Home-field advantage affects the local adaptive interaction between *Andropogon gerardii* ecotypes and rhizobiome

Anna Kazarina[1], Soumyadev Sarkar[1], Shiva Thapa[2], Leah Heeren[1], Abigail Kamke[1], Kaitlyn Ward[1], Eli Hartung[1], Qinghong Ran[1], Matthew Galliart[3], Ari Jumpponen[1], Loretta Johnson[1], Sonny T.M. Lee[1]*

[1] Division of Biology, Kansas State University, Manhattan, Kansas, United States

[2] Department of Biology, University of North Carolina at Greensboro, North Carolina, United States

[3] Department of Biological Sciences, Fort Hays State University, Hays, Kansas, United States

* Corresponding author, e-mail: leet1@ksu.edu

***Keywords:** Rhizosphere, plant microbiome, ecotypic variation, local adaptation, precipitation gradient

Abstract

Due to climate change, drought frequencies and severities are predicted to increase across the United States. Plant responses and adaptation to stresses depend on plant genetic and environmental factors. Understanding the effect of those factors on plant performance is required to predict the response of species to the environmental change. We used reciprocal gardens planted with dry, mesic and wet regional ecotypes of *Andropogon gerardii* to characterize the rhizosphere communities using 16S rRNA metabarcode sequencing. Even though the local microbial pool was the main driver of the rhizosphere microbial communities, the significant ecotypic effect highlighted active plant microbial recruitment driven by genetic variations. We also showed that ecotypes do better in the recruitment of microbes when planted at homesite, supporting the “home field advantage” hypothesis. At homesites, ecotypes were more successful at recruiting rhizosphere community members unique to the locations - microbial specialists that were potentially linked to the plant stress response functions. In addition, we showed the support for ecotypic variations in the recruitment of bacterial variants from the same genera, highlighting the effect of the plant ecotypes on the rhizosphere microbiome recruitment. The results of this study should facilitate expanded studies on understanding the complexity of relationships between plant host interactions with local soil microbes and identification of functional potential of recruited microbes. Our study has the potential for further predicting ecosystem responses to climate change and the impact of management on restoration practices.

Introduction

The rhizosphere is a dynamic region characterized by the complex interaction between the plant host and associated microbial communities [1,2]. It has been widely recognized that plants directly and indirectly benefit from associated microbial activities and resultant microbial products [3,4]. Complex microbe-microbe interactions around the rhizosphere results in facilitating nutrient transformations, uptake, and cycling as well as alternating soil structure and soil moisture availability [5,6]. Similarly, plant host-microbe interactions can also greatly affect the overall plant health and productivity [7,8]. Root associated microorganisms (hereafter referred to as rhizobiome) can affect plant resistance to biotic and abiotic stress, help with nutrient intake and even alter the plant morphology and phenology [9,10]. Given the crucial roles of the rhizobiome, understanding what shapes the microbial assembly, function, and mechanisms, as well as adaptive responses between plant host and associated microbes is critical in predicting the response of this system to changing environmental conditions [11,12].

Numerous studies have demonstrated that we need to consider the interactive effects of the location and plant host genetics in understanding the rhizobiome. The chemical and physical characteristics of local soil source can directly affect plant physiology, which in turn can have consequential influence on the composition of the rhizobiome [11,13,14]. Plant hosts actively modulate associated microbial communities by releasing various signaling molecules (phytohormones) and compounds into the surrounding soil environment [11,15]. Phytohormones are structurally diverse secondary metabolites released by the plant to activate the immune system [16,17], in response to microbial pathogens [18] and even insect herbivores [19]. Outside of the direct immune responses, plants produce phytohormones and compounds in response to abiotic stress such as nutrient or water deficiency, or promote symbiotic interactions between plants and soil microbes [20]. Although there are numerous studies on plant host influence on rhizobiome composition, there is still a lack of information when considering the interactive impact of the host-environment on the rhizobiome. The rhizobiome is a subset of microorganisms available from the surrounding soil microbial pool [15], thus, it is no surprise that the same plants would perform differently in distinct locations. Some studies have described the increase in efficacy of the plant host-associated rhizobiome interaction due to the "*home field advantage*" [21,22]. However, questions remain if plants locally adapted to different locations can take advantage of the local soil microbes equally or if plants favor microbiomes similar to their home environment.

Due to climate change, drought frequencies and severity are predicted to increase across the United States [23-25]. In the Great Plains, drought events limit productivity especially in tallgrass prairies [24]. Thus, understanding the effect of drought in shaping rhizobiome and the mechanisms of mutual adaptation between plants and associated microbes is critical in the prediction of the ecosystem's response to changing climate. Unfortunately, studies [26-28] on the effect of drought on plant-microbe interactions have been under *in vitro* conditions using model organisms, lacking the complexity and dynamics of the natural system application [29,30].

To address the question if there is a co-adaptation of the plant host and its associated rhizobiome in a non-model plant system, our study took the opportunity to investigate the rhizobiome composition of three big bluestem (*Andropogon gerardii* Vitman) ecotypes in reciprocal common gardens across the precipitation gradient in Kansas. *Andropogon gerardii* is a perennial C4 grass that is widely distributed across the Great Plains of North America [31,32], and covers up to 80% of the biomass in tallgrass prairie [32-35]. Within the Great Plains, *A. gerardii* has been growing for over 10,000 years along prominent sharp rainfall gradients that range from semiarid to heavy rainfall [36,37]. Time and environmental variations lent support for local adaptation of *A. gerardii*, giving rise to distinct ecotypes (dry, mesic, and wet) [36,38,39] as well as populations of *A. gerardii* [36,39,40] . Previous investigations revealed that *A. gerardii* ecotypes vary in functional traits known to influence microbially mediated processes [40,41]. Although there are studies investigating intraspecific [42] and interspecific (reviewed in [40]) plants' response to climate [43], the role of the rhizobiome in the plant host environmental adaptation in the natural system remains unclear.

Here, we (1) investigated the overall relative importance of the plant local environment and phenotypic variation of *A. gerardii* on establishing plant rhizobiome; (2) compared ecotypic responses in their ability to recruit rhizosphere microbes under reciprocally transplanted, local and non-local environments; and (3) examined rhizosphere community members with the potential link to the recruitment microorganism for the plant hosts' stress response functions. We hypothesize that *A. gerardii* ecotypes will perform differently at the different locations, highlighting the impact of the plant genetics on the rhizosphere community composition. We also predict that ecotypes will have a "*home field advantage*" in recruiting microorganisms that can potentially increase their resilience under environmental stress. Our work contributes to a clearer understanding of the factors that influence the plant host in recruitment of rhizobiome

members, and will help to provide insights into *A. gerardii* ecotypic responses to a future changing climate.

Materials and Methods

Study sites, samples collection and processing

We collected samples from three *Andropogon gerardii* reciprocal gardens (Hays Kansas, Manhattan Kansas, Carbondale Illinois) in the summer of 2019. The gardens were established ten years ago at the following three sites: Hays, KS (H) at Kansas State University Agriculture Experimental Station (38°85'N, 99°34'W), Manhattan, KS (MHK) at USDA Plant Materials Facility (39°19'N, 96°58'W), and Carbondale, Illinois (C) at Southern Illinois University Agriculture Research Station (37°73'N, 89°17'W), giving us an excellent opportunity to study the interactive effects of location and hosts on the rhizobiome (Supplementary Table S1). Experimental details are published in Galliart et al [44] - briefly, in 2009, *A. gerardii* seeds were collected from four different sites (hereafter referred to as *A. gerardii* populations) at three different locations: mixed grass Central Kansas (CKS/Dry: CDB, REL, SAL, WEB), tallgrass Eastern Kansas (EKS/Mesic: CAR, KON, TAL, TOW) and Southern Illinois savanna (SIL/Wet: 12MI, DES, FUL, WAL) prairies across the natural rainfall gradient with 580 mm/year, 871 mm/year and 1167 mm/year of mean annual precipitation respectively. We defined the ecotypic variation of *A. gerardii* based on the locations they were collected (Dry: Hays; Mesic: Manhattan and Wet: Carbondale). Collected seeds from all three ecotypes were germinated and grown in a greenhouse using potting mix (Metro-Mix 510). Established 3- to 4-months-old plants were then planted at each three garden sites (size - 4 × 8 m), in which 12 plants (4 populations x 3 ecotypes) were planted in a complete randomized block design with 10 blocks (rows) for a total of 120 plants per site. Plants were planted 0.5 m apart along each block, and the soil around the plants was covered with the water-penetrable landscape cloth for weed control.

Not all plants survived transplantation or through the years of growth in the common gardens. In this study, we used a soil core and collected a total of 284 rhizosphere soil cores (15 cm deep x 1.25 cm diameter) across the three locations (Supplementary Table S2). Samples were sealed in ziplock bags, transported on ice, and were placed in -20 °C freezer until genomic DNA extraction.

We extracted genomic DNA from 0.150 g of rhizospheric roots and soil using an Omega E.Z.N.A. Soil DNA Kit (Omega Bio-Tek, Inc., Norcross, GA, USA) as per the manufacturer's

protocol with a slight modification. We shook off as much as the soil from the plant roots, and any soil that was attached to the roots were considered as part of the rhizospheric soil [45,46]. We mechanically lysed the cells on a Qiagen TissueLyser II (Qiagen, Hilden, Germany) using glass beads for 2 mins at 20 rev/s prior to any downstream genomic DNA extraction steps. The extracted and purified DNA was eluted to a final volume of 100 µL. All samples were measured for the DNA yield and concentration using a Nanodrop and a Qubit™ dsDNA BR Assay Kit. Extracted DNA were sequenced (2 x 250 cycles) using Illumina MiSeq with the 16S rRNA V4 region amplified using the primers 515F and 806R at the Kansas State University Integrated Genomics Facility.

Sequence data processing and analyses

We used QIIME 2 v. 2021.4 [47] to process a total of 8,353,179 raw sequences, and this resulted in 5,628,314 bacterial sequences after QC. We used QIIME 2 plugin cutadapt [48] to remove the primer sequences. Any sequences with ambiguous bases, reads with no primer, sequences with more than 0.1 error rate mismatch with primer and any mismatches to the sample-specific 12 bp molecular identifiers (MIDs) were also discarded. Following initial quality control, we used DADA2 [49] with the same parameters across different runs and truncated the reads to length where the 25th percentile of the reads had a quality score below 10. We used the pre-trained SILVA database (v. 138) in QIIME 2 for taxonomic assignment of the bacteria. We rarefied the data set to 10,000 number of reads per sample to minimize biases resulting from differences in sequencing depth among samples before estimating diversity indices and downstream analyses [50].

We used ANOVA statistical analysis on observed (S_{Obs}) richness, community (Shannon's $_{H'}$) and phylogenetic (Faith's PD) diversity indices on the rhizosphere associated bacterial communities to test the overall effects of the locations (Hays (H), Carbondale (C), Manhattan (MHK)), ecotypes (dry, mesic, wet) and populations (12MI, CAR, CDB, DES, FUL, KON, REL, SAL, TAL, TOW, WAL, WEB) on α-diversity. Following overall ANOVA, we performed pairwise comparisons using Kruskal-Wallis test to identify factors that were driving the significant effects.

We estimated pairwise Bray-Curtis distances to compare the bacterial community dissimilarity among the different factors, and visualized these data using Non-Metric Multidimensional Scaling (NMDS) ordinations. We used a nonparametric permutational analog of traditional analysis of variance (PERMANOVA) to determine whether bacterial composition differed among

locations, ecotypes and populations. In this model, "population" was nested within "ecotype" to account for the split-plot design. Following the PERMANOVA model, we performed pairwise comparisons using pairwise.adonis function. We also used betadispr function to test whether the community dispersion differed between any significant groups. To identify bacteria populations that were disproportionately more abundant in one significant group than in another, we analyzed these data for indicator species. The community composition data analyses were conducted in R ape [51], indicspecies [52], lme4 [53], phyloseq v 1.42.0 [54], stat v 4.1.1, vegan [55], R studio [56].

Oligotyping analyses

We used algorithm minimum entropy decomposition (MED) [57] with default parameters to identify sequence variants in high-throughput 16S rRNA amplicon sequences. We used MED to partition the sequences into discrete sequence groups by minimizing the total entropy in the dataset. We then concatenated the sequences assigned to a specific genus and performed the oligotyping pipeline using the supervised oligotyping method [58]. In the supervised oligotyping method, we used Shannon entropy, with a threshold value of minimum 0.2 and minimum substantive abundance threshold of 10, to obtain genus-level oligotypes.

Results and discussions

We analyzed a total of 2,104,416 (19,131 ± 4,115 per sample) high quality sequences assigned to 1,157 ASVs. Of the recovered counts, an average of 90% bacterial counts were annotated to the genus level on SILVA classifier. Any unknown or unclassified ASVs were removed from downstream analyses. The bacterial assignment along with their counts in each sample are provided in Supplementary Table S3. The sequence yields were dominated by the phylum Proteobacteria (45% of all sequences), followed by Actinobacteria (15%), Acidobacteria (12%) and Bacteroidata (6%). A small proportion of sequences remained unclassified (0.29%). ASVs relative abundance was dominated by Proteobacteria (28% of all ASVs), Actinobacteria (14%), Firmicutes (12%) and Bacteroids (9%). Similar to sequences, the proportion of unassigned ASVs was small (0.3%).

Location had a strong impact on the ecotypic rhizobiome richness and diversity

We showed that location was the main driver on the bacterial communities, with a strong effect on bacterial richness and diversity (ANOVA, $S_{Obs:}$ $F_{2,245} = 7.13$; $P < 0.001$; Shannon's H' index: $F_{2,245} = 26.56$; $P < 0.001$; Faith's PD index: $F_{2,245} = 4.09$; $P = 0.018$) (Figure 1A). We further

conducted a pairwise test, and showed that communities richness (S_{Obs}) and Shannon's diversity indices were statistically lower in Manhattan as compared to other locations (Table 1). On the other hand, we noticed that the phylogenetic diversity (Faith's PD) in Carbondale was marginally higher compared to Hays and Manhattan (Table 1). The higher bacterial diversity we observed in this study could be highly attributed to the amount of precipitation among the locations.

We observed a significant clustering of the samples indicating that locations had strong effects on bacterial composition (PERMANOVA, $F_{2,245}$ = 102.53; P = 0.001; Figure 1B). Our pairwise comparisons further corroborated that all locations had significantly different bacterial compositions (Pairwise Adonis, C vs H: R^2 = 0.435; P = 0.001 P_{adj} = 0.003; C vs MHK: R^2 = 0.313, P = 0.001 P_{adj} = 0.003; H vs MHK: R^2 = 0.274, P = 0.001 P_{adj} = 0.003). We conducted a dispersion analysis, and observed that bacterial communities in Manhattan ($F_{2,279}$ = 3.899; P = 0.015) were more varied than Carbondale (P = 0.020). Similarly to bacterial richness, the variation in bacterial community compositions among the locations were likely a result of precipitation-associated biotic and abiotic differences [59]. For example, the mean precipitation in Carbondale is 1167 mm/yr which is drastically different from that in Hays (580 mm/yr). This precipitation gradient among the 3 locations would result in differences in pH which is known to be a key factor influencing bacterial diversity [60,61]. In this study, we showed that location had a strong effect on bacterial diversity and composition, but were there any bacterial populations that were disproportionately higher in relative abundance among the locations?

We used indicator taxon analysis and identified 194 taxa that differed among the locations. We noticed that the majority of the taxa were associated with location Carbondale (n=181) and Hays (n=151), whereas fewer were associated with Manhattan (n=38) (Supplementary Table S4), suggesting that Carbondale and Hays harbored higher number of habitat specialist microbes due to their environmental conditions [62,63]. Of our three common gardens, Manhattan had the most neutral conditions for growth of *A. gerardii*, where plants were less likely to experience abiotic stress including water availability stress such as in Hays and Carbondale. We further observed that the majority of soil bacterial indicator ASVs were assigned to these four main phyla - Acidobacteria (Total n=31; C = 21, H = 5, MHK = 5); Actinobacteria (Total n=66; C = 15, H = 47, MHK = 4); Planctomycetes (Total n=20; C = 13, H = 7, MHK = 0); and Proteobacteria (Total n=109; C = 53, H = 41, MHK = 15); and Verrucomicrobia (Total n=23; C = 14, H = 9, MHK = 0) (Supplementary Table S4). It was not surprising to see those phyla dominating our indicator

taxon analysis since they are ubiquitous among rhizosphere associated bacterial communities [41,64-66]. However, we also noticed that indicators were not evenly distributed across locations, suggesting that this pattern was due to the soil moisture affecting the bacterial distribution. Soil moisture can directly affect the soil microbial composition and functionality by differentiating drought tolerance among taxonomic and functional groups of microorganisms [67,68]. For example, limited soil moisture restricts the solute mobility and therefore decreases substrate supply to the soil microbes. Therefore, highly sensitive to moisture Gram-negative bacteria populations (Acidobacteria, Planctomycetes, Verrucomicrobia) were affected by the limited water, resulting in lower number indicators in Hays and disproportionately higher in Carbondale [69-71]. In line with this argument, we also observed that Gram-positive bacteria (Actinobacteria) was disproportionately higher in Hays than in Carbondale and Manhattan [72].

Ecotypes shaped the rhizosphere inhibiting bacterial richness and diversity

While there was a strong location effect on all alpha diversity metrics, we noticed that the ecotypic effect was marginally observed only in (S_{Obs}) richness (ANOVA, $S_{Obs:}$ $F_{2,245} = 3.46$; $P = 0.033$). The pairwise comparison among ecotypes indicated that mesic ecotypic rhizobiome had a higher observed richness (S_{Obs}) than wet ecotype (Mesic vs Wet: $H = 6.86$, $P_{adj} = 0.026$). We observed no differences in bacterial diversity and phylogenetic diversity among host ecotypes (ANOVA, Shannon's H' index: $F_{2,245} = 0.91$; $P = 0.404$; Faith's PD index: $F_{2,245} = 2.51$; $P = 0.108$) (Figure 2A). It was not surprising that the effect of ecotype was lower than the effect of location. It is well discussed across the literature that the plant ecotypic effect can be suppressed by the local biotic and abiotic environmental factors. For example, the environmental gradient defines the local microbial source pool available to the plant and therefore directly affects the rhizosphere communities [18,73-75]. Taking into consideration the overwhelming effect of the local environment (location), we aimed to test if our ecotypes differed in bacterial richness (S_{Obs}) matrics locally. For that, we split our data set by locations, and performed separate ANOVA models for each location with ecotype, population and their interaction as the main factors. Following that, we observed that only Hays ($F_{2,87} = 15.06$; $P < 0.001$), but not Manhattan ($F_{2,87} = 0.10$; $P = 0.905$) or Carbondale ($F_{2,79} = 0.41$; $P = 0.668$) showed the statistical differences by ecotype. We further used a pairwise test and identified that the wet ecotype in Hays was significantly lower in (S_{Obs}) richness when compared to dry (Wet vs Dry: $P_{adj} < 0.001$) and mesic (Wet vs Mesic: $P_{adj} < 0.001$) ecotypes. These results highlight the potential differences in ecotypes' performance in the recruitment and structuring of the rhizosphere communities even when planted in a common environment. The overall effect of ecotype on bacterial community

composition was also weaker compared to the location effect in the overall model (PERMANOVA, $F_{2,245}$ = 2.91; P = 0.012). We used pairwise comparisons and showed that the difference among the ecotypic bacterial composition was driven by the wet (Wet vs Dry: R^2 = 0.028, P_{adj} = 0.015) and mesic ecotype (Wet vs Mesic: R^2 = 0.038, P_{adj} = 0.015; Figure 2B).

Putting together our data on locations and ecotypic effects on rhizobiome, we surmised that interaction between plant ecotypes and locations resulted in the wet and dry ecotypes harboring a higher number of habitat specialist microbes in Carbondale and Hays ([62, 63]). While the dry ecotype was well-suited to its native environment, the wet ecotypic rhizobiome was significantly different suggesting that the wet ecotypic rhizobiome was not well-adapted to an environment (Hays) that is extremely different from its native location (Carbondale). Therefore, with a plant-host-rhizobiome mismatch in Hays, the wet ecotype would not be able to get a "*home field advantage*", resulting in a higher number of generalists - abundant soil microbes that are good at colonizing plants [2,4,63,76,77]. Another limiting factor for wet ecotype to recruit and retain native specialist microbes in Hays is driven by lower drought stress tolerance of the plant host [36]. Wet ecotype physiologically is not well adapted to the drier environment of Hays - which results in the weaker performance of lower biomass production and therefore lower photosynthetic rate [36]. We surmise that lowered photosynthetic products released in the soil by the wet ecotype in Hays would limit the number of microbes the wet ecotype can support in the drier environment. In addition, the limiting photosynthates that were released by wet ecotype would then be metabolized by the more abundant and faster colonizing generalists [63]. Due to the general lower relative abundance of specialists in the samples, statistical analysis on ecotypic Shannon's diversity and Faith PD as well as indicator taxon might not be sensitive enough to show the impact of ecotypes on its associated rhizobiome [78-80]. In order to test that idea, we calculated how many microbial taxa were uniquely observed in each location, to provide insights into the environmental and functional selection of potential specialists microbial populations. We showed that Carbondale (133) harbored the highest number of unique microbial taxa, followed by Hays (120) and Manhattan (79) (Figure 3A, Supplementary Table S5). We then looked at the unique taxa associated with ecotypes across all locations. Wet ecotype had the highest number of unique microbes (107), followed by Dry (92) and Mesic (66) (Figure 3B, Supplementary Table S5). When we considered the impact of ecotypes on the unique microbial populations at each location. Interestingly, we noticed that dry and wet ecotypes harbored more unique taxa when they were planted at their "*home field*", except for mesic ecotype planted in Manhattan (C: Dry = 79, Mesic = 39, Wet = 127), (H: Dry = 121, Mesic

= 71, Wet = 49) (MHK: Dry = 77, Mesic = 67, Wet = 72) (Figure 3C). Our results highlighted that ecotypes gained a "*home field advantage*" when planted in their native environment, and were able to match the plant host ecotypes to recruit and retain a higher number of unique microbial populations. On the other hand, the mesic ecotype was constantly associated with a lower number of unique microbial taxa, leading us to hypothesize that due to the highly equable environment for *A. gerardii* in Manhattan, mesic ecotype had not adaptively need to harbor a variety of specialist microbes for survival, and therefore was associated with a lower number of unique taxa across all the locations.

Matching of the plant host ecotype and rhizobiome was evident at the ecotypic native location

We used indicator taxon analysis to give insights into the interactive relationship between the ecotypic plant host and its associated rhizobiome (Supplementary Table S6). We identified numerous indicator taxa that were significantly different among the ecotypes. We further showed that, considering individual locations, there was a strong effect of the ecotypes on the indicator taxa. Our study demonstrated that plant host ecotypes matched strongest to their rhizobiome, showing the highest number of indicator taxa, when the plant ecotypes were at their "*home field".*

In the overall indicator taxon analysis across all the locations, we identified 26 indicator taxa that differed among the ecotypes. Wet ecotype was associated with the highest number of indicators (n=20), followed by mesic (n=6) and dry (n=0) ecotypes (Supplementary Table S6). The majority of soil bacterial indicator ASVs were assigned to Acidobacteria (Total n=10; Dry = 0, Mesic = 2, Wet = 8) and Proteobacteria (Total n=10; Dry = 0, Mesic = 1, Wet = 9). Similarly, taking into consideration the strong effects of location, we further focused our analysis by studying the ecotypic effects at different locations. We observed that while ecotypes differed at all locations (PERMANOVA, H: $F_{2,109}$ = 2.55; P = 0.021, MHK: $F_{2,89}$ = 2.87; P = 0.014, IL:$F_{2,81}$ = 2.55; P = 0.015) (Figure 3C), in our pairwise comparisons of communities composition in Carbondale and Manhattan, wet ecotype only differed from mesic (C: Wet vs Mesic: P_{adj} = 0.033, MHK: Wet vs Mesic: P_{adj} = 0.042), while other ecotype comparisons across all locations were not significant (P_{adj} > 0.05).

In Carbondale, we further observed that even though the ecotypic rhizobiome dispersion were significantly different ($F_{2,79}$ = 3.84; P = 0.026), dry ecotypic rhizobiome were more dispersed as

compared to mesic and wet ecotypes. In addition, we did not identify ecotype-associated indicator taxa in Carbondale across all the ecotypes (n=0), highlighting that the differences in ecotypic recruitment might be on a smaller scale of unique and lower abundance taxa (Supplementary Table S7). In Manhattan, mesic ecotype was significantly more dispersed ($F_{2,87}$ = 10.72; P = 0.01) when compared to dry and wet ecotypes. In Manhattan, we identified 11 indicator taxa - 4 indicators were associated with mesic (Actinobacteria=2; Proteobacteria=1; Verrucomicrobia=2) and 7 indicators with wet ecotypes (Actinobacteria=3; Proteobacteria=3; Cyanobacteria = 1). We observed that in Hays, wet ecotype differed in composition from dry and mesic ecotypes (Dry vs Wet: P=0.046, Mesic vs Wet: P=0.030), but no significant differences were observed after adjusting for multiple comparisons (P_{adj} =0.05). Interestingly, ecotypes did not differ in Hays (P_{adj} =0.05). Hays is at the very edge of where *A. gerardii* are commonly found [36], suggesting that the drier environment might have a strong impact on diversity of bacterial populations that can proliferate under the arid conditions [81, 82] . Therefore, in Hays, we hypothesize that *A. gerardii* ecotypes 1) had a lower diversity of bacterial populations for recruitment; 2) experienced high abiotic stress from the drier conditions; and 3) had to compete for the recruitment of the low microbial specialist populations. Although our results suggest that all ecotypes had a more challenging survivorship under the harsher environment, will the dry and wet *A. gerardii* ecotypes be more resilient and successful in recruiting microbes due to their "*memory*" from surviving in a harsh "*home*" environment [21,83]? Will ecotypes get a "*home field advantage* " in the recruitment of microbes at their "*home*" locations?

To test that, we performed the indicator taxon analysis on ecotypes at each location (Supplementary Table S8). Dry ecotype recruited 64 indicator taxa ASVs in Hays, 43 in Carbondale and only 15 in Manhattan. Similarly, wet ecotype in Carbondale has the highest number of indicators (120), followed by Hays (76) and Manhattan (19). Mesic ecotype recruited 87 indicators in Carbondale, 51 in Hays and only 7 in Manhattan. The majority of the indicator taxa from dry ecotype were Proteobacteria (41), Actinobacteria (32), followed by Acidobacteria (12). On the other hand, wet ecotype had disproportionately higher relative abundance in Proteobacteria (69), Actinobacteria (37), followed by Verrucomicrobia (19). Even though lower microbial recruitment in Manhattan could be generally due to lower number of indicators in Manhattan as we discussed earlier, it is clear that both wet and dry ecotypes recruited more indicator taxa when they were growing in their home environments, suggesting how "*home field*" confer a physiological and adaptive advantage to the plant host and associated rhizobiome.

Since we observed differences in indicator taxa and unique ASVs across locations and ecotypes, we further conducted oligotyping analysis to inspect the concealed diversity within ASVs at a higher resolution. We identified a total of 92 oligotypes across 6 genera (Supplementary Table S9). We selected *Pseudomonas* and *Rhizobium* oligotypes for further analysis due to the overall high relative abundance across the bacterial ASVs and generated oligotypes (Oligos: *Pseudomonas*-Oligos (n=9); *Rhizobium*-Oligos (n=32)). We noticed that the relative abundance of ASVs and oligos associated with the two bacterial genera displaying opposite abundance patterns across the locations (Figure 4). Pseudomonadales had lower relative abundance of ASVs across samples from Hays and Carbondale as compared to samples from Manhattan. However, we noticed that there were more dissimilarities among ecotypes and samples in *Pseudomonas*-Oligos in Hays as compared to Carbondale and Manhattan (Figure 4A). Furthermore, although the relative abundance of Rhizobiales was similar throughout all locations, there were high degrees of differences among ecotypes and samples in the relative abundance of *Rhizobium*-Oligos (Figure 4B). Further work needs to be done to provide more insights into recruitment patterns of strain-level Pseudomonadales and Rhizobiales populations by the plant host to understand the impact of bacterial populations on hosts' resilience to environmental stresses. However, our results suggested that precipitation-induced stress (drier in Hays and wetter in Carbondale) could result in a shift of plant host-rhizobiome interaction, changing the stable *Pseudomonas*-Oligos composition as shown in Manhattan (Figure 4A). The differences in the *Pseudomonas*-Oligos and *Rhizobium*-Oligos across the locations potentially supports the "*home field advantage*" and tendency of plants to recruit microbial strains that could contribute to the plant hosts' ecotypic resilience [21,84].

Conclusion

Plant responses and adaptation to stress depend on a combination of environmental factors and plant genetics [1,2]. While the environment defines the soil-associated microbial pool, our results highlighted the plant-host's ability to recruit these soil microbial communities under different environmental conditions. We showed that plant hosts were more successful in the recruitment of both the general and unique microbial population when grown at their homesite [85]. Our observations also suggested the "*home field advantage*" and mutual recognition between plant and specific soil microbes [21,22,84]. From our study, we further propose that, at their home sites, ecotypes originating from these harsher environments, experiencing constant abiotic stresses, were more able to recruit specialist microbes with the potential stress relief

functions [85]. We argue that in the study of plant host-rhizobiome, in line with the generalist and specialist hypothesis, plant host resiliency under abiotic stress are more dependent on specialized microbes [2,4,63,76,77] than the core microbiome [15,86-88], Our study suggests that in terms of the resistance to abiotic stress, the key factor is in less abundant and specialized microbes with specific functions rather than general common microbes which are abundant in soil. We further observed, in our study, the fragile relationships between plant hosts and associated specialized microbes. Although it might be challenging to tease apart the "*specialist vs generalists*" and "*home field advantage*" concepts, we used oligotyping analysis and showed the ecotypic variations in recruitment of bacterial stains from the same genera. These observations even further highlight the complexity of these symbiotic relationships. After growing in a common garden for over 10 years, we could still see the distinct microbial communities recruited by the ecotypes. However, the disconnect between the plant host ecotypes and rhizobiome in the harsher environment of Hays demonstrated that the plant host-rhizobiome interaction is much more fragile than we imagined. Taking all these factors in consideration, there is a crucial gap to identify specialist microbes, and understanding these relationships and communication signals with plant hosts, to predict the response of species to the changing climate change.

Data availability

The raw sequence data are available through the Sequence Read Archive under BioProjectBioSamples PRJNA911775, while bioinformatic and statistical codes are available through figshare (10.6084/m9.figshare.21791306).

Acknowledgements

This work was supported by the National Science Foundation EPSCoR Award No. OIA-1656006 and matching support from the State of Kansas Board of Regents. This study was supported by the United States Department of Agriculture, National Institute of Food and Agriculture (USDA NIFA), under the Award Number: 2020-67019-3180. We would like to thank Sara Baer for aiding in the designing of the reciprocal gardens. We would like to thank all of those who assisted in sampling and data acquisitions. We are grateful for the help of Tanner Richie, Brandi Feehan with the discussion on bioinformatics and data analysis. We are grateful for the technical assistance by Alina Akhunova, Sarah Bastian and Samantha Elledge at the Integrated Genomic Facility at Kansas State University (https://www.k-state.edu/igenomics/).

Author Contributions

A.J., L.J. and S.T.M.L. designed the study. L.J. designed the reciprocal gardens experimental design, and A.J., L.J. and S.T.M.L. maintained sites. Sample collection was performed by S.S., E.H., M.G., A.J., S.T.M.L. and S.T.. S.S., A.K., K.W. extracted DNA with Nanodrop and Qubit quality analysis. A.K. and Q.R. performed 16S rRNA sequencing bioinformatic analysis. Q.R. and S.T.M.L generated oligotypes data. A.K. performed statistical analyses. A.K. and S.T.M.L wrote the manuscript, prepared figures, and supplementary files. A.J. and L.J. authors aided in manuscript and figure revisions. S.T.M.L., A.J. and L.J.acquired fundings for this study. All authors read, contributed to manuscript revision, and approved the submitted version.

Conflict of Interest

The authors disclose no conflicts of interest.

References

1. Mendes R, Garbeva P, Raaijmakers JM. The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms. FEMS Microbiol Rev. 2013;37: 634–663.

2. Hayat R, Ali S, Amara U, Khalid R, Ahmed I. Soil beneficial bacteria and their role in plant growth promotion: a review. Ann Microbiol. 2010;60: 579–598.

3. Mendes R, Kruijt M, de Bruijn I, Dekkers E, van der Voort M, Schneider JHM, et al. Deciphering the rhizosphere microbiome for disease-suppressive bacteria. Science. 2011;332: 1097–1100.

4. Wagg C, Bender SF, Widmer F, van der Heijden MGA. Soil biodiversity and soil community composition determine ecosystem multifunctionality. Proc Natl Acad Sci U S A. 2014;111: 5266–5270.

5. Ahkami AH, Allen White R, Handakumbura PP, Jansson C. Rhizosphere engineering: Enhancing sustainable plant ecosystem productivity. Rhizosphere. 2017;3: 233–243.

6. Hunter P. Plant microbiomes and sustainable agriculture. EMBO Rep. 2016;17: 1696–1699.

7. Adl S. Rhizosphere, food security, and climate change: a critical role for plant-soil research. Rhizosphere. Elsevier; 2016. pp. 1–3.

8. Vacher C, Hampe A, Porté AJ, Sauer U, Compant S, Morris CE. The Phyllosphere: Microbial Jungle at the Plant–Climate Interface. Annu Rev Ecol Evol Syst. 2016;47: 1–24.

9. Bakker PAHM, Pieterse CMJ, de Jonge R, Berendsen RL. The Soil-Borne Legacy. Cell. 2018;172: 1178–1180.

10. Raaijmakers JM, Mazzola M. Diversity and natural functions of antibiotics produced by beneficial and plant pathogenic bacteria. Annu Rev Phytopathol. 2012;50: 403–424.

11. Liu F, Hewezi T, Lebeis SL, Pantalone V, Grewal PS, Staton ME. Soil indigenous microbiome and plant genotypes cooperatively modify soybean rhizosphere microbiome assembly. BMC Microbiol. 2019;19: 201.

12. Srivastava AK, Kashyap PL, Newcombe G, Santoyo G. Plant Microbiome: Interactions, Mechanisms of Action, and Applications. Frontiers Media SA; 2021.

13. Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH. Going back to the roots: the microbial ecology of the rhizosphere. Nat Rev Microbiol. 2013;11: 789–799.

14. Fitzpatrick CR, Copeland J, Wang PW, Guttman DS, Kotanen PM, Johnson MTJ. Assembly and ecological function of the root microbiome across angiosperm plant species. Proc Natl Acad Sci U S A. 2018;115: E1157–E1165.

15. Lundberg DS, Lebeis SL, Paredes SH, Yourstone S, Gehring J, Malfatti S, et al. Defining the core Arabidopsis thaliana root microbiome. Nature. 2012;488: 86–90.

16. Pieterse CMJ, Van der Does D, Zamioudis C, Leon-Reyes A, Van Wees SCM. Hormonal

modulation of plant immunity. Annu Rev Cell Dev Biol. 2012;28: 489–521.

17. Jones JDG, Dangl JL. The plant immune system. Nature. 2006;444: 323–329.

18. Lebeis SL, Paredes SH, Lundberg DS, Breakfield N, Gehring J, McDonald M, et al. PLANT MICROBIOME. Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. Science. 2015;349: 860–864.

19. Carvalhais LC, Dennis PG, Badri DV, Kidd BN, Vivanco JM, Schenk PM. Linking Jasmonic Acid Signaling, Root Exudates, and Rhizosphere Microbiomes. Mol Plant Microbe Interact. 2015;28: 1049–1058.

20. Smith SM. Q&A: What are strigolactones and why are they important to plants and soil microbes? BMC Biol. 2014;12: 19.

21. Ewing PM, Runck BC, Kono TYJ, Kantar MB. The home field advantage of modern plant breeding. PLoS One. 2019;14: e0227079.

22. Meng Y, Hui D, Huangfu C. Site conditions interact with litter quality to affect home-field advantage and rhizosphere effect of litter decomposition in a subtropical wetland ecosystem. Sci Total Environ. 2020;749: 141442.

23. Craine JM, Nippert JB, Elmore AJ, Skibbe AM, Hutchinson SL, Brunsell NA. Timing of climate variability and grassland productivity. Proc Natl Acad Sci U S A. 2012;109: 3401–3405.

24. Knapp AK, Briggs JM, Koelliker JK. Frequency and Extent of Water Limitation to Primary Production in a Mesic Temperate Grassland. Ecosystems. 2001;4: 19–28.

25. Knapp AK, Smith MD. Variation among biomes in temporal dynamics of aboveground primary production. Science. 2001. pp. 481–484.

26. Panke-Buisse K, Poole AC, Goodrich JK, Ley RE, Kao-Kniffin J. Selection on soil microbiomes reveals reproducible impacts on plant function. ISME J. 2015;9: 980–989.

27. Rolli E, Marasco R, Vigani G, Ettoumi B, Mapelli F, Deangelis ML, et al. Improved plant resistance to drought is promoted by the root-associated microbiome as a water stress-dependent trait. Environ Microbiol. 2015;17: 316–331.

28. Marasco R, Rolli E, Ettoumi B, Vigani G, Mapelli F, Borin S, et al. A drought resistance-promoting microbiome is selected by root system under desert farming. PLoS One. 2012;7: e48479.

29. Limpens J, Granath G, Aerts R, Heijmans MMPD, Sheppard LJ, Bragazza L, et al. Glasshouse vs field experiments: do they yield ecologically similar results for assessing N impacts on peat mosses? New Phytol. 2012;195: 408–418.

30. Schittko C, Runge C, Strupp M, Wolff S, Wurst S. No evidence that plant-soil feedback effects of native and invasive plant species under glasshouse conditions are reflected in the field. J Ecol. 2016;104: 1243–1249.

31. Sala OE, Parton WJ, Joyce LA, Lauenroth WK. Primary production of the central grassland region of the United States. Ecology. 1988;69: 40–45.

32. Epstein HE, Lauenroth WK, Burke IC, Coffin DP. Regional productivities of plant species in the Great Plains of the United States. Plant Ecol. 1998;134: 173–195.

33. Gibson DJ. Grasses and Grassland Ecology. Oxford University Press; 2009.

34. Knapp AK, Briggs JM, Blair JM, Turner CL. Patterns and controls of aboveground net primary production in tallgrass prairie. : long-term ecological research in tallgrass …. 1998.

35. Toju H, Peay KG, Yamamichi M, Narisawa K, Hiruma K, Naito K, et al. Core microbiomes for sustainable agroecosystems. Nat Plants. 2018;4: 247–257.

36. Johnson LC, Olsen JT, Tetreault H, DeLaCruz A, Bryant J, Morgan TJ, et al. Intraspecific variation of a dominant grass and local adaptation in reciprocal garden communities along a US Great Plains' precipitation gradient: implications for grassland restoration with climate change. Evol Appl. 2015;8: 705–723.

37. Olsen JT, Caudle KL, Johnson LC, Baer SG, Maricle BR. Environmental and genetic variation in leaf anatomy among populations of Andropogon gerardii (Poaceae) along a precipitation gradient. Am J Bot. 2013;100: 1957–1968.

38. Caudle KL, Johnson LC, Baer SG, Maricle BR. A comparison of seasonal foliar chlorophyll change among ecotypes and cultivars of Andropogon gerardii (Poaceae) by using nondestructive and destructive methods. Photosynthetica. 2014;52: 511–518.

39. Galliart M, Bello N, Knapp M, Poland J, St Amand P, Baer S, et al. Local adaptation, genetic divergence, and experimental selection in a foundation grass across the US Great Plains' climate gradient. Glob Chang Biol. 2019;25: 850–868.

40. Johnson LC, Galliart MB, Alsdurf JD, Maricle BR, Baer SG, Bello NM, et al. Reciprocal transplant gardens as gold standard to detect local adaptation in grassland species: New opportunities moving into the 21st century. J Ecol. 2021. doi:10.1111/1365-2745.13695

41. Sarkar S, Kamke A, Ward K, Rudick AK, Baer SG, Ran Q, et al. Bacterial but Not Fungal Rhizosphere Community Composition Differ among Perennial Grass Ecotypes under Abiotic Environmental Stress. Microbiol Spectr. 2022;10: e0239121.

42. Raffard A, Santoul F, Cucherousset J, Blanchet S. The community and ecosystem consequences of intraspecific diversity: a meta-analysis. Biol Rev Camb Philos Soc. 2019;94: 648–661.

43. Kokko H, Chaturvedi A, Croll D, Fischer MC, Guillaume F, Karrenberg S, et al. Can Evolution Supply What Ecology Demands? Trends Ecol Evol. 2017;32: 187–197.

44. Galliart M, Sabates S, Tetreault H, DeLaCruz A, Bryant J, Alsdurf J, et al. Adaptive genetic potential and plasticity of trait variation in the foundation prairie grass Andropogon gerardii across the US Great Plains' climate gradient: Implications for climate change and restoration. Evol Appl. 2020;13: 2333–2356.

45. Smalla K, Wieland G, Buchner A, Zock A, Parzy J, Kaiser S, et al. Bulk and rhizosphere soil bacterial communities studied by denaturing gradient gel electrophoresis: plant-dependent enrichment and seasonal shifts revealed. Appl Environ Microbiol. 2001;67: 4742–4751.

46. Sanguin H, Remenant B, Dechesne A, Thioulouse J, Vogel TM, Nesme X, et al. Potential of

a 16S rRNA-based taxonomic microarray for analyzing the rhizosphere effects of maize on Agrobacterium spp. and bacterial communities. Appl Environ Microbiol. 2006;72: 4302–4312.

47. Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, Al-Ghalith GA, et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nat Biotechnol. 2019;37: 852–857.

48. Martin M. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal. 2011;17: 10–12.

49. Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJA, Holmes SP. DADA2: High-resolution sample inference from Illumina amplicon data. Nat Methods. 2016;13: 581–583.

50. Gihring TM, Green SJ, Schadt CW. Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. Environ Microbiol. 2012;14: 285–290.

51. Paradis E, Schliep K. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. Bioinformatics. 2018;35: 526–528.

52. De Cáceres M, Legendre P. Associations between species and groups of sites: indices and statistical inference. Ecology. 2009;90: 3566–3574.

53. Bates D, Mächler M, Bolker B, Walker S. Fitting Linear Mixed-Effects Models Using lme4. J Stat Softw. 2015;67: 1–48.

54. McMurdie PJ, Holmes S. phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. PLoS One. 2013;8: e61217.

55. Oksanen J, Blanchet FG, Friendly M, Kindt R. vegan: Community Ecology Package. R package version 2.5-6. 2019. 2020. Available: https://scholar.google.ca/scholar?cluster=11712188988930644900&hl=en&as_sdt=0,5&sciodt=0,5

56. Team RC. R: A language and environment for statistical computing. R Foundation for Statistical Computing; 2020. Available: https://www.R-project.org/

57. Eren AM, Morrison HG, Lescault PJ, Reveillaud J, Vineis JH, Sogin ML. Minimum entropy decomposition: unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. ISME J. 2015;9: 968–979.

58. Eren AM, Maignien L, Sul WJ, Murphy LG, Grim SL, Morrison HG, et al. Oligotyping: Differentiating between closely related microbial taxa using 16S rRNA gene data. Methods Ecol Evol. 2013;4: 1111–1119.

59. Lumibao CY, Borer ET, Condon B, Kinkel L, May G, Seabloom EW. Site-specific responses of foliar fungal microbiomes to nutrient addition and herbivory at different spatial scales. Ecol Evol. 2019;9: 12231–12244.

60. Brady, N. (1990) The nature and properties of soils. 10th Edition, Macmillan Publishing Company, Cranbury.

61. Wei Z, Hu X, Li X, Zhang Y, Jiang L, Li J, et al. The rhizospheric microbial community structure and diversity of deciduous and evergreen forests in Taihu Lake area, China. PLoS One. 2017;12: e0174411.

62. Liao J, Cao X, Zhao L, Wang J, Gao Z, Wang MC, et al. The importance of neutral and niche processes for bacterial community assembly differs between habitat generalists and specialists. FEMS Microbiol Ecol. 2016;92. doi:10.1093/femsec/fiw174

63. Xu Q, Vandenkoornhuyse P, Li L, Guo J, Zhu C, Guo S, et al. Microbial generalists and specialists differently contribute to the community diversity in farmland soils. J Advert Res. 2022;40: 17–27.

64. Chu H, Fierer N, Lauber CL, Caporaso JG, Knight R, Grogan P. Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. Environ Microbiol. 2010;12: 2998–3006.

65. Nacke H, Thürmer A, Wollherr A, Will C, Hodac L, Herold N, et al. Pyrosequencing-based assessment of bacterial community structure along different management types in German forest and grassland soils. PLoS One. 2011;6: e17000.

66. Sul WJ, Asuming-Brempong S, Wang Q, Tourlousse DM, Penton CR, Deng Y, et al. Tropical agricultural land management influences on soil microbial communities through its effect on soil organic carbon. Soil Biol Biochem. 2013;65: 33–38.

67. Clark JS, Campbell JH, Grizzle H, Acosta-Martìnez V, Zak JC. Soil microbial community response to drought and precipitation variability in the Chihuahuan Desert. Microb Ecol. 2009;57: 248–260.

68. Zhou Z, Wang C, Luo Y. Response of soil microbial communities to altered precipitation: A global synthesis. Glob Ecol Biogeogr. 2018;27: 1121–1136.

69. Fierer N, Bradford MA, Jackson RB. Toward an ecological classification of soil bacteria. Ecology. 2007;88: 1354–1364.

70. Bardgett RD, Freeman C, Ostle NJ. Microbial contributions to climate change through carbon cycle feedbacks. ISME J. 2008;2: 805–814.

71. Manzoni S, Schimel JP, Porporato A. Responses of soil microbial communities to water stress: results from a meta-analysis. Ecology. 2012;93: 930–938.

72. Schimel J, Balser TC, Wallenstein M. Microbial stress-response physiology and its implications for ecosystem function. Ecology. 2007;88: 1386–1394.

73. de Wit R, Bouvier T. “Everything is everywhere, but, the environment selects”; what did Baas Becking and Beijerinck really say? Environ Microbiol. 2006;8: 755–758.

74. Marschner P, Crowley D, Yang CH. Development of specific rhizosphere bacterial communities in relation to plant species, nutrition and soil type. Plant Soil. 2004;261: 199–208.

75. Veach AM, Morris R, Yip DZ, Yang ZK, Engle NL, Cregger MA, et al. Rhizosphere microbiomes diverge among Populus trichocarpa plant-host genotypes and chemotypes, but it depends on soil origin. Microbiome. 2019;7: 76.

76. Székely AJ, Langenheder S. The importance of species sorting differs between habitat generalists and specialists in bacterial communities. FEMS Microbiol Ecol. 2014;87: 102–112.

77. Xiong C, He J-Z, Singh BK, Zhu Y-G, Wang J-T, Li P-P, et al. Rare taxa maintain the stability of crop mycobiomes and ecosystem functions. Environ Microbiol. 2021;23: 1907–1924.

78. Bent SJ, Forney LJ. The tragedy of the uncommon: understanding limitations in the analysis of microbial diversity. ISME J. 2008;2: 689–695.

79. DeJong TM. A Comparison of Three Diversity Indices Based on Their Components of Richness and Evenness. Oikos. 1975;26: 222–227.

80. Larsen FW, Bladt J, Rahbek C. Indicator taxa revisited: useful for conservation planning? Divers Distrib. 2009;15: 70–79.

81. Bachar A, Al-Ashhab A, Soares MIM, Sklarz MY, Angel R, Ungar ED, et al. Soil microbial abundance and diversity along a low precipitation gradient. Microb Ecol. 2010;60: 453–461.

82. Naylor D, Coleman-Derr D. Drought Stress and Root-Associated Bacterial Communities. Front Plant Sci. 2017;8: 2223.

83. Levins R. Theory of Fitness in a Heterogeneous Environment. I. The Fitness Set and Adaptive Function. Am Nat. 1962;96: 361–373.

84. Fanin N, Lin D, Freschet GT, Keiser AD, Augusto L, Wardle DA, et al. Home-field advantage of litter decomposition: from the phyllosphere to the soil. New Phytol. 2021;231: 1353–1358.

85. Gregory TR. Understanding Natural Selection: Essential Concepts and Common Misconceptions. Evolution: Education and Outreach. 2009;2: 156–175.

86. Chen ECH, Morin E, Beaudet D, Noel J, Yildirir G, Ndikumana S, et al. High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont Rhizophagus irregularis. New Phytol. 2018;220: 1161–1171.

87. Qiu Z, Verma JP, Liu H, Wang J, Batista BD, Kaur S, et al. Response of the plant core microbiome to Fusarium oxysporum infection and identification of the pathobiome. Environ Microbiol. 2022;24: 4652–4669.

88. Risely A. Applying the core microbiome to understand host-microbe systems. J Anim Ecol. 2020;89: 1549–1558.

Figure and Table Legends

Figure 1. (A) Bacterial α-diversity indices among three sites located across precipitation gradient: Hays, Manhattan, and Carbondale. Species observed richness (S_{Obs}), Shannon's H index, and Faith-PD index. (B) Location impact on *Andropogon gerardii* rhizosphere bacterial composition. Non-metric multidimensional (NMDS) scaling plot of *A. gerardii* rhizosphere communities associated with three site locations across the precipitation gradient: Hays, Manhattan and Carbondale. NMDS ordinations were obtained from Bray-Curtis similarity matrix. (p-values: * - 0.05, ** - 0.01, *** - <0.01).

Figure 2. (A) Bacterial α-diversity indices among the dry, mesic, and wet ecotypes across all locations Species observed richness (S_{Obs}), Shannon's H index, Faith-PD index. (B) Ecotype impact on *Andropogon gerardii* rhizosphere bacterial composition. Non-metric multidimensional (NMDS) scaling plot of *A. gerardii* rhizosphere communities associated with three ecotypes across three site locations. NMDS ordinations were obtained from Bray-Curtis similarity matrix. (p-values: * - 0.05, ** - 0.01, *** - <0.01).

Figure 3. Venn diagrams representing the overlapping and unique ASVs (numbers in the circle) among (A) all locations, (B) all ecotypes, (C) ecotypes in Carbondale, ecotypes in Hays, ecotypes in Manhattan. The circle with a red edge represents the home ecotype for that location. Inserts represent the top three genera. Partial information on unique ASVs are shown here, full information is in Supplementary Table S5. Higher numbers of unique ASVs suggest the "*home field advantage*" of the *Andropogon gerardii* ecotypes.

Figure 4. Relative abundance of each oligotype within the Pseudomonadales and Rhizobiales diversity for each sample among three sites located across precipitation gradient. The proportion of the relative abundance of the (A) Pseudomonadales (red, top) and *Pseudomonas*-Oligos (bottom), and (B) Rhizobiales (purple) and *Rhizobium*-Oligos (bottom) suggest the impact of locations and ecotypes on rhizobiome strain-level composition.

Table 1. Statistical analyses (ANOVA and pairwise test) reveal locations (C-Carbondale, H-Hays, MHK-Manhattan) had a strong influence on the rhizobiome diversity and richness.

Supplementary Tables

Supplementary Table S1. Locations of seeds and populations collected from *Andropogon gerardii*.

Supplementary Table S2. Samples names and details for the soil cores collected for this study.

Supplementary Table S3. Raw sequence analysis by QIIME 2 Version 2019.7. The number of counts of bacteria and fungi initially obtained, and the counts that were considered after primer trimming and DADA2 quality control per sample. Bacterial identifications along with the number of counts per sample.

Supplementary Table S4. Indicator taxon analysis on different locations (irrespective of ecotypes) - Hays, Manhattan and Carbondale.

Supplementary Table S5. Unique taxa for locations and ecotypes.

Supplementary Table S6. Indicator taxon analysis on ecotypes (irrespective of locations) - Dry, Mesic and Wet.

Supplementary Table S7. Indicator taxon analysis on locations by individual ecotypes.

Supplementary Table S8. Indicator taxon analysis on ecotypes by individual locations.

Supplementary Table S9. Genus-level oligotyping analysis.

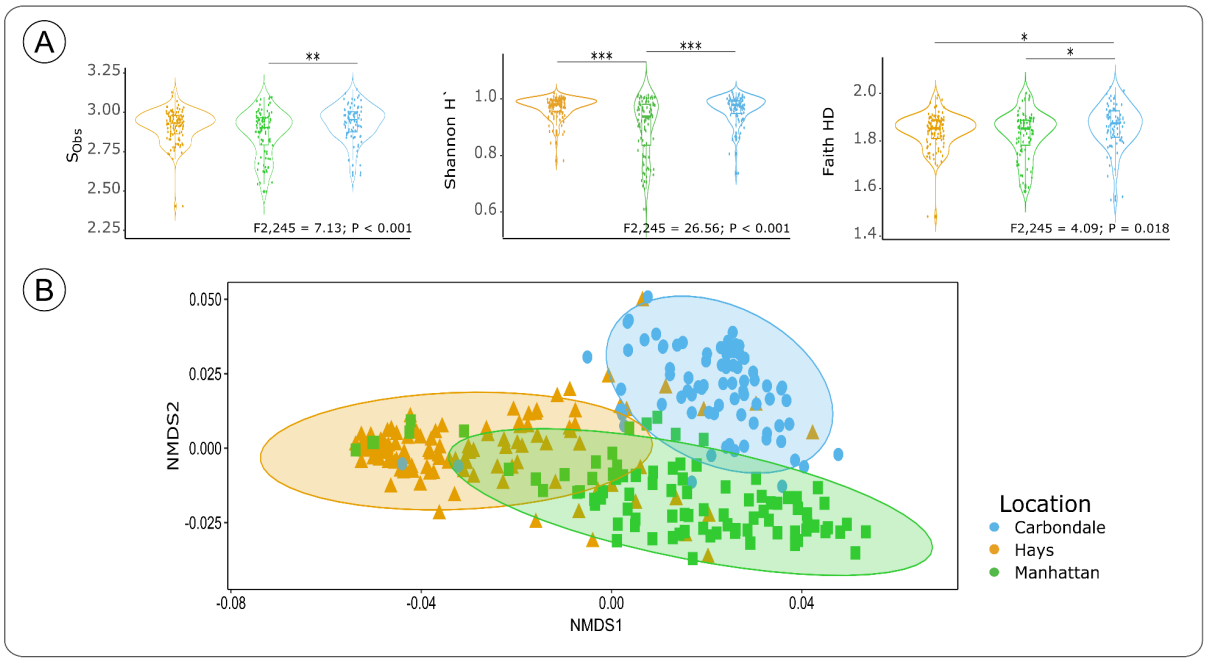
A
B
S_{Obs}
Shannon H`
Faith HD
F2,245 = 7.13; P < 0.001
F2,245 = 26.56; P < 0.001
F2,245 = 4.09; P = 0.018
NMDS1
NMDS2
Location
Carbondale
Hays
Manhattan

Figure 1

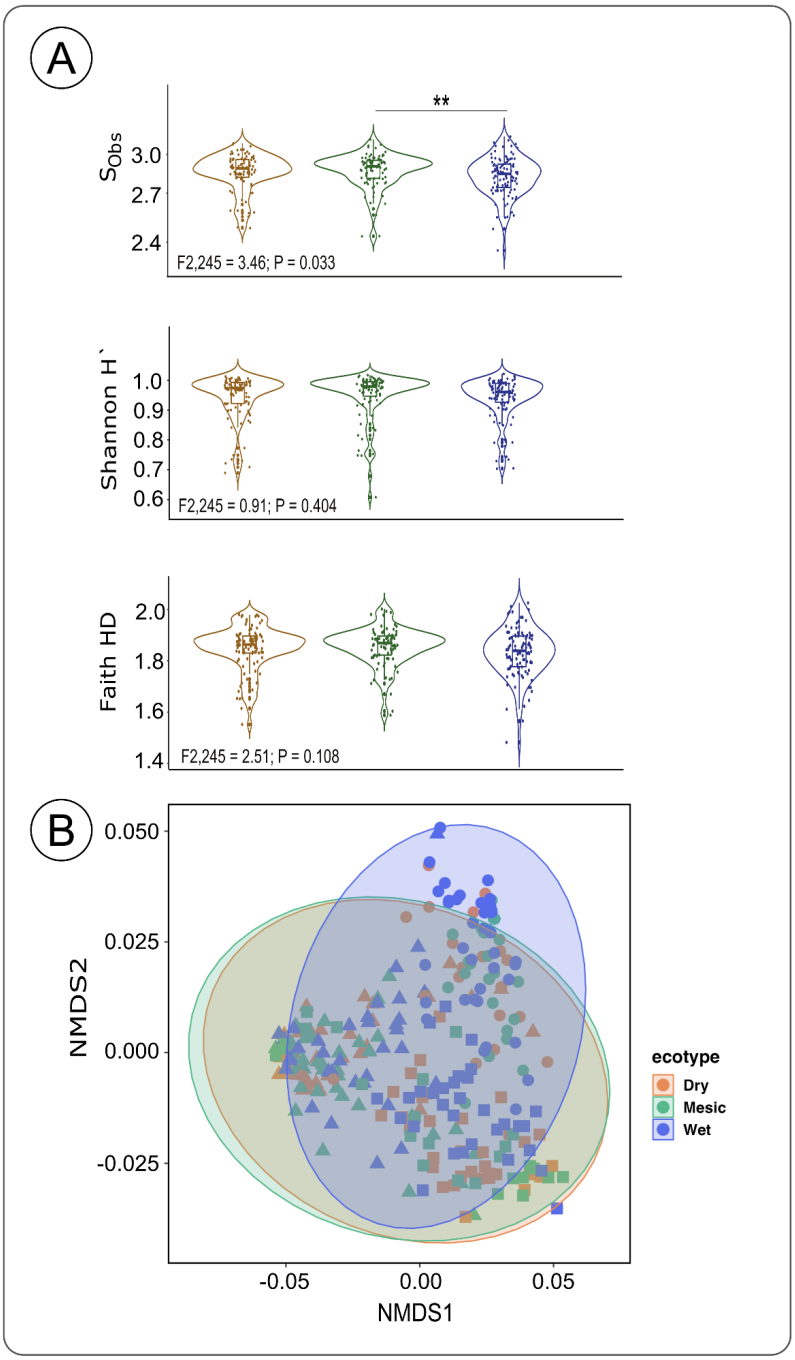
A
**
S_{Obs}
3.0
2.7
2.4
F2,245 = 3.46; P = 0.033
Shannon H`
1.0
0.9
0.8
0.7
0.6
F2,245 = 0.91; P = 0.404
Faith HD
2.0
1.8
1.6
1.4
F2,245 = 2.51; P = 0.108
B
0.050
0.025
0.000
-0.025
NMDS2
-0.05
0.00
0.05
NMDS1
ecotype
Dry
Mesic
Wet

Figure 2

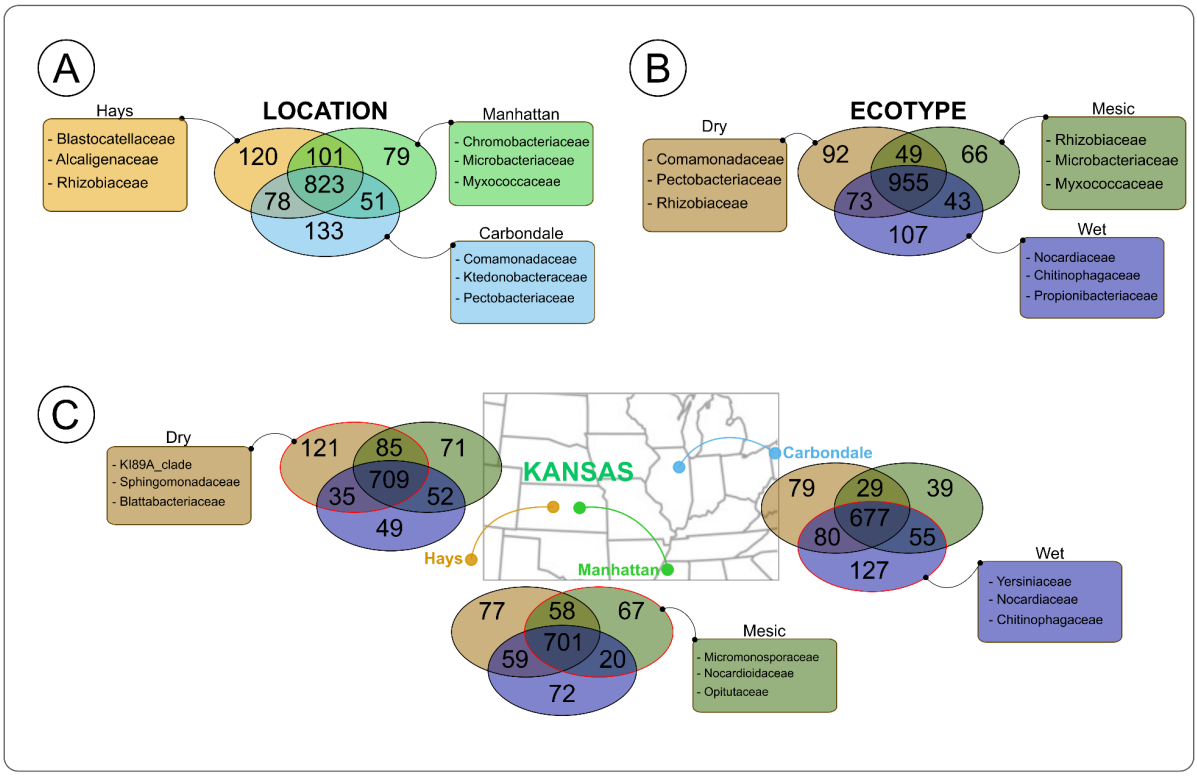
A
LOCATION
Hays
- Blastocatellaceae
- Alcaligenaceae
- Rhizobiaceae
Manhattan
- Chromobacteriaceae
- Microbacteriaceae
- Myxococcaceae
Carbondale
- Comamonadaceae
- Ktedonobacteraceae
- Pectobacteriaceae
120
101
79
823
78
51
133
B
ECOTYPE
Dry
- Comamonadaceae
- Pectobacteriaceae
- Rhizobiaceae
Mesic
- Rhizobiaceae
- Microbacteriaceae
- Myxococcaceae
Wet
- Nocardiaceae
- Chitinophagaceae
- Propionibacteriaceae
92
49
66
955
73
43
107
C
Dry
- KI89A_clade
- Sphingomonadaceae
- Blattabacteriaceae
121
85
71
709
35
52
49
KANSAS
Carbondale
Hays
Manhattan
79
29
39
677
80
55
127
Wet
- Yersiniaceae
- Nocardiaceae
- Chitinophagaceae
77
58
67
701
59
20
72
Mesic
- Micromonosporaceae
- Nocardioidaceae
- Opitutaceae

Figure 3

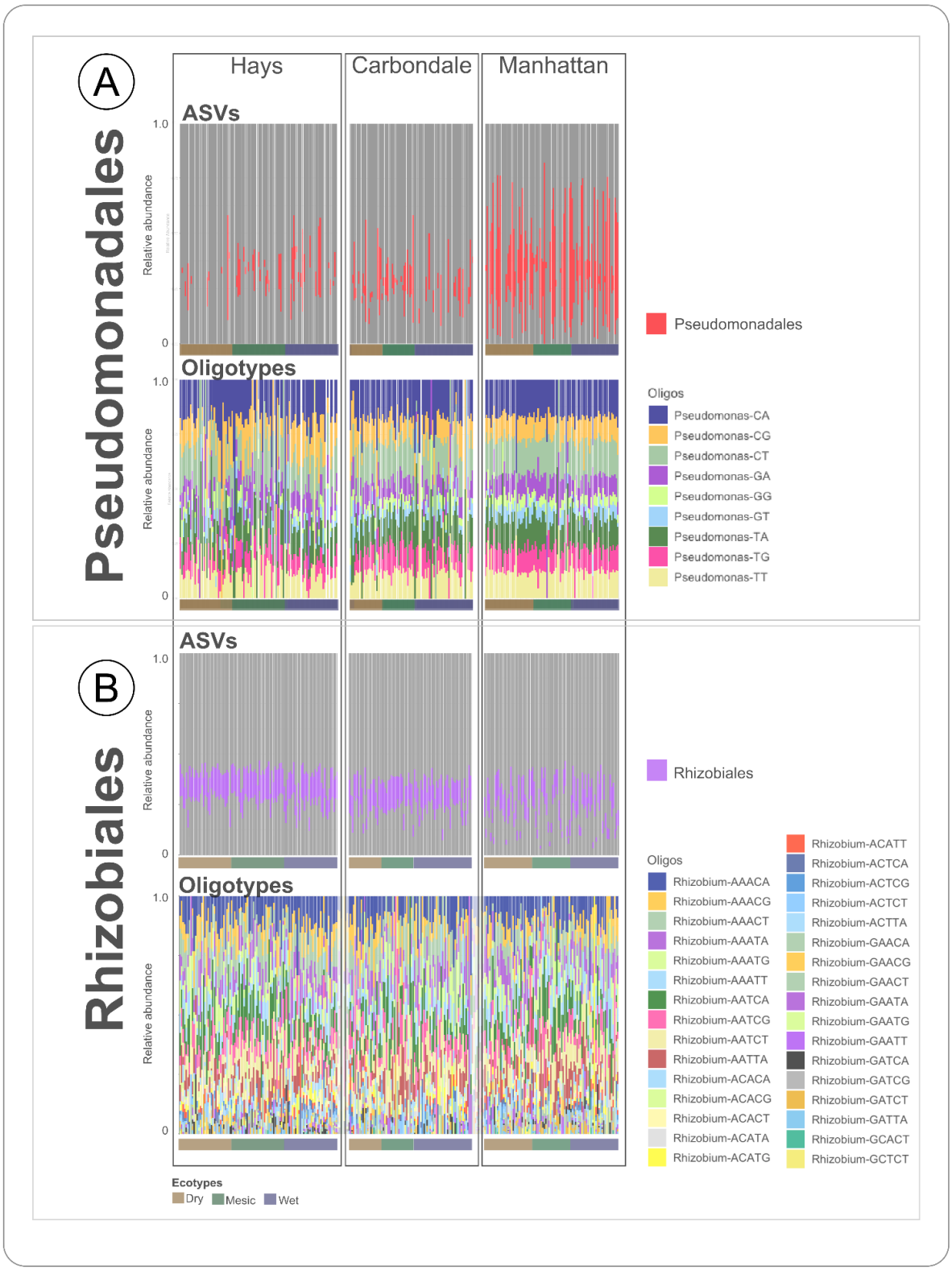
A
Pseudomonadales
Hays
Carbondale
Manhattan
ASVs
Oligotypes
Relative abundance
1.0
0
Pseudomonadales
Oligos
Pseudomonas-CA
Pseudomonas-CG
Pseudomonas-CT
Pseudomonas-GA
Pseudomonas-GG
Pseudomonas-GT
Pseudomonas-TA
Pseudomonas-TG
Pseudomonas-TT
B
Rhizobiales
Rhizobiales
Oligos
Rhizobium-AAACA
Rhizobium-AAACG
Rhizobium-AAACT
Rhizobium-AAATA
Rhizobium-AAATG
Rhizobium-AAATT
Rhizobium-AATCA
Rhizobium-AATCG
Rhizobium-AATCT
Rhizobium-AATTA
Rhizobium-ACACA
Rhizobium-ACACG
Rhizobium-ACACT
Rhizobium-ACATA
Rhizobium-ACATG
Rhizobium-ACATT
Rhizobium-ACTCA
Rhizobium-ACTCG
Rhizobium-ACTCT
Rhizobium-ACTTA
Rhizobium-GAACA
Rhizobium-GAACG
Rhizobium-GAACT
Rhizobium-GAATA
Rhizobium-GAATG
Rhizobium-GAATT
Rhizobium-GATCA
Rhizobium-GATCG
Rhizobium-GATCT
Rhizobium-GATTA
Rhizobium-GCACT
Rhizobium-GCTCT
Ecotypes
Dry
Mesic
Wet

Figure 4

Table 1

Index	ANOVA		Pairwise test		
	chi-squared	P-value	C	H	
SObs	10.42	0.005	0.1005	-	H
			0.0067	0.0653	MHK
Shannon's H	25.171	3.422e-o6	0.7	-	H
			6.90E-05	1.40E-05	MHK
Faith's PD	6.7829	0.03366	0.044	-	H
			0.044	0.585	MHK

Index	ANOVA		Pairwise test		
	chi-squared	P-value	Dry	Mesic	
SObs	3.46	0.033	0.585	-	Mesic
			0.078	0.026	Wet
Shannon's H	0.91	0.404	0.285	-	Mesic
			0.285	0.061	Wet
Faith's PD	2.51	0.0108	0.78	-	Mesic
			0.14	0.13	Wet