatic processing of sequencing data

A total of 1,122,767 raw sequence reads were demultiplexed and imported in QIIME 2 version 2019.10 (Bolyen et al., 2019). Sequencing adapters and primers were removed using cutadapt (Martin, 2011), and read quality was assessed using the 'q2-demux' plugin. Forward and reverse reads were truncated to 220 and 195 bp, respectively; quality-filtered; and merged. Chimera and singletons were removed using DADA2 (Callahan et al., 2016). Amplicon sequence variants (ASVs) were taxonomically classified against the SILVA SSU database release 138 (Quast et al., 2013) at 100% identity threshold using VSEARCH (Rognes et al., 2016), and nonbacterial reads were removed. Differences in sequencing depth were corrected using scaling with ranked subsampling (SRS) (Beule & Karlovsky, 2020). The SRS curves were plotted using the 'SRScurve' function, and the ASV table was normalized to 4,798 reads per sample using the 'SRS' function of the 'SRS' R-package (Beule & Karlovsky, 2020).

2.5 | Statistical analysis

Alpha diversity was assessed by determining the Shannon diversity index *H'*, and species richness determined using the 'diversity' and 'specnumber' function in the 'vegan' R package v2.5-6 (Oksanen, 2017). Differences in exponentially transformed Shannon diversity index *H'* values and species richness among N treatments were tested using one-way ANOVA with Tukey's honestly significant difference test for separating means. Treatment was considered as fixed effect, and block was considered as random effect. Nonmetric, multidimensional scaling of Bray–Curtis dissimilarities was performed by using the 'metaMDS' function in the 'vegan' R package (Oksanen, 2017). Canonical analysis of principal coordinates (Anderson & Willis, 2003) of Bray–Curtis dissimilarities was performed using the 'CAPdiscrim' function in the 'BiodiversityR' R package v2.11-3 (Kindt & Coe, 2005).

Differences in community dispersion within treatments were examined using a test for homogeneity of multivariate dispersions (PERMDISP) (Anderson, 2006) using 9,999 permutations. PERMDISP was performed using the 'betadisper' function in the 'vegan' R package (Oksanen, 2017). If a homogenous dispersion was given, dissimilarities of soil bacterial community composition in response to N management were tested using nonparametric permutational multivariate ANOVA (Anderson, 2001) using 9,999 permutations. The permutational multivariate ANOVA was performed using the 'adonis2' function in the 'vegan' R package (Oksanen, 2017). Differences in soil bacterial genera abundance were tested using Kruskal–Wallis test with the multiple comparison extension. Statistical significance was considered at $\alpha \leq .05$, and parameters with $p > .05 \leq .08$ are mentioned as marginally significant. All statistical analyses were carried out in R environment v4.0.0 (R Core Team, 2017).

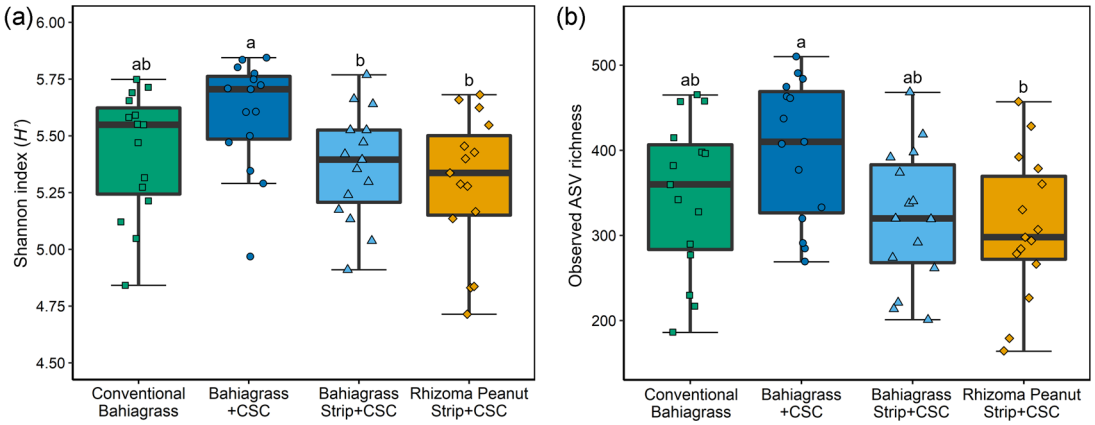

FIGURE 2 Alpha diversity indices of soil bacterial communities across different N management treatments. Boxplot displaying (a) amplicon sequence variant (ASV) diversity (Shannon index H') and (b) ASV richness. Squares, circles, triangles, and rhombi represent individual data points. Different lowercase letters indicate differences in the alpha diversity of soil bacteria (one-way ANOVA with Tukey's honestly significant difference test at $\alpha \leq .05$). CSC, cool-season clover

3 | RESULTS AND DISCUSSION

3.1 | Soil bacterial community composition

Quality-filtered reads from all samples were grouped into 1,069 unique ASVs assigned to 12 phyla. Among all samples, dominant (>0.5%) phyla included Proteobacteria (24.8 ± 4.5%), Acidobacteria (23.0 ± 7.0%), Actinobacteria (15.0 ± 5.1%), Firmicutes (8.5 ± 5.6%), Verrucomicrobia (6.0 ± 2.0%), and Bacteroidetes (5.5 ± 2.4%). Unassigned and rare (<0.5%) phyla accounted for 2.6 ± 1.1% of all sequences. Phyla representing <5% relative abundance included Gemmatimonadetes, Myxococcota, Nitrospirae, and Plantomycetes. Bacteria classes Acidobacteriae (Acidobacteria, 17.9 ± 7.7%), Alphaproteobacteria (Proteobacteria, 14.1 ± 3.1%), and Gammaproteobacteria (Proteobacteria, 10.8 ± 2.7%) dominated the samples (Supplemental Figure S1). Approximately 64% of total sequences were assigned at the genus level. We classified ASVs at 100% identity threshold, which likely reduced the number of sequences classified to the genus level but improved taxonomic classification certainty. Among the 27 genera of bacteria observed, the most common across samples included *Bacillus* (Firmicutes, 6.8 ± 4.6%), *Bryobacter* (Acidobacteria, 2.7 ± 1.0%), *Candidatus Udaeobacter* (Verrucomicrobia, 2.5 ± 1.0%), and *Bradyrhizobium* (Proteobacteria, 2.3 ± 0.8%).

3.2 | Soil bacteria community diversity

Soil bacterial diversity (Shannon index *H'*; $P = .010$) and richness (observed ASV richness; $P = .022$) were affected by pasture treatments (Figure 2). There was greater bacterial alpha diversity in the Bahiagrass+CSC treatment than in the Bahiagrass Strip+CSC treatment ($P = .049$) or the Rhizoma Peanut Strip+CSC treatment ($P = .008$) (Figure 2a). In comparison, ASV richness in the Bahiagrass+CSC treatment was greater than in the Rhizoma Peanut Strip+CSC, whereas other treatments were comparable to both ($P = .022$) (Figure 2b). In this case, increasing vegetation diversity did not translate into greater soil bacterial diversity. Successful characterization of the relationship between pasture vegetation diversity and soil microbial diversity remains elusive despite targeted efforts using a range of methods (Kowalchuk et al., 2002; Leff et al., 2015; Millard & Singh, 2010; Prober et al., 2015; Schlatter et al., 2015; Wardle, 2006).

Soil bacteria community composition differed most between the Conventional Bahiagrass treatment and Rhizoma Peanut Strip+CSC based on Bray–Curtis dissimilarities ($P = .025$) (Figure 3). More specifically, pairwise comparisons identified marginal differences between the Conventional Bahiagrass and Rhizoma Peanut Strip+CSC treatments ($P = .076$), as illustrated by nonmetric, multidimensional scaling clustering (Figure 3a). The canonical analysis of principal coordinate analysis also showed differences among treatments ($P < .001$) (Figure 3b). In contrast to the Conventional Bahiagrass treatment without legumes, the Rhizoma Peanut Strip+CSC treatment included legumes throughout the year (Garcia-Jimenez, 2019). Previous reports also have demonstrated that legume inclusion affected soil bacterial communities (Grayston et al., 2001; van Eekeren et al., 2009; Zhou et al., 2017). Additionally, Millard and Singh (2010) indicated that the quality of organic matter inputs to soil from different vegetation types may be more important in shaping soil bacterial communities than the plant species themselves. Our results suggest that differentiation between soil bacterial communities in conventional grass pastures versus mixed grass–legume pastures was most likely

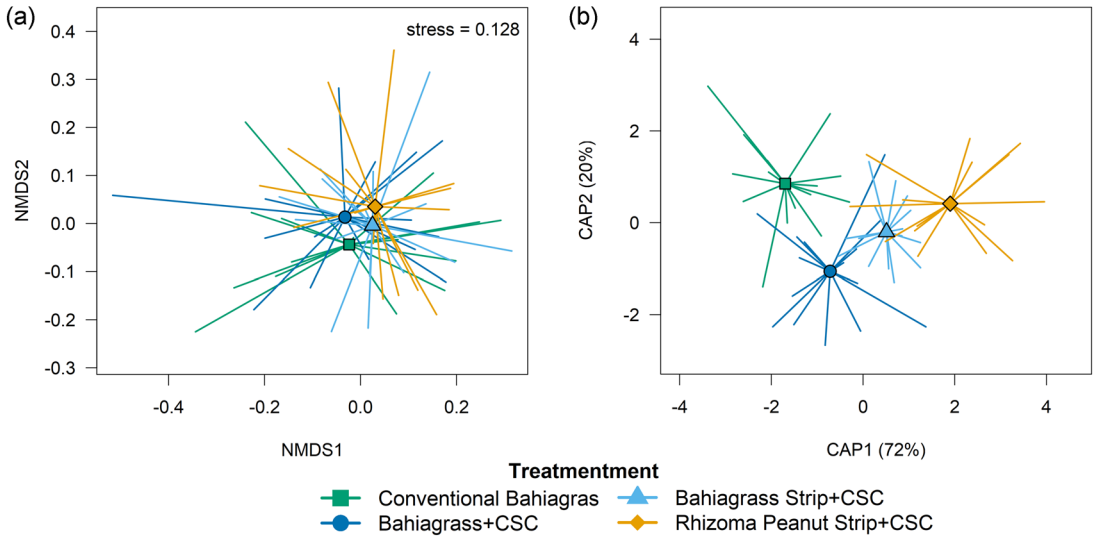

FIGURE 3 Beta diversity among soil bacterial communities under different N management. Nonmetric multidimensional scaling (NMDS) plot of Bray–Curtis dissimilarities calculated for (a) amplicon sequence variants and (b) canonical analysis of principal coordinates (CAP). CSC, cool-season clover

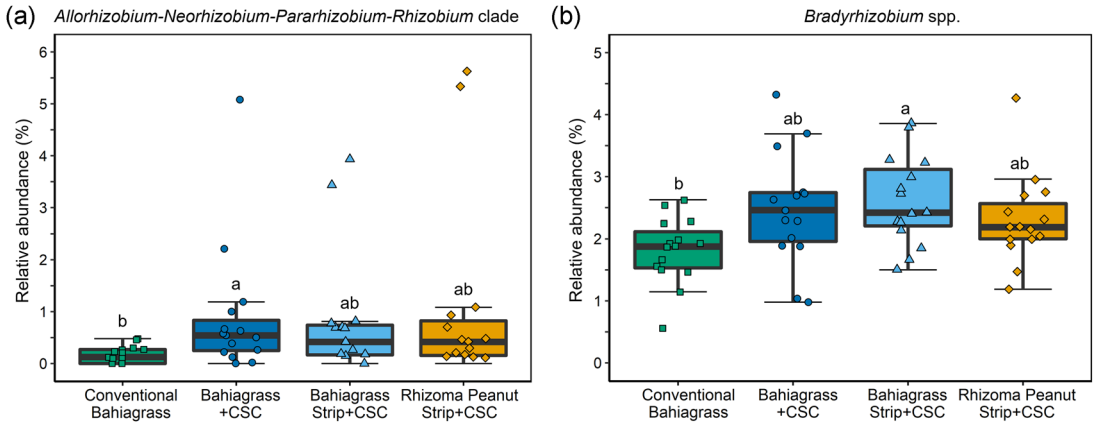

FIGURE 4 Relative abundances of sequences assigned to (a) *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium* clade and (b) *Bradyrhizobium* spp. observed in soil samples taken in pastures under different N management treatments. Squares, circles, triangles, and rhombi represent individual data points. Different lowercase letters indicate differences among treatments (Kruskal–Wallis test with multiple comparison extension at $\alpha \leq .05$). CSC, cool-season clover

when there was year-round legume inclusion (i.e., Rhizoma Peanut Strip+CSC).

3.3 | Soil bacteria genera relative abundance characteristics

The relative abundances of specific soil bacterial genera known to be involved in N-cycling differed across some treatments (Figure 4). For example, sequences assigned to the *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium* clade (Proteobacteria) were found in greater abundance in the Bahiagrass+CSC than in the Conventional Bahiagrass treatment ($P = .024$) (Figure 4a), whereas the Bahiagrass Strip+CSC had a greater abundance of *Bradyrhizobium* spp. than the Conventional Bahiagrass treatment ($P = .012$) (Figure 4b). The genus *Bradyrhizobium* is among the most ubiquitous N_2–fixing bacteria genera in soil (Nelson et al., 2016), although some species have also been identified as denitrifiers (Bedmar et al., 2005; Ishii et al., 2011). Additionally, some *Bradyrhizobium* spp. are known to persist in soil years after host plant cultivation has terminated (Crozat et al., 1982; Obaton et al., 2002). Even so, shifts in relative abundance of *Bradyrhizobium* among

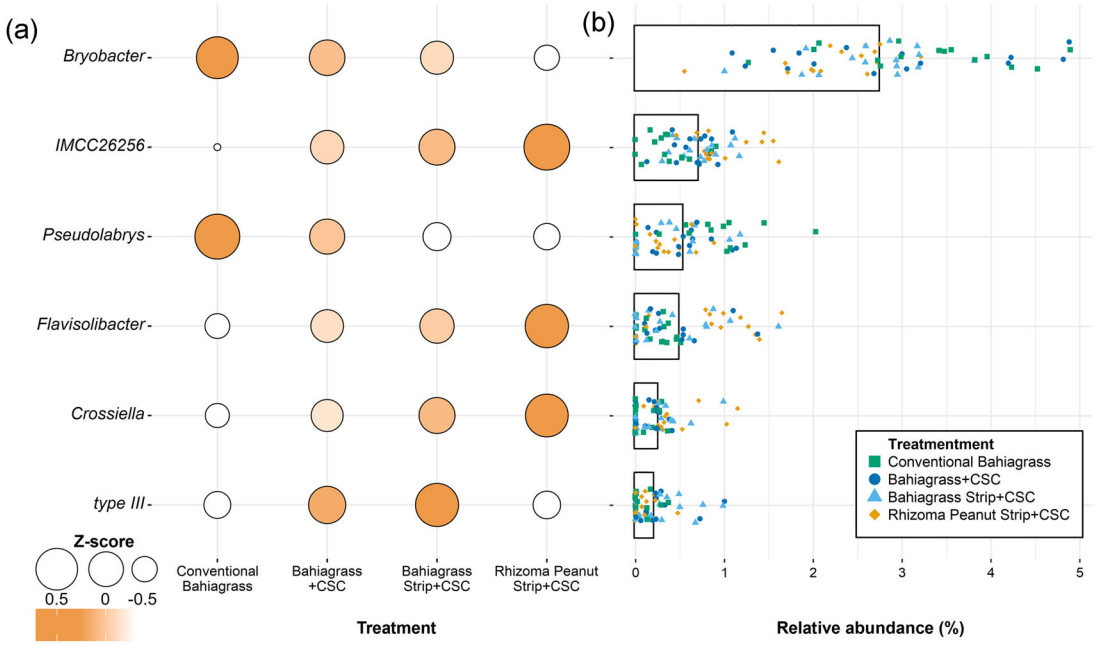

FIGURE 5 *Z*-score–transformed (a) mean relative abundances and (b) relative abundances of soil bacterial genera identified as having differences among pastures under different N management strategies (Kruskal–Wallis test with multiple comparison extension at $\alpha \leq .05$). CSC, cool-season clover

treatments demonstrate the influential role legume inclusion plays in shaping the soil bacterial community in pastures. Wang et al. (2019) listed *Bradyrhizobium* among the most dominant genera observed in plots across seven different rhizoma peanut cultivars. However, at a nearby site, Beule et al. (2019) reported *Bradyrhizobium* to be the second most abundant genus present among different bahiagrass cultivars.

There was greater relative abundance of *Crossiella* (Actinobacteria) in the Rhizoma Peanut Strip+CSC than in the Conventional Bahiagrass treatment ($P = .017$) (Figure 5a). Sequences assigned to the bacterial genus *type III* (*Firmicutes*) were found in greater abundance in the Bahiagrass Strip+CSC than in the Rhizoma Peanut Strip+CSC, which lie adjacent to one another, or Conventional Bahiagrass treatments ($P = .010$). Sequences assigned to *type III*, *Crossiella*, and *Flavisolibacter* represented rare taxa (<0.5% relative abundance) whose relative abundances were affected by treatment (Figure 5b).

Flavisolibacter (Bacteroidetes) ($P = .012$) was less abundant in the Conventional Bahiagrass treatment compared with the Rhizoma Peanut Strip+CSC treatment, which was represented by legume species year-round. Additionally, the Bahiagrass Strip+CSC and Rhizoma Peanut Strip+CSC treatments resulted in a greater abundance of uncultured *Actinobacteria* IMCC26256 spp. ($P = .0001$).

There was greater abundance of *Bryobacter* (Acidobacteria) ($P = .032$) in the Conventional Bahiagrass compared with the Rhizoma Peanut Strip+CSC treatment (Figure 5a). Dedysh et al. (2017) reported that the genus *Bryobacter* preferred substrates composed of sugars, polysaccharides, and organic acids, whereas Rosier et al. (2021) reported a greater abundance of *Bryobacter* in soils at forest edges, which were also positively correlated with soil organic matter. *Bryobacter* spp. were among the most abundant identified soil bacteria across all treatments ($2.7 \pm 1.0\%$) (Figure 5b) and have been suggested to be a keystone taxon among different vegetation types (Xue et al., 2017).

Similar to *Bryobacter*, sequences assigned to the genus *Pseudolabrys* (Proteobacteria) were in greater abundance in the Conventional Bahiagrass treatment compared with the Rhizoma Peanut Strip+CSC but also greater compared with the Bahiagrass Strip+CSC ($P = .009$) (Figure 5a). *Pseudolabrys* was reported to be positively associated with management practices that increase soil organic carbon (Guo et al., 2016; Ho Joa et al., 2014). Patterns of *Bryobacter* and *Pseudolabrys* abundance in this study coincide with Jaramillo, Dubeux, Sollenberger, Mackowiak, et al. (2021), who reported that Conventional Bahiagrass also had the greatest litter deposition among treatments at this site.

Other research has identified positive correlations between the abundance of *Bryobacter* and soil phosphorous availability (Liang et al., 2020; Malviya et al., 2021; Rosier et al., 2021). *Bryobacter*, along with other dominant soil genera in this study, likely contribute significantly to soil nutrient and carbon cycling processes. However, their contributions to soil processes under different land-use and pasture management

practices are far from being fully identified and substantiated. Linkages between soil bacteria community structure and pasture management that affect herbage and root litter, root exudates, and livestock excreta inputs to the soil require further study.

4 | CONCLUSIONS

Changes to soil bacterial community composition under bahiagrass pasture were identified in the southeastern United States in response to different methods of pasture N management. Legume inclusion demonstrated a potential for increasing the proportion soil bacteria capable of performing BNF by up to 44%, whereas mineral N fertilization tended to be affiliated with other soil bacteria, such as *Bryobacter* and *Pseudolabrys* spp., that are associated with more abundant C substrates and nutrient cycling. Increased plant species diversity in pastures did not correlate with increased soil bacterial diversity. However, treatments that contrasted most in their botanical composition also differed in soil bacteria community structure (i.e., relative abundance). Furthermore, our study used next-generation sequencing technology to identify with high taxonomic resolution soil bacterial communities associated with conventional pasture systems found in North Florida. This information contributes to our understanding of how pasture management influences soil bacterial communities, particularly members that are associated with soil C and nutrient cycling. As next generation sequencing becomes a more accessible tool for reseachers and as reference taxonomy databases are expanded, investigations into bacterial community diversity and associations between specific taxa and substrate quality and quantity in pasture systems should continue.

ACKNOWLEDGMENTS

This project was supported by Agriculture and Food Research Initiative Competitive Grant 2019-67013-29107 from the USDA National Institute of Food and Agriculture (USDA-NIFA). We thank USDA-NIFA National Needs Graduate and Postgraduate Fellowship Program for the funds granted for this research (Award 2015-38420-23700). Lukas Beule was supported by the German Federal Ministry of Education and Research in the framework of the Bonares-SIGNAL project (funding codes: 031A562A and 031B0510A). We thank Chih-Ming Hsu for extracting the soil DNA.

AUTHOR CONTRIBUTIONS

Victor A. Guerra: Formal analysis; Visualization; Writing-original draft; Writing-review & editing. Lukas Beule: Formal analysis; Visualization; Writing-original draft; Writing-review & editing. Hui-Ling Liao: Conceptualization; Funding acquisition; Methodology; Project administration; Resources; Writing-review & editing. Jose C.B. Dubeux: Funding acquisition; Project administration; Writing-review & editing. Ann R.S. Blount: Writing-review & editing. Xiao-Bo Wang: Writing-review & editing. Diane L. Rowland: Writing-review & editing. Xiao-bo Wang: Writing-review & editing. Cheryl L. Mackowiak: Funding acquisition; Supervision; Writing-original draft; Writing-review & editing.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ORCID

Victor A. Guerra https://orcid.org/0000-0003-1431-7650
Lukas Beule https://orcid.org/0000-0003-1107-7540
Xiao-Bo Wang https://orcid.org/0000-0003-2278-2464

REFERENCES

Anderson, M. J. (2001). A new method for non-parametric multivariate analysis of variance. *Austral Ecology*, *26*(1), 32–46. https://doi.org/10.1111/j.1442-9993.2001.01070.pp.x

Anderson, M. J. (2006). Distance-based tests for homogeneity of multivariate dispersions. *Biometrics*, *62*, 245–253. https://doi.org/10.1111/j.1541-0420.2005.00440.x

Anderson, M. J., & Willis, T. J. (2003). Canonical analysis of principal coordinates: A useful method of constrained ordination for ecology. *Ecology*, *84*, 511–525. https://doi.org/10.1890/0012-9658(2003)084(0511:CAOPCA)2.0.CO;2

Bedmar, E. J., Robles, E. F., & Delgado, M. J. (2005). The complete denitrification pathway of the symbiotic, nitrogen-fixing bacterium *Bradyrhizobium japonicum*. *Biochemical Society Transactions*, *33*(1), 141–144. https://doi.org/10.1042/BST0330141

Berg, G., & Smalla, K. (2009). Plant species and soil type cooperatively shape the structure and function of microbial communities in the rhizosphere. *FEMS Microbiology Ecology*, *68*(1), 1–13. https://doi.org/10.1111/j.1574-6941.2009.00654.x

Beule, L., Chen, K.-H., Hsu, C.-M., Mackowiak, C., Dubeux, J. C. B. Jr., Blount, A., & Liao, H.-L. (2019). Soil bacterial and fungal communities of six bahiagrass cultivars. *PeerJ*, *7*, e7014. https://doi.org/10.7717/peerj.7014

Beule, L., & Karlovsky, P. (2020). Improved normalization of species count data in ecology by scaling with ranked subsampling (SRS): Application to microbial communities. *PeerJ*, *8*, e9593. https://doi.org/10.7717/peerj.9593

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., …, Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods*, *13*, 581–583 https://doi.org/10.1038/nmeth.3869

Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., Fierer, N., & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the National Academy of Sciences of the United States of America*, *108*(SUPPL. 1), 4516–4522. https://doi.org/10.1073/pnas.1000080107

Chen, K.-H., Liao, H.-L., Arnold, A. E., Bonito, G., & Lutzoni, F. (2018). RNA-based analyses reveal fungal communities structured by a senescence gradient in the moss *Dicranum scoparium* and the presence of putative multi-trophic fungi. *New Phytologist*, *218*(4), 1597–1611. https://doi.org/10.1111/nph.15092

Crozat, Y., Cleyet-Marel, J. C., Giraud, J. J., & Obaton, M. (1982). Survival rates of *Rhizobium japonicum* populations introduced into different soils. *Soil Biology and Biochemistry*, *14*(4), 401–405. https://doi.org/10.1016/0038-0717(82)90012-8

Dedysh, S. N., Kulichevskaya, I. S., Huber, K. J., & Overmann, J. (2017). Defining the taxonomic status of described subdivision 3 *Acidobacteria*: Proposal of *Bryobacteraceae* fam. nov. *International Journal of Systematic and Evolutionary Microbiology*, *67*(2), 498–501. https://doi.org/10.1099/ijsem.0.001687

Dubeux, J. C. B., Blount, A. R. S., Mackowiak, C., Santos, E. R. S., Pereira Neto, J. D., Riveros, U., Garcia, L., Jaramillo, D. M., & Ruiz-Moreno, M. (2017). Biological N_2 fixation, belowground responses, and forage potential of rhizoma peanut cultivars. *Crop Science*, *57*(2), 1027–1038. https://doi.org/10.2135/cropsci2016.09.0810

Dubeux, J. C. B., Mackowiak, C. L., Blount, A. R. S., Wright, D. L., & Dantas, L. Q. (2019). Overseeding rhizoma perennial peanut pasture and hay fields during the cool-season. *EDIS*, *2019*(1). https://doi.org/10.32473/edis-ag426-2019

Fierer, N., Lauber, C. L., Ramirez, K. S., Zaneveld, J., Bradford, M. A., & Knight, R. (2012). Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. *ISME Journal*, *6*(5), 1007–1017. https://doi.org/10.1038/ismej.2011.159

Garcia-Jimenez, L. M. (2019). *Ecosystem services provided by contrasting grazing systems in North Florida* [Doctoral dissertation, University of Florida]. https://ufdc.ufl.edu/UFE0055613/00001

Grayston, S. J., Griffith, G. S., Mawdsley, J. L., Campbell, C. D., & Bardgett, R. D. (2001). Accounting for variability in soil microbial communities of temperate upland grassland ecosystems. *Soil Biology and Biochemistry*, *33*(4–5), 533–551. https://doi.org/10.1016/S0038-0717(00)00194-2

Guo, L., Zheng, S., Cao, C., & Li, C. (2016). Tillage practices and straw-returning methods affect topsoil bacterial community and organic C under a rice-wheat cropping system in central China. *Scientific Reports*, *6*(1), 1–10. https://doi.org/10.1038/srep33155

Ho Joa, J., Weon, H. Y., Hyun, H. N., Jeun, Y. C., & Koh, S. W. (2014). Effect of long-term different fertilization on bacterial community structures and diversity in citrus orchard soil of volcanic ash. *Journal of Microbiology*, *52*(12), 995–1001. https://doi.org/10.1007/s12275-014-4129-6

Ishii, S., Ashida, N., Otsuka, S., & Senoo, K. (2011). Isolation of oligotrophic denitrifiers carrying previously uncharacterized functional gene sequences. *Applied and Environmental Microbiology*, *77*(1), 338–342. https://doi.org/10.1128/AEM.02189-10

Jaramillo, D. M., Dubeux, J. C. B., Mackowiak, C., Sollenberger, L. E., DiLorenzo, N., Rowland, D. L., Blount, A. R. S., Santos, E. R. S., Garcia, L., & Ruiz-Moreno, M. (2018). Annual and perennial peanut mixed with 'Pensacola' bahiagrass in North Florida. *Crop Science*, *58*(2), 982–992. https://doi.org/10.2135/cropsci2017.09.0542

Jaramillo, D. M., Dubeux, J. C. B., Sollenberger, L. E., Mackowiak, C., Vendramini, J. M. B., DiLorenzo, N., Queiroz, L. M. D., Santos, E. R. S., Garcia, L., Ruiz-Moreno, M., & van Santen, E. (2021). Litter mass, deposition rate, and decomposition in nitrogen-fertilized or gass-legume grazing systems. *Crop Science*, *61*, 2176–2189. https://doi.org/10.1002/csc2.20475

Jaramillo, D. M., Dubeux, J. C. B., Sollenberger, L. E., Vendramini, J. M. B., Mackowiak, C., DiLorenzo, N., Garcia, L., Queiroz, L. M. D., Santos, E. R. S., Homem, B. G. C., van Cleef, F., & Ruiz-Moreno, M. (2021). Water footprint, herbage, and livestock responses for nitrogen-fertilized grass and grass–legume grazing systems. *Crop Science*, *61*(5), 3844–3858. https://doi.org/10.1002/CSC2.20568

Kindt, R., & Coe, R. (2005). *Tree diversity analysis. A manual and software for common statistical methods and biodiversity studies*. World Agroforestry Centre. (ICRAF).

Kowalchuk, G. A., Buma, D. S., de Boer, W., Klinkhamer, P. G. L., & van Veen, J. A. (2002). Effects of above-ground plant species composition and diversity on the diversity of soil-borne microorganisms. *Antonie Van Leeuwenhoek*, *81*(1), 509–520. https://doi.org/10.1023/A:1020565523615

Leff, J. W., Jones, S. E., Prober, S. M., Barberán, A., Borer, E. T., Firn, J. L., Harpole, W. S., Hobbie, S. E., Hofmockel, K. S., Knops, J. M. H., Mcculley, R. L., Pierre, K. L.a, Risch, A. C., Seabloom, E. W., Schütz, M., Steenbock, C., Stevens, C. J., Fierer, N., & Performed, C. J. S. (2015). Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. *Proceedings of the National Academy of Sciences of the United States of America*, *112*, 2020. https://doi.org/10.1073/pnas.1508382112

Liang, X., Li, F., Wang, S., Hua, G., He, M., Tian, G., Khan, S., Poudel, R., & Garrett, K. A. (2020). A rice variety with a high straw biomass retained nitrogen and phosphorus without affecting soil bacterial species. *Soil Ecology Letters*, *2*(2), 131–144. https://doi.org/10.1007/S42832-020-0029-3

Lundberg, D. S., Lebeis, S. L., Paredes, S. H., Yourstone, S., Gehring, J., Malfatti, S., Tremblay, J., Engelbrektson, A., Kunin, V., del Rio, T. G., Edgar, R. C., Eickhorst, T., Ley, R. E., Hugenholtz, P., Tringe, S. G., & Dangl, J. L. (2012). Defining the core *Arabidopsis thaliana* root microbiome. *Nature*, *488*(7409), 86–90. https://doi.org/10.1038/nature11237

Malviya, M. K., Solanki, M. K., Li, C.-N., Wang, Z., Zeng, Y., Verma, K. K., Singh, R. K., Singh, P., Huang, H.-R., Yang, L.-T., Song, X.-P., & Li, Y.-R. (2021). Sugarcane-legume intercropping can enrich the soil microbiome and plant growth. *Frontiers in Sustainable Food Systems*, *5*, 285. https://doi.org/10.3389/FSUFS.2021.606595

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.Journal*, *17*(1). https://doi.org/10.14806/ej.17.1.200

McCaig, A. E., Glover, L. A., & Prosser, J. I. (1999). Molecular analysis of bacterial community structure and diversity in unimproved and improved upland grass pastures. *Applied and Environmental Microbiology*, *65*(4), 1721–1730. https://doi.org/10.1128/AEM.65.4.1721-1730.1999

McCormick, M. E., Han, K. J., Moreira, V. R., & Blouin, D. C. (2014). Evaluation of alfalfa inter-seeding effect on bahiagrass baleage fermentation and lactating Holstein performance. *Journal of Animal*

Science and Biotechnology, *5*(1), 1–9. https://doi.org/10.1186/2049-1891-5-38

Millard, P., & Singh, B. K. (2010). Does grassland vegetation drive soil microbial diversity? *Nutrient Cycling in Agroecosystems*, *88*(2), 147–158. https://doi.org/10.1007/s10705-009-9314-3

Muir, J. P., Pitman, W. D., & Foster, J. L. (2011). Sustainable, low-input, warm-season, grass-legume grassland mixtures: Mission (nearly) impossible? *Grass and Forage Science*, *66*(3), 301–315. https://doi.org/10.1111/j.1365-2494.2011.00806.x

Mullenix, M. K., Sollenberger, L. E., Wallau, M. O., Blount, A. R., Vendramini, J. M. B., & Silveira, M. L. (2016). Herbage accumulation, nutritive value, and persistence responses of rhizoma peanut cultivars and germplasm to grazing management. *Crop Science*, *56*(2), 907–915. https://doi.org/10.2135/cropsci2015.08.0507

Mylavarapu, R., Wright, D., Kidder, G., & Chambliss, C. G. (2009). *UF/IFAS standardized fertilization recommendations for agronomic crops*. University of Florida IFAS Extension. http://edis.ifas.ufl.edu/ss163

Nelson, M. B., Martiny, A. C., & Martiny, J. B. H. (2016). Global biogeography of microbial nitrogen-cycling traits in soil. *Proceedings of the National Academy of Sciences of the United States of America*, *113*(29), 8033–8040. https://doi.org/10.1073/pnas.1601070113

Obaton, M., Bouniols, A., Piva, G., & Vadez, V. (2002). Are *Bradyrhizobium japonicum* stable during a long stay in soil? *Plant and Soil*, *245*(2), 315–326. https://doi.org/10.1023/A:1020447928911

Oksanen, J. (2017). *Vegan: Ecological diversity*. R Package Version 2.4-4. https://cran.r-project.org, https://github.com/vegandevs/vegan

Prober, S. M., Leff, J. W., Bates, S. T., Borer, E. T., Firn, J., Harpole, W. S., Lind, E. M., Seabloom, E. W., Adler, P. B., Bakker, J. D., Cleland, E. E., Decrappeo, N. M., Delorenze, E., Hagenah, N., Hautier, Y., Hofmockel, K. S., Kirkman, K. P., Knops, J. M. H., La Pierre, K. J., …, Fierer, N. (2015). Plant diversity predicts beta but not alpha diversity of soil microbes across grasslands worldwide. *Ecology Letters*, *18*(1), 85–95. https://doi.org/10.1111/ele.12381

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., & Glöckner, F. O. (2013). The SILVA ribosomal RNA gene database project: Improved data processing and web-based tools. *Nucleic Acids Research*, *41*(1), 590. https://doi.org/10.1093/nar/gks1219

R Core Team. (2017). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. https://www.R-project.org/

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

Rosier, C. L., Polson, S. W., D'Amico, V., Kan, J., & Trammell, T. L. E. (2021). Urbanization pressures alter tree rhizosphere microbiomes. *Scientific Reports*, *11*(1), 1–12. https://doi.org/10.1038/s41598-021-88839-8

Rouquette, F. M., & Smith, G. R. (2010). Review: Effects of biological nitrogen fixation and nutrient cycling on stocking strategies for cow-calf and stocker programs. *Professional Animal Scientist*, *26*(2), 131–141. https://doi.org/10.15232/S1080-7446(15)30572-6

Santos, E. R. S., Dubeux, J. C. B., Sollenberger, L. E., Blount, A. R. S., Mackowiak, C., Dilorenzo, N., Jaramillo, D. M., Garcia, L., Pereira, T. P., & Ruiz-Moreno, M. (2018). Herbage responses and biological N2 fixation of bahiagrass and rhizoma peanut monocultures compared with their binary mixtures. *Crop Science*, *58*(5), 2149–2163. https://doi.org/10.2135/cropsci2018.02.0128

Schlatter, D. C., Bakker, M. G., Bradeen, J. M., & Kinkel, L. L. (2015). Plant community richness and microbial interactions structure bacterial communities in soil. *Ecology*, *96*(1), 134–142. https://doi.org/10.1890/13-1648.1

Silveira, M. L., & Kohmann, M. M. (2020). Maintaining soil fertility and health for sustainable pastures. In M. Rouquette & G. E. Aiken (Eds.), *Management strategies for sustainable cattle production in southern pastures* (pp. 35–58). Academic Press. https://doi.org/10.1016/B978-0-12-814474-9.00003-7

Silveira, M. L., Rouquette, F. M., Smith, G. R., da Silva, H. M. S., & Dubeux, J. C. B. (2014). Soil-fertility principles for warm-season perennial forages and sustainable pasture production. *Forage and Grazinglands*, *12*(1). https://doi.org/10.2134/FG-2013-0041-RV

Silveira, M. L., Vendramini, J. M. B., Sellers, B., Monteiro, F. A., Artur, A. G., & Dupas, E. (2015). Bahiagrass response and N loss from selected N fertilizer sources. *Grass and Forage Science*, *70*(1), 154–160. https://doi.org/10.1111/gfs.12078

Soil Survey Staff. (2019). *Web soil survey*. USDA Natural Resources Conservation Service. http://websoilsurvey.sc.egov.usda.gov/

van der Heijden, M. G. A., Bakker, R., Verwaal, J., Scheublin, T. R., Rutten, M., Van Logtestijn, R., & Staehelin, C. (2006). Symbiotic bacteria as a determinant of plant community structure and plant productivity in dune grassland. *FEMS Microbiology Ecology*, *56*(2), 178–187. https://doi.org/10.1111/j.1574-6941.2006.00086.x

van der Heijden, M. G. A., Bardgett, R. D., & van Straalen, N. M. (2008). The unseen majority: Soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecology Letters*, *11*(3), 296–310. https://doi.org/10.1111/j.1461-0248.2007.01139.x

van Eekeren, N., van Liere, D., de Vries, F., Rutgers, M., de Goede, R., & Brussaard, L. (2009). A mixture of grass and clover combines the positive effects of both plant species on selected soil biota. *Applied Soil Ecology*, *42*(3), 254–263. https://doi.org/10.1016/j.apsoil.2009.04.006

Vendramini, J. M. B., Sollenberger, L. E., Blount, A. R., Aguiar, A. D., Galzerano, L., Valente, A. L. S., Alves, E., & Custodio, L. (2013). Bahiagrass cultivar response to grazing frequency with limited nitrogen fertilization. *Agronomy Journal*, *105*(4), 938–944. https://doi.org/10.2134/agronj2012.0404

Vose, R. S., Applequist, S., Squires, M., Durre, I., Menne, C. J., Williams, C. N., Fenimore, C., Gleason, K., & Arndt, D. (2014). Improved historical temperature and precipitation time series for U.S. climate divisions. *Journal of Applied Meteorology and Climatology*, *53*(5), 1232–1251. https://doi.org/10.1175/JAMC-D-13-0248.1

Wang, X., Hsu, C., Dubeux, J. C. B., Mackowiak, C., Blount, A., Han, X., & Liao, H. (2019). Effects of rhizoma peanut cultivars (*Arachis glabrata* Benth.) on the soil bacterial diversity and predicted function in nitrogen fixation. *Ecology and Evolution*, *9*(22), 12676–12687. https://doi.org/10.1002/ece3.5735

Wardle, D. A. (2006). The influence of biotic interactions on soil biodiversity. *Ecology Letters*, *9*(7), 870–886. https://doi.org/10.1111/j.1461-0248.2006.00931.x

Xue, L., Ren, H., Li, S., Leng, X., & Yao, X. (2017). Soil bacterial community structure and co-occurrence pattern during vegetation restoration in karst rocky desertification area. *Frontiers in Microbiology*, *8*, 2377. https://doi.org/10.3389/fmicb.2017.02377

Zeng, J., Liu, X., Song, L., Lin, X., Zhang, H., Shen, C., & Chu, H. (2016). Nitrogen fertilization directly affects soil bacterial diversity and indirectly affects bacterial community composition. *Soil Biology and Biochemistry*, *92*, 41–49. https://doi.org/10.1016/j.soilbio.2015.09.018

Zhou, Y., Qin, Y., Liu, X., Feng, Z., Zhu, H., & Yao, Q. (2019). Soil bacterial function associated with stylo (legume) and bahiagrass (grass) is affected more strongly by soil chemical property than by bacterial community composition. *Frontiers in Microbiology*, *10*, 798. https://doi.org/10.3389/fmicb.2019.00798

Zhou, Y., Zhu, H., Fu, S., & Yao, Q. (2017). Variation in soil microbial community structure associated with different legume species is greater than that associated with different grass species. *Frontiers in Microbiology*, *8*, 1007. https://doi.org/10.3389/fmicb.2017.01007

SUPPORTING INFORMATION

Additional supporting information may be found in the online version of the article at the publisher's website.

How to cite this article: Guerra, V. A., Beule, L., Mackowiak, C. L., Dubeux, J. C. B., Blount, A. R. S., Wang, X. B., Rowland, D. L., & Liao, H.-L. (2022). Soil bacterial community response to rhizoma peanut incorporation into Florida pastures. *J Environ Qual*, *51,* 55–65. https://doi.org/10.1002/jeq2.20307