

Nutrient and Microbiome-Mediated Plant–Soil Feedback in Domesticated and Wild *Andropogoneae*: Implications for Agroecosystems

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Appendix S1: Supplemental Methods

Conditioning phase: Seed collection

Seeds of *Zea mays* ssp. *mays* *B73-wt*, *B73-rth3*, *b58*, and *HP301* were obtained from in-house collections bulked in the greenhouse through self-pollination (Lincoln, Nebraska). For the *B73-rth3* seedlings that were used to generate seeds, the absence of both *rth3* alleles was confirmed through PCR. Seed batches of these seedlings were tested for the root-hairless phenotype by germinating 10 seeds per ear on petri dishes to a primary root length of 10 cm and confirming the absence of root hair using a stereo microscope. *Zea mays* ssp. *parviglumis* seeds were bulked in field growth through open pollination by Petcher Seeds, LLC (Fruitdale, AL). Seeds of *Andropogon gerardii* were obtained from Prairie Legacy, LLC (Witt's End Homestead, NE). from locally sourced plants that were grown in species-specific gardens and open-pollinated. Seeds of *Tripsacum dactyloides* were collected from a prairie in southeastern Nebraska.

Appendix S2: Supplemental tables and figures

Table S1. Numbers of reads (amplicons) and ASVs after filtering across conditioning genotypes in the rhizosphere. Read counts and the number of amplicon sequence variants (ASVs) used in analyses. Negative control (unconditioned) soils were soils from pots with no plants that were treated identically to pots with plants. Preconditioned soils pertain to one biological replicate of the initial soil community prior to planting in pots.

	Abbreviation	Number of reads	Number of ASVs
Maize functional group		155544	2878
<i>Zea mays parviglumis</i>	teo	23523	588
<i>Zea mays mays b58</i>	b58	33599	827
<i>Zea mays mays B73-wt</i>	b73	23916	585
<i>Zea mays mays B73-rth3</i>	rth	39730	884
<i>Zea mays mays HP301</i>	pop	34776	833
Prairie grass functional group		55469	1075
<i>Tripsacum dactyloides</i>	tri	28800	649
<i>Andropogon gerardii</i>	and	26669	567
Other soils		NA	NA
Preconditioned soil	ini	2726	269
Unconditioned soils	neg	5862	177

Table S2. Effects of conditioning genotype on soil microbial abundance and community alpha diversity metrics. Type III analysis of variance (ANOVA) tests assessed the significance of the conditioning genotype effect using separate models with or without unconditioned soil controls from the conditioning phase. Tests were based on amplicon sequence variant (ASV) relative abundance. The observed richness was the total number of ASVs, diversity was measured using Shannon's diversity index and Fisher's alpha diversity index, and Simpson's evenness.

Response variable	With soil controls	No soil controls
Log(abundance)	$F_{7,69} = 0.84$ $p = 0.524$	$F_{6,65} = 0.87$ $p = 0.499$
Observed ASV richness	$F_{7,74} = 1.70$ $p = 0.121$	$F_{6,72} = 1.88$ $p = 0.097$
Shannon's diversity	$F_{7,74} = 1.46$ $p = 0.193$	$F_{6,72} = 1.66$ $p = 0.143$
Fisher's alpha diversity	$F_{7,74} = 1.71$ $p = 0.101$	$F_{6,72} = 2.01$ $p = 0.076$
Simpson's evenness	$F_{7,74} = 1.93$ $p = 0.077$	$F_{6,72} = 2.19$ $p = 0.053$

Table S3. Microbial indicator taxa of conditioning genotype rhizobiomes. A point biserial correlation analysis of rhizosphere amplicon sequence variants (ASVs) to assess for microbial taxa which are more prevalent in soils of specific conditioning genotypes or shared by conditioning genotypes. Indicator ASVs included a biserial correlation coefficient (r_{pb}) and correlation probability (p_{corr}) for significant ($p_{corr} < 0.05$) comparisons within an associated conditioning genotype(s). Each ASV shows the phylum, family, and genus-level classification trained using the SILVA v 132 database. Unclassified taxonomic levels from the SILVA database were marked with “NA”.

Conditioning genotype(s)	r_{pb}	p_{corr}	Phylum	Family	Genus
and	0.50	0.002	Actinobacteria	Nocardioideaceae	Kribbella
and	0.47	0.001	Actinobacteria	Micromonosporaceae	Actinocatenispora
and	0.45	0.008	Actinobacteria	Micromonosporaceae	Actinocatenispora
and	0.42	0.029	Actinobacteria	Streptomycetaceae	Streptomyces
and	0.42	0.032	Actinobacteria	Streptomycetaceae	Streptomyces
and	0.42	0.030	Actinobacteria	Nocardioideaceae	Marmoricola
and	0.42	0.031	Patescibacteria	NA	NA
and	0.41	0.018	Proteobacteria	Xanthomonadaceae	Luteimonas
and	0.41	0.029	Proteobacteria	Rhodanobacteraceae	Dyella
and	0.41	0.036	Patescibacteria	NA	NA
and	0.41	0.036	Proteobacteria	Rhodanobacteraceae	Fulvimonas
and	0.41	0.024	Patescibacteria	Saccharimonadaceae	NA
and	0.40	0.025	Proteobacteria	Rhodanobacteraceae	Fulvimonas
and	0.40	0.032	Bacteroidetes	Chitinophagaceae	NA
and	0.39	0.031	Actinobacteria	Micromonosporaceae	Actinocatenispora
and	0.37	0.031	Bacteroidetes	Chitinophagaceae	Niastella
and	0.36	0.030	Actinobacteria	Streptomycetaceae	Streptomyces
and	0.36	0.048	Actinobacteria	Streptomycetaceae	Allostreptomyces
and	0.35	0.039	Actinobacteria	67-14	NA
and	0.32	0.030	Actinobacteria	Streptomycetaceae	Streptomyces
b58	0.42	0.018	Bacteroidetes	Microscillaceae	NA
b58	0.38	0.026	Proteobacteria	Burkholderiaceae	Ralstonia
b73	0.57	0.001	Actinobacteria	Intrasporangiaceae	Janibacter
					Burkholderia- Caballeronia- Paraburkholderia
b73	0.40	0.047	Proteobacteria	Burkholderiaceae	Paraburkholderia
b73	0.39	0.039	Planctomycetes	Pirellulaceae	NA
b73	0.37	0.044	Verrucomicrobia	Pedosphaeraceae	NA
b73	0.36	0.045	Bacteroidetes	env.OPS 17	NA
b73	0.34	0.048	Proteobacteria	KD3-10	NA
b73	0.34	0.048	Proteobacteria	Sphingomonadaceae	Sphingomonas
pop	0.51	0.003	Actinobacteria	Intrasporangiaceae	Janibacter
pop	0.45	0.014	Proteobacteria	Burkholderiaceae	Pseudoduganella
pop	0.41	0.018	Proteobacteria	Burkholderiaceae	Ralstonia

pop	0.40	0.028	<i>Gemmatimonadetes</i>	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>
pop	0.38	0.029	<i>Actinobacteria</i>	<i>Nocardoidaceae</i>	<i>Nocardioides</i>
rth	0.60	0.001	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.46	0.004	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.44	0.015	<i>Verrucomicrobia</i>	<i>Pedosphaeraceae</i>	NA
rth	0.42	0.014	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.41	0.013	<i>Gemmatimonadetes</i>	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>
rth	0.41	0.010	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.40	0.013	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.38	0.023	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>
rth	0.37	0.049	<i>Verrucomicrobia</i>	<i>Pedosphaeraceae</i>	NA
teo	0.43	0.010	<i>Actinobacteria</i>	67-14	NA
teo	0.42	0.038	<i>Bacteroidetes</i>	NA	NA
teo	0.42	0.035	<i>Proteobacteria</i>	<i>Acetobacteraceae</i>	<i>Rhodovastum</i>
teo	0.41	0.034	<i>Gemmatimonadetes</i>	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>
teo	0.40	0.039	<i>Actinobacteria</i>	<i>Nocardoidaceae</i>	<i>Nocardioides</i>
teo	0.40	0.037	<i>Acidobacteria</i>	NA	NA
teo	0.39	0.029	<i>Chloroflexi</i>	NA	NA
teo	0.38	0.028	<i>Acidobacteria</i>	<i>Unknown_Family</i>	<i>Vicinamibacter</i>
teo	0.38	0.030	<i>Proteobacteria</i>	<i>Micropepsaceae</i>	NA
teo	0.38	0.030	<i>Planctomycetes</i>	<i>Phycisphaeraceae</i>	NA
teo	0.38	0.029	<i>Fibrobacteres</i>	<i>Fibrobacteraceae</i>	<i>Possible genus 04</i>
teo	0.37	0.027	<i>Actinobacteria</i>	NA	NA
teo	0.37	0.038	<i>Verrucomicrobia</i>	<i>Verrucomicrobiaceae</i>	<i>Prostheco bacter</i>
teo	0.36	0.028	<i>Verrucomicrobia</i>	<i>Pedosphaeraceae</i>	NA
tri	0.44	0.011	<i>Proteobacteria</i>	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>
tri	0.44	0.017	<i>Patescibacteria</i>	<i>Saccharimonadaceae</i>	NA
tri	0.43	0.018	<i>Actinobacteria</i>	<i>Streptomycetaceae</i>	<i>Streptomyces</i>
tri	0.41	0.020	<i>Actinobacteria</i>	<i>Streptomycetaceae</i>	<i>Streptomyces</i>
tri	0.41	0.020	<i>Proteobacteria</i>	<i>Dongiaceae</i>	<i>Dongia</i>
and:tri	0.36	0.047	<i>Bacteroidetes</i>	env.OPS 17	NA
b58:b73	0.45	0.010	<i>Verrucomicrobia</i>	<i>Opitutaceae</i>	<i>Opitutus</i>
b58:tri	0.36	0.041	<i>Proteobacteria</i>	<i>Burkholderiaceae</i>	<i>Massilia</i>
rth:teo	0.39	0.035	<i>Proteobacteria</i>	<i>Haliangiaceae</i>	<i>Haliangium</i>
and:b73:					<i>Candidatus</i>
pop:rth	0.38	0.031	<i>Verrucomicrobia</i>	<i>Xiphinematobacteraceae</i>	<i>Xiphinematobacter</i>

Table S4. Effects of feedback genotype, conditioning genotype, and their interaction on foliar nutrient composition. Permutational multivariate analyses of variance (perMANOVA) and homogeneity of dispersion analyses were performed based on an abundance-weighted (Gower) distance metric to separately test the effects of feedback genotype, conditioning genotype, their interaction, and conditioning functional group on the foliar nutrient composition. The perMANOVA numerator degrees of freedom (*df*) were 1 for functional group, 2 for feedback genotype, 5 for conditioning genotype nested within their respective functional group, and 12 *df* for the interaction of conditioning and feedback genotypes, with denominator degrees of 219. Separate tests of dispersion were conducted for main effects of feedback genotype and functional group, where the numerator *df* were 2 for feedback genotype, and 1 for functional group, with denominator degrees of 241 and 242, respectively. Homogeneity of multivariate dispersion was assessed by calculating the both the ordination methods to estimate the distances from the centroid, followed by an ANOVA for separate analyses of conditioning functional group.

Factor	perMANOVA			Test of Dispersion	
	<i>F</i>	Probability	<i>R</i>²	<i>F</i>	Probability
Functional group	56.13	$p = 0.001$	0.12	30.36	$p < 0.001$
Feedback genotype	70.22	$p = 0.001$	0.30	0.51	$p = 0.599$
Functional group: conditioning genotype	2.30	$p = 0.001$	0.02	-	-
Feedback × conditioning genotype	3.99	$p = 0.001$	0.10	-	-

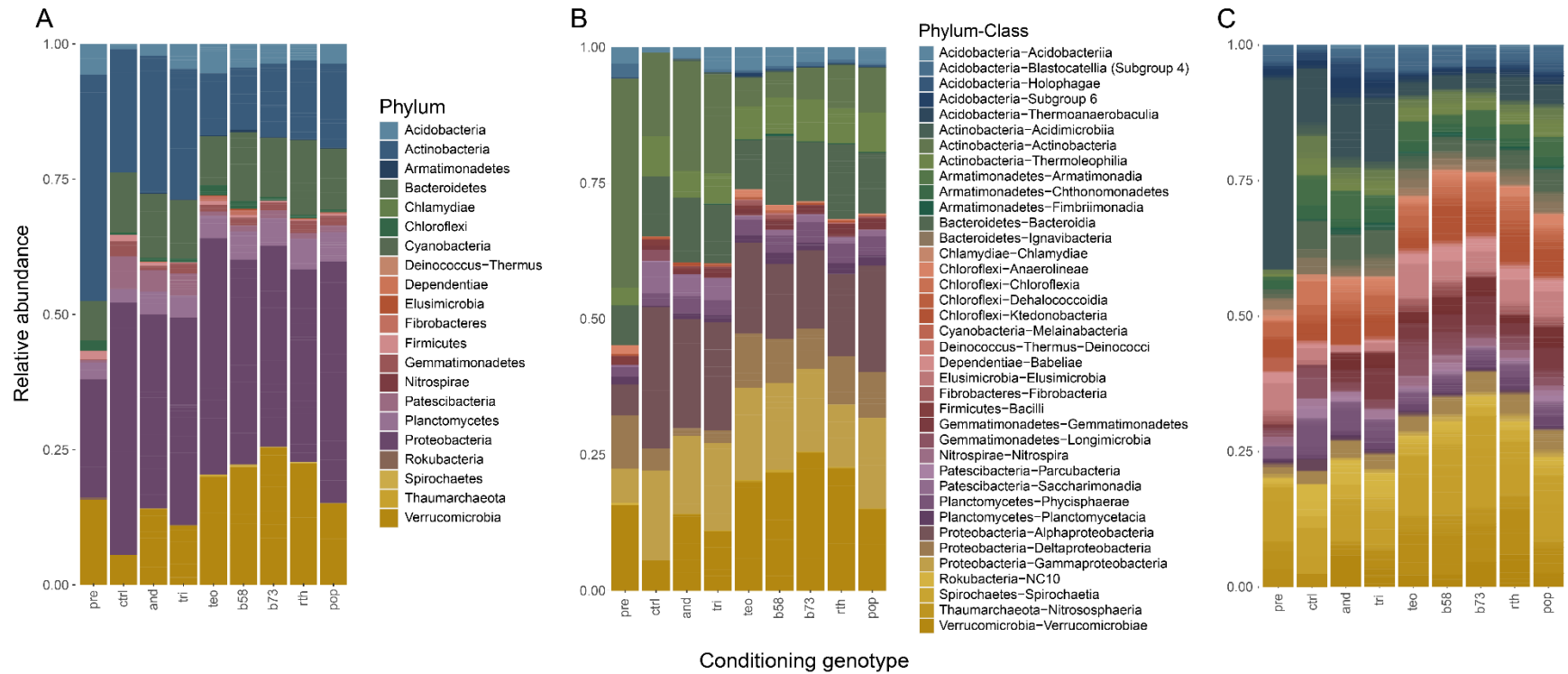


Figure S1. Variation in taxonomic classification for pre-conditioned, unconditioned controls, and different conditioning genotype soil microbial communities. Taxonomic bar plots of the relative abundance of amplicon sequence variants (ASVs) at the A) phylum, B) class level, grouped at the phylum level, and C) the genus level, grouped at the family level, nested in the class level of taxonomic classification (legend below). 47% of the genus-level classification was unclassified, while 15% of the family-level classification was unclassified by the SILVA v 132 database. 21 Phyla, 38 classes, 144 families, and 204 genera (315 unique genera, if “unclassified” genera are nested on a phylogenetic basis into family and class level groupings).

Class-Family-Genus

Acidimicrobia-Iamiaceae-Iamia	Alphaproteobacteria-Devosiaceae-Devosia	Bacteroidia-Chitinophagaceae-Flaviaestuariibacter
Acidimicrobia-Ilumotobacteraceae-Ilumotobacter	Alphaproteobacteria-Devosiaceae-Unclassified	Bacteroidia-Chitinophagaceae-Flavisolibacter
Acidimicrobia-Ilumotobacteraceae-Unclassified	Alphaproteobacteria-Dongiaceae-Dongia	Bacteroidia-Chitinophagaceae-Flavitalea
Acidimicrobia-Unclassified-Unclassified	Alphaproteobacteria-Fistriaceae-Fistria	Bacteroidia-Chitinophagaceae-Helimonas
Acidobacteria-Acidobacteriaceae_(Subgroup 1)-Acidipila	Alphaproteobacteria-Elsteriaceae-Unclassified	Bacteroidia-Chitinophagaceae-Niastella
Acidobacteria-Acidobacteriaceae_(Subgroup 1)-Edaphobacter	Alphaproteobacteria-Hyphomicrobiaceae-Hyphomicrobium	Bacteroidia-Chitinophagaceae-Niveltalea
Acidobacteria-Acidobacteriaceae_(Subgroup 1)-Occallatibacter	Alphaproteobacteria-Hyphomondadaceae-Hirschia	Bacteroidia-Chitinophagaceae-Paraffimonas
Acidobacteria-Acidobacteriaceae_(Subgroup 1)-Temiglobus	Alphaproteobacteria-Hyphomondadaceae-SW602	Bacteroidia-Chitinophagaceae-Sediminibacterium
Acidobacteria-Koribacteraceae-Candidatus Koribacter	Alphaproteobacteria-Inquilinaceae-Inquilinus	Bacteroidia-Chitinophagaceae-Sogetibacter
Acidobacteria-Solibacteraceae_(Subgroup 3)-Bryobacter	Alphaproteobacteria-Kaistiaaceae-Kaistia	Bacteroidia-Chitinophagaceae-Taibaiella
Acidobacteria-Solibacteraceae_(Subgroup 3)-Candidatus Solibacter	Alphaproteobacteria-KF-JG30-B3-Unclassified	Bacteroidia-Chitinophagaceae-Terimonas
Acidobacteria-Unclassified-Unclassified	Alphaproteobacteria-Magnetospiraceae-Unclassified	Bacteroidia-Chitinophagaceae-Unclassified
Actinobacteria-Acidothermaceae-Acidothermus	Alphaproteobacteria-Magnetospirillaceae-Phaeospirillum	Bacteroidia-Crocinotomacaceae-Fluvicola
Actinobacteria-Catenulisporaceae-Catenulispora	Alphaproteobacteria-Magnetospirillaceae-Unclassified	Bacteroidia-Cytophagaceae-Cytophaga
Actinobacteria-Cellulomonadaceae-Cellulomonas	Alphaproteobacteria-Micavibrionaceae-Micavibrio	Bacteroidia-Cytophagaceae-Sporocytophaga
Actinobacteria-Gemmatimonadaceae-Blasococcus	Alphaproteobacteria-Micavibrionaceae-Unclassified	Bacteroidia-envi GPS 17-Unclassified
Actinobacteria-Intrasporangiaceae-Jenibacter	Alphaproteobacteria-Micropepsaceae-Micropepsis	Bacteroidia-Flavobacteriaceae-Flavobacterium
Actinobacteria-Intrasporangiaceae-Terrabacter	Alphaproteobacteria-Micropepsaceae-Unclassified	Bacteroidia-Microsillaceae-Chryseolinea
Actinobacteria-Microbacteriaceae-Lysinimonas	Alphaproteobacteria-Midichloriaceae-Candidatus Jidaibacter	Bacteroidia-Microsillaceae-Ohtakawangia
Actinobacteria-Microbacteriaceae-Microbacterium	Alphaproteobacteria-Mitochondria-Unclassified	Bacteroidia-Microsillaceae-OLB12
Actinobacteria-Microbacteriaceae-Unclassified	Alphaproteobacteria-Paracaeobacteraceae-Candidatus Paracaeobacter	Bacteroidia-Microsillaceae-Unclassified
Actinobacteria-Micrococcaleae-Paenarthrobacter	Alphaproteobacteria-Reynanellaceae-Reynanella	Bacteroidia-NS11-12 marine group-Unclassified
Actinobacteria-Micrococcaleae-Pseudarthrobacter	Alphaproteobacteria-Rhizobiaceae-Altorrhizobium-Neorhizobium-Pararhizobium-Rhizobium	Bacteroidia-Sagropiraceae-Unclassified
Actinobacteria-Micromonosporaceae-Actinocatenispora	Alphaproteobacteria-Rhizobiaceae-Mesorhizobium	Bacteroidia-Sphingobacteriaceae-Arcisibacter
Actinobacteria-Micromonosporaceae-Dactylosporangium	Alphaproteobacteria-Rhizobiaceae-Shinella	Bacteroidia-Sphingobacteriaceae-Mucilaginibacter
Actinobacteria-Micromonosporaceae-Unclassified	Alphaproteobacteria-Rhizobiaceae-Unclassified	Bacteroidia-Sphingobacteriaceae-Pedobacter
Actinobacteria-Mycobacteriaceae-Mycobacterium	Alphaproteobacteria-Rhizobiales Incertae Sedis-Nordella	Bacteroidia-Spirosomaceae-Dyadobacter
Actinobacteria-Nocardiaceae-Nocardia	Alphaproteobacteria-Rhizobiales Incertae Sedis-Phreatobacter	Bacteroidia-Unclassified-Unclassified
Actinobacteria-Nocardiaceae-Unclassified	Alphaproteobacteria-Rhodospirillaceae-Unclassified	Bacteroidia-Weeksellaceae-Chryseobacterium
Actinobacteria-Nocardioidiaceae-Kribbella	Alphaproteobacteria-Rickettsiaceae-Unclassified	Blastocatella_(Subgroup 4)-Blastocatellaceae-JGI 0001001-H03
Actinobacteria-Nocardioidiaceae-Marmoricola	Alphaproteobacteria-SM2D12-Unclassified	Blastocatella_(Subgroup 4)-Blastocatellaceae-Unclassified
Actinobacteria-Nocardioidiaceae-Nocardioides	Alphaproteobacteria-Sphingomonadaceae-Altererythrobacter	Blastocatella_(Subgroup 4)-Pyrimonomadaceae-RB11
Actinobacteria-Pseudonocardiaceae-Actinophytocola	Alphaproteobacteria-Sphingomonadaceae-Elin6055	Blastocatella_(Subgroup 4)-Unclassified-Unclassified
Actinobacteria-Pseudonocardiaceae-Amycolatopsis	Alphaproteobacteria-Sphingomonadaceae-Novosphingobium	Chlamydiae-cvF6-Unclassified
Actinobacteria-Pseudonocardiaceae-Pseudonocardia	Alphaproteobacteria-Sphingomonadaceae-Porphyrabacter	Chlamydiae-Simkaniaceae-Unclassified
Actinobacteria-Pseudonocardiaceae-Unclassified	Alphaproteobacteria-Sphingomonadaceae-Qipengyuania	Chloroflexia-JG30-KF-CM45-Unclassified
Actinobacteria-Streptomyetaceae-Alostreptomycetes	Alphaproteobacteria-Sphingomonadaceae-Sphingosauribaculus	Chloroflexia-Roseiflexaceae-Unclassified
Actinobacteria-Streptomyetaceae-Kitasatospora	Alphaproteobacteria-Sphingomonadaceae-Sphingobium	Chloroflexia-Thermomicrobiaceae-Nitrolancea
Actinobacteria-Streptomyetaceae-Streptomyces	Alphaproteobacteria-Sphingomonadaceae-Sphingomonas	Chthonomonadetes-Chthonomonadaceae-Chthonomonas
Actinobacteria-Streptomyetaceae-Unclassified	Alphaproteobacteria-Sphingomonadaceae-Stakelama	Chthonomonadetes-Unclassified-Unclassified
Actinobacteria-Streptosporangiaceae-Nonomuraea	Alphaproteobacteria-Sphingomonadaceae-Unclassified	Dehalococcoida-Unclassified-Unclassified
Actinobacteria-Thermomonosporaceae-Actinoinformus	Alphaproteobacteria-Unclassified-Unclassified	Deinococci-Deinococcaceae-Deinococcus
Actinobacteria-Thermomonosporaceae-Actinomadura	Alphaproteobacteria-URHD0085-Unclassified	Deltaproteobacteria-0319-6G20-Unclassified
Actinobacteria-Thermomonosporaceae-Spirillospora	Alphaproteobacteria-Xanthobacteraceae-Bradyrhizobium	Deltaproteobacteria-Archangiaceae-Anaeromyxobacter
Actinobacteria-Unclassified-Unclassified	Alphaproteobacteria-Xanthobacteraceae-Nitrobacter	Deltaproteobacteria-Archangiaceae-Archangium
Alphaproteobacteria-Acetobacteraceae-Acidicoccus	Alphaproteobacteria-Xanthobacteraceae-Pseudolabrys	Deltaproteobacteria-Archangiaceae-Unclassified
Alphaproteobacteria-Acetobacteraceae-Rhodospila	Alphaproteobacteria-Xanthobacteraceae-Unclassified	Deltaproteobacteria-bacteriap25-Unclassified
Alphaproteobacteria-Acetobacteraceae-Rhodovastum	Anaerolineae-A4b-Unclassified	Deltaproteobacteria-Bacterioviraceae-Bacteriovorax
Alphaproteobacteria-Acetobacteraceae-Unclassified	Anaerolineae-Anaerolineaceae-Unclassified	Deltaproteobacteria-Bacterioviraceae-Peredibacter
Alphaproteobacteria-bac2nt3-Unclassified	Anaerolineae-Unclassified-Unclassified	Deltaproteobacteria-Bdellovibrionaceae-Bdellovibrio
Alphaproteobacteria-Bejerinckiacae-Methylobacterium	Armatimonadia-Unclassified-Unclassified	Deltaproteobacteria-Bdellovibrionaceae-OM27_clade
Alphaproteobacteria-Caulobacteraceae-Asticcacaulis	Babellae-Unclassified-Unclassified	Deltaproteobacteria-Bifid11-Unclassified
Alphaproteobacteria-Caulobacteraceae-Caulobacter	Bacilli-Alicyclobacillaceae-Turnebacillus	Deltaproteobacteria-Bifid19-Unclassified
Alphaproteobacteria-Caulobacteraceae-Phenyllobacterium	Bacilli-Bacillaceae-Bacillus	Deltaproteobacteria-Desulfarutaceae-Unclassified
Alphaproteobacteria-Caulobacteraceae-Unclassified	Bacilli-Bacillaceae-Unclassified	Deltaproteobacteria-Geobacteraceae-Geobacter
Alphaproteobacteria-Devisiaceae-Arsenicitalea	Bacilli-Paenibacillaceae-Paenibacillus	Deltaproteobacteria-Haliangiaceae-Haliangium
	Bacilli-Paenibacillaceae-Unclassified	Deltaproteobacteria-KD3-10-Unclassified
	Bacilli-Planococcaceae-Chungangia	Deltaproteobacteria-mle1-27-Unclassified
	Bacilli-Planococcaceae-Unclassified	Deltaproteobacteria-MSB-4B10-Unclassified
	Bacilli-Unclassified-Unclassified	Deltaproteobacteria-Myxococcaceae-Unclassified
Bacteroidia-37-13-Unclassified	Bacteroidia-37-13-Unclassified	Deltaproteobacteria-Oligoflexaceae-Unclassified
Bacteroidia-AKYH767-Unclassified	Bacteroidia-AKYH767-Unclassified	Deltaproteobacteria-P30B-42-Unclassified
Bacteroidia-Chitinophagaceae-Chitinophaga	Bacteroidia-Chitinophagaceae-Chitinophaga	Deltaproteobacteria-Phascolystidaceae-Phascolystis
Bacteroidia-Chitinophagaceae-Ferruginibacter	Bacteroidia-Chitinophagaceae-Ferruginibacter	Deltaproteobacteria-Polyangiaceae-Minicystis
Bacteroidia-Chitinophagaceae-Filimonas	Bacteroidia-Chitinophagaceae-Filimonas	Deltaproteobacteria-Polyangiaceae-Pajaroellobacter

Class-Family-Genus continued

■	Deltaproteobacteria-Polyangiaceae-Unclassified	■	Gemmatimonadetes-Gemmatimonadaceae-Gemmatimonas
■	Deltaproteobacteria-Sandaracinaceae-Sandaracinus	■	Gemmatimonadetes-Gemmatimonadaceae-Gemmatirosa
■	Deltaproteobacteria-Sandaracinaceae-Unclassified	■	Gemmatimonadetes-Gemmatimonadaceae-Unclassified
■	Deltaproteobacteria-Unclassified-Unclassified	■	Holophagae-Holophagaceae-Geothrix
■	Elusimicrobia-Unclassified-Unclassified	■	Holophagae-Unclassified-Unclassified
■	Fibrobacteria-Fibrobacteraceae-possible genus 04	■	Ignavibacteria-Unclassified-Unclassified
■	Fibrobacteria-Fibrobacteraceae-Unclassified	■	Ktedonobacteria-Ktedonobacteraceae-HSB OF53-F07
■	Fimbrimonadia-Fimbrimonadaceae-Fimbrimonas	■	Ktedonobacteria-Ktedonobacteraceae-Ktedonobacter
■	Fimbrimonadia-Fimbrimonadaceae-Unclassified	■	Ktedonobacteria-Ktedonobacteraceae-Unclassified
■	Gammaproteobacteria-A21b-Unclassified	■	Ktedonobacteria-Unclassified-Unclassified
■	Gammaproteobacteria-B1-7BS-Unclassified	■	Longimicrobia-Longimicrobiaceae-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Achromobacter	■	Melainabacteria-Unclassified-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Aquincola	■	NC10-Unclassified-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Azohydromonas	■	Nitrososphaeria-Nitrososphaeraceae-Candidatus Nitrososmicus
■	Gammaproteobacteria-Burkholderiaceae-Burkholderia-Caballeronia-Paraburkholderia	■	Nitrososphaeria-Nitrososphaeraceae-Candidatus Nitrososphaera
■	Gammaproteobacteria-Burkholderiaceae-Caenimonas	■	Nitrososphaeria-Nitrososphaeraceae-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Cupriavidus	■	Nitrospira-Nitrospiraceae-Nitrospira
■	Gammaproteobacteria-Burkholderiaceae-Duganella	■	Parcubacteria-Unclassified-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Kinnerella	■	Phycisphaerae-CPla-3 termite group-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Massilia	■	Phycisphaerae-Phycisphaeraceae-SM1A02
■	Gammaproteobacteria-Burkholderiaceae-Mitsuaria	■	Phycisphaerae-Phycisphaeraceae-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Paolibacter	■	Phycisphaerae-Tepidisphaeraceae-Tepidisphaera
■	Gammaproteobacteria-Burkholderiaceae-Piscinibacter	■	Phycisphaerae-Tepidisphaeraceae-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Pseudoduganella	■	Phycisphaerae-Unclassified-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Ralstonia	■	Phycisphaerae-WD2101 soil group-Unclassified
■	Gammaproteobacteria-Burkholderiaceae-Ramlibacter	■	Planctomycetacia-Gemmataceae-Fimbriglobus
■	Gammaproteobacteria-Burkholderiaceae-Roseateles	■	Planctomycetacia-Gemmataceae-Gemmata
■	Gammaproteobacteria-Burkholderiaceae-Unclassified	■	Planctomycetacia-Gemmataceae-Unclassified
■	Gammaproteobacteria-Diploricetaceae-Aquicella	■	Planctomycetacia-Gemmataceae-Zavarzinella
■	Gammaproteobacteria-Diploricetaceae-Unclassified	■	Planctomycetacia-Isosphaeraceae-Singulisphaera
■	Gammaproteobacteria-Enterobacteriaceae-Unclassified	■	Planctomycetacia-Pirellulaceae-Pirellula
■	Gammaproteobacteria-Legionellaceae-Legionella	■	Planctomycetacia-Pirellulaceae-Unclassified
■	Gammaproteobacteria-Methylophilaceae-Methylophilus	■	Planctomycetacia-Rubinisphaeraceae-Planctomicrobium
■	Gammaproteobacteria-Moraxellaceae-Cavicella	■	Planctomycetacia-Rubinisphaeraceae-SH-PL14
■	Gammaproteobacteria-Moraxellaceae-Unclassified	■	Planctomycetacia-Schlesneriaceae-Schlesneria
■	Gammaproteobacteria-Nitrosomonadaceae-Elin6067	■	Planctomycetacia-Unclassified-Unclassified
■	Gammaproteobacteria-Nitrosomonadaceae-MND1	■	Saccharimonadia-Saccharimonadaceae-Unclassified
■	Gammaproteobacteria-Nitrosomonadaceae-Unclassified	■	Saccharimonadia-Unclassified-Unclassified
■	Gammaproteobacteria-Pseudomonadaceae-Pseudomonas	■	Spirochaetia-Spirochaetaceae-Salinispira
■	Gammaproteobacteria-Rhodanobacteraceae-Dokdonella	■	Spirochaetia-Spirochaetaceae-Spirochaeta 2
■	Gammaproteobacteria-Rhodanobacteraceae-Dyella	■	Subgroup_6-Unknown Family-Vicinambacter
■	Gammaproteobacteria-Rhodanobacteraceae-Frateuria	■	Thermoanaerobaculia-Thermoanaerobaculaceae-Subgroup 10
■	Gammaproteobacteria-Rhodanobacteraceae-Fulvimonas	■	Thermoleophilia-67-14-Unclassified
■	Gammaproteobacteria-Rhodanobacteraceae-Luteibacter	■	Thermoleophilia-Gallaceae-Gallia
■	Gammaproteobacteria-Rhodanobacteraceae-Rhodanobacter	■	Thermoleophilia-Solirubrobacteraceae-Conexibacter
■	Gammaproteobacteria-Rhodanobacteraceae-Tahibacter	■	Thermoleophilia-Solirubrobacteraceae-Parviterribacter
■	Gammaproteobacteria-Rhodanobacteraceae-Unclassified	■	Thermoleophilia-Solirubrobacteraceae-Solirubrobacter
■	Gammaproteobacteria-Rhodocyclaceae-Unclassified	■	Thermoleophilia-Solirubrobacteraceae-Unclassified
■	Gammaproteobacteria-SC-I-84-Unclassified	■	Thermoleophilia-Unclassified-Unclassified
■	Gammaproteobacteria-Solimonadaceae-Alkanibacter	■	Verrucomicrobiae-Chthoniobacteraceae-Candidatus Udaebacter
■	Gammaproteobacteria-Solimonadaceae-Fontimonas	■	Verrucomicrobiae-Chthoniobacteraceae-Chthoniobacter
■	Gammaproteobacteria-Solimonadaceae-Nevskia	■	Verrucomicrobiae-Chthoniobacteraceae-LD29
■	Gammaproteobacteria-Solimonadaceae-Panacagrimonas	■	Verrucomicrobiae-Chthoniobacteraceae-Unclassified
■	Gammaproteobacteria-Solimonadaceae-Polycyclovorans	■	Verrucomicrobiae-Methylacidiphilaceae-Unclassified
■	Gammaproteobacteria-Steroidobacteraceae-Povalibacter	■	Verrucomicrobiae-Opitutaceae-Lacunisphaera
■	Gammaproteobacteria-Steroidobacteraceae-Steroidobacter	■	Verrucomicrobiae-Opitutaceae-Opitutus
■	Gammaproteobacteria-Steroidobacteraceae-Unclassified	■	Verrucomicrobiae-Opitutaceae-Unclassified
■	Gammaproteobacteria-TRA3-20-Unclassified	■	Verrucomicrobiae-Pedospaeraceae-ADurb.Bin063-1
■	Gammaproteobacteria-Unclassified-Unclassified	■	Verrucomicrobiae-Pedospaeraceae-Pedospaera
■	Gammaproteobacteria-Unknown_Family-Acidibacter	■	Verrucomicrobiae-Pedospaeraceae-Unclassified
■	Gammaproteobacteria-Xanthomonadaceae-Arenimonas	■	Verrucomicrobiae-Terrimicrobiaceae-Terrimicrobium
■	Gammaproteobacteria-Xanthomonadaceae-Luteimonas	■	Verrucomicrobiae-Verrucomicrobiaceae-Prosthecobacter
■	Gammaproteobacteria-Xanthomonadaceae-Lysobacter	■	Verrucomicrobiae-Verrucomicrobiaceae-Unclassified
■	Gammaproteobacteria-Xanthomonadaceae-Thermomonas	■	Verrucomicrobiae-Xiphinematobacteraceae-Candidatus Xiphinematobacter
■	Gammaproteobacteria-Xanthomonadaceae-Unclassified		

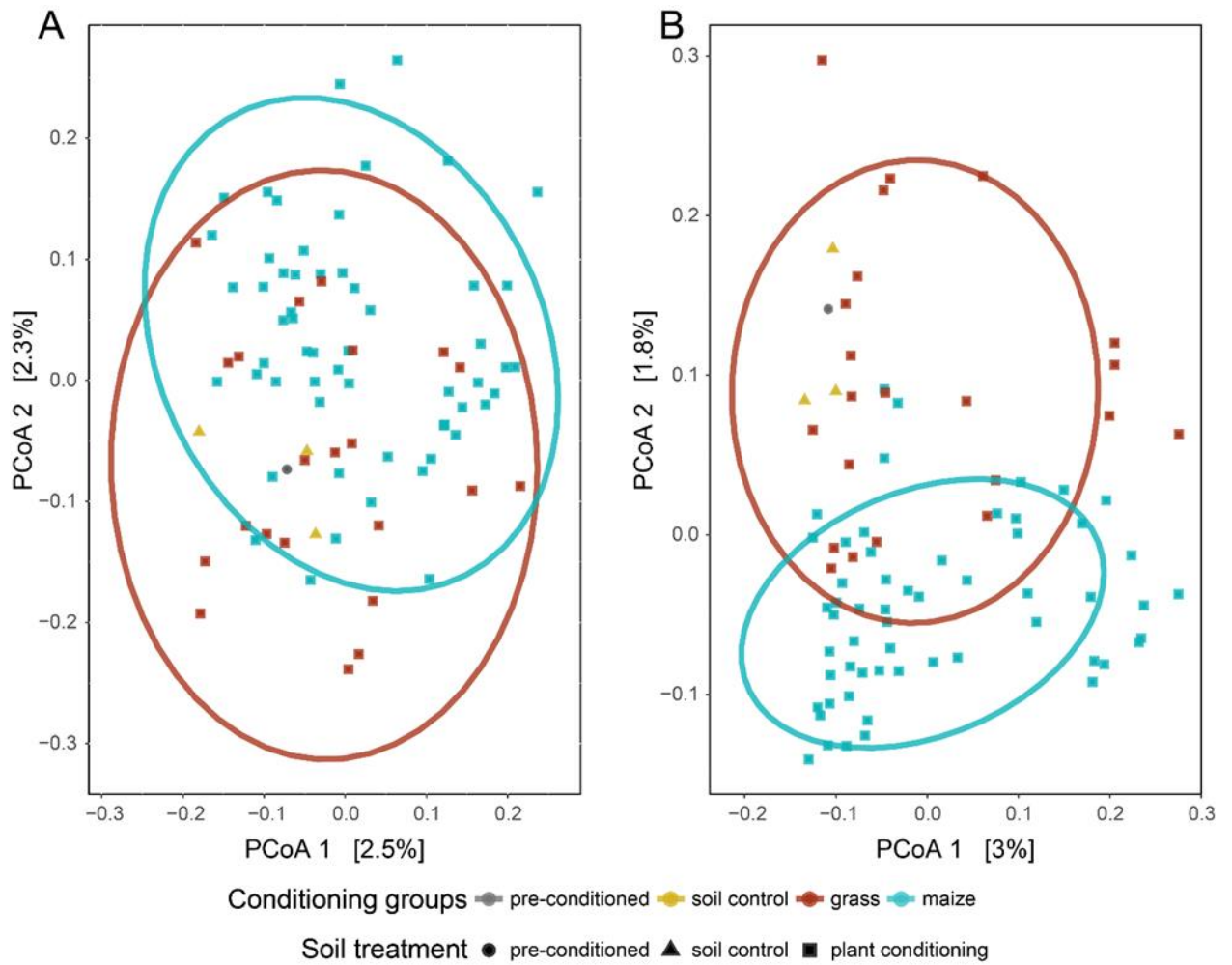


Figure S2. Variation in ASV microbial community composition between soil conditioning types. Principle coordinate analysis (PCoA) using a Bray-Curtis (abundance-weighted) (A) and Jaccard (presence-absence) (B) dissimilarity distance indices of amplicon sequence variants (ASVs) between soil conditioning treatments. Points correspond to samples from individual pots (square points) conditioned by prairie grasses (red) or maize genotypes (aqua), from pre-conditioned soil (gray circles), and from negative control soil (yellow triangles). Colors and symbols indicate conditioning functional groups and soil treatments, respectively. The soil treatments include pre-conditioned soil samples (grey circles) and unconditioned control pots that were not conditioned by plants (yellow triangles). The conditioning functional groups are indicated by square points and were colored so the prairie grass spp. group (*A. gerardii* and *T. dactyloides*) coordinated with a red-orange hue while the maize genotypes groups (*Z. mays* ssp. *parviglumis*, *Z. mays* ssp. *mays* b58, B73-wt, B73-rth3, and HP301) coordinated with a light blue hue. Ellipses represent the 95% confidence ellipse based on the standard deviation around the centroid for conditioning treatments with more than 5 biological replicates.

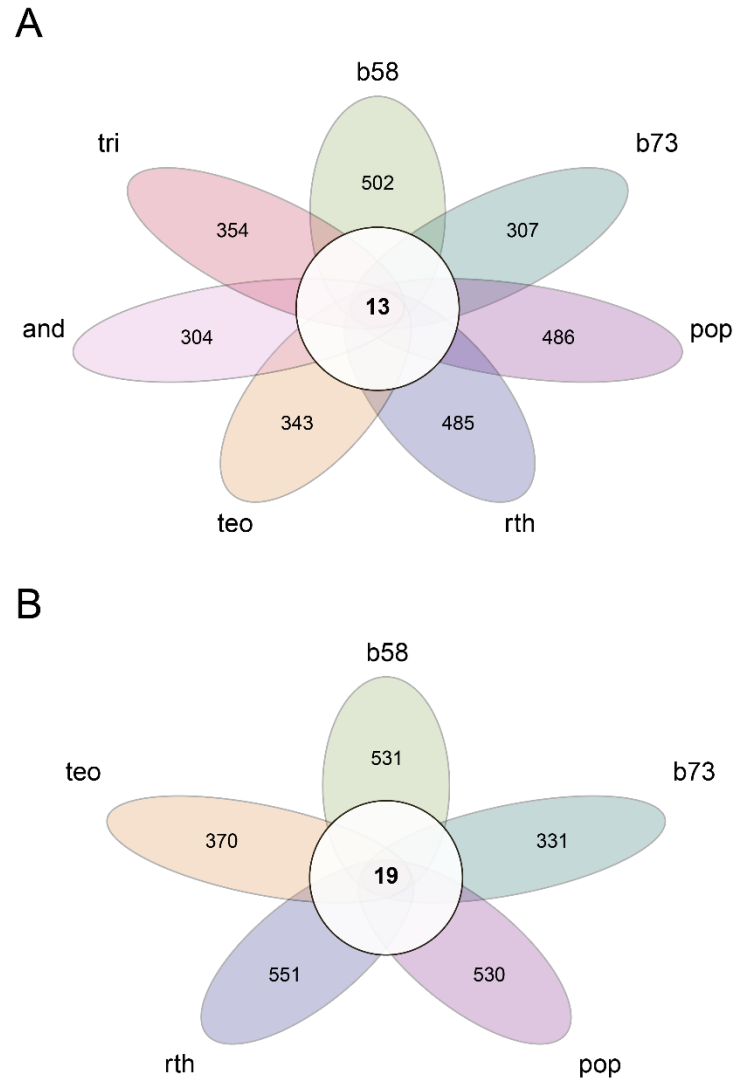


Figure S3. Shared and unique microbial taxa in maize and Poaceae rhizobiomes. Petal plots of amplicon sequence variants (ASV) of A) all conditioning genotypes included in this study (*A. gerardii*, *T. dactyloides*, *Z. mays* ssp. *parviglumis*, *Z. mays* ssp. *mays* b58, B73-wt, B73-rth3, and HP301) and B) the maize conditioning genotypes (*Z. mays* ssp. *parviglumis*, *Z. mays* ssp. *mays* b58, B73-wt, B73-rth3, and HP301). The number within each ellipse represents the number of ASVs unique to each conditioning genotype within each analysis, along with a centroid including the total shared ASVs across conditioning genotypes in each analysis. The microbiota of all rhizosphere conditioning genotype communities included 3592 ASVs and the maize conditioning genotype microbiota included 2890 ASVs.

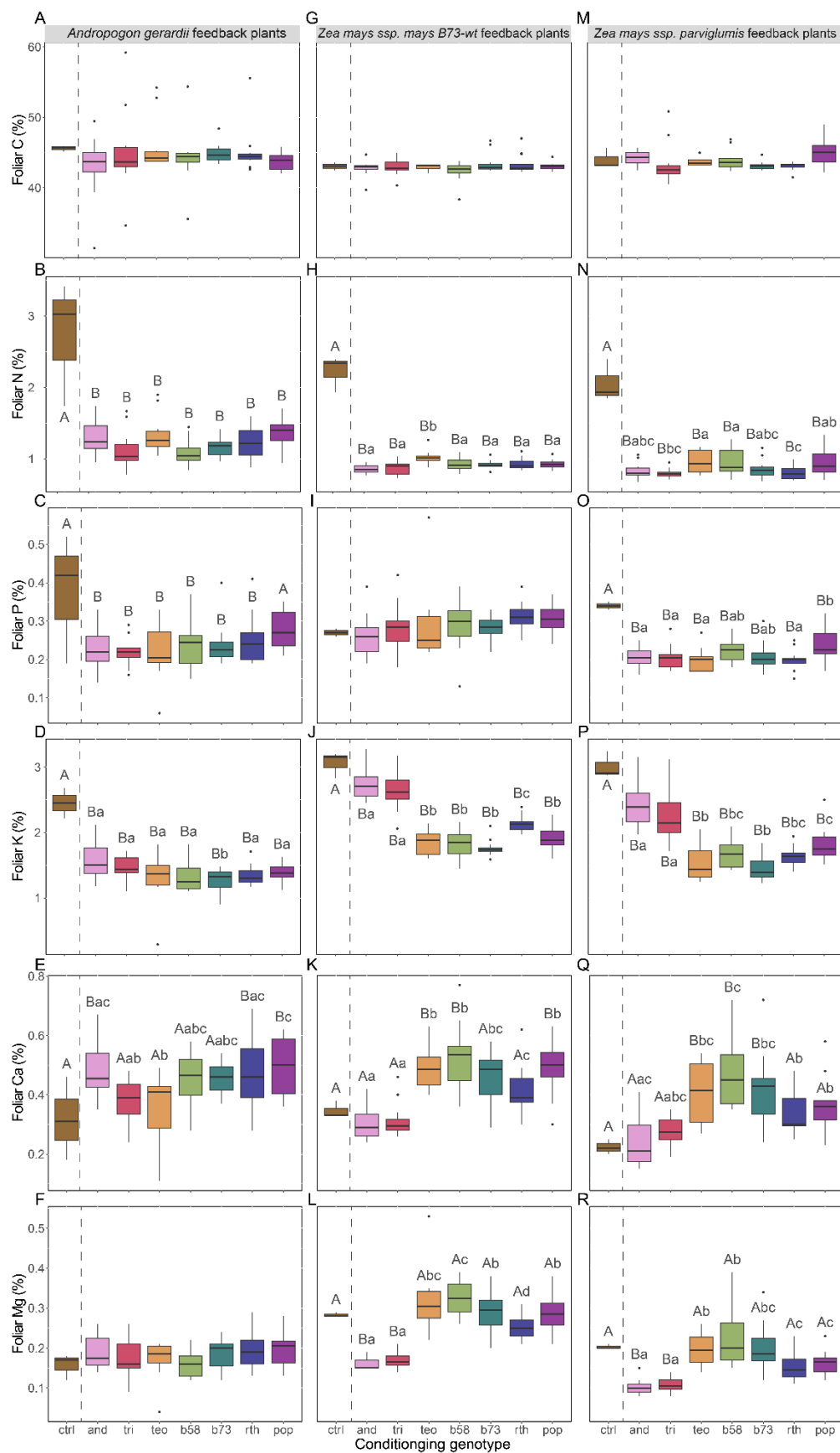


Figure S4. Variation in foliar nutrient concentrations of feedback plants among conditioning genotypes and controls. Foliar nutrient concentrations were quantified for conditioning genotype effect using type III analysis of variance (ANOVAs) of separate linear mixed models for leaf carbon (A, G, and M), nitrogen (B, H, and N), phosphorus (C, I, and O), potassium (D, J, and P), calcium (E, K, and Q), and magnesium (F, L, and R) in *A. gerardii* (A-F), maize *B73-wt* (G-L), and teosinte feedback plants (M-R). Colors indicate conditioning genotypes and other soil treatments. The leftmost category includes soil samples from unconditioned control pots that were not conditioned by plants but did have feedback plants growing in them (brown, “ctrl”). Thus, the difference between the plant-conditioned versus the unconditioned soils reflects the effects of plant conditioning. The prairie grass species are pink (*Andropogon gerardii*; ‘and’) and red (*Tripsacum dactyloides*; ‘tri’). Maize genotypes of *Z. mays* ssp. *parviglumis* are light orange (teosinte, ‘teo’) and the *Z. mays* ssp. *mays* genotypes are in cooler colors: *b58* is light green, *B73-wt* is dark green, *B73-rth3* (‘rth’) is dark blue, and *HP301* (‘pop’) is purple. Lowercase letters indicate significant differences between conditioning genotypes and uppercase letters indicate significant differences between conditioning and negative controls, from *post-hoc* pairwise comparisons using Benjamini-Hochberg correction. Refer to Table 3 for omnibus tests of conditioning genotype effects.

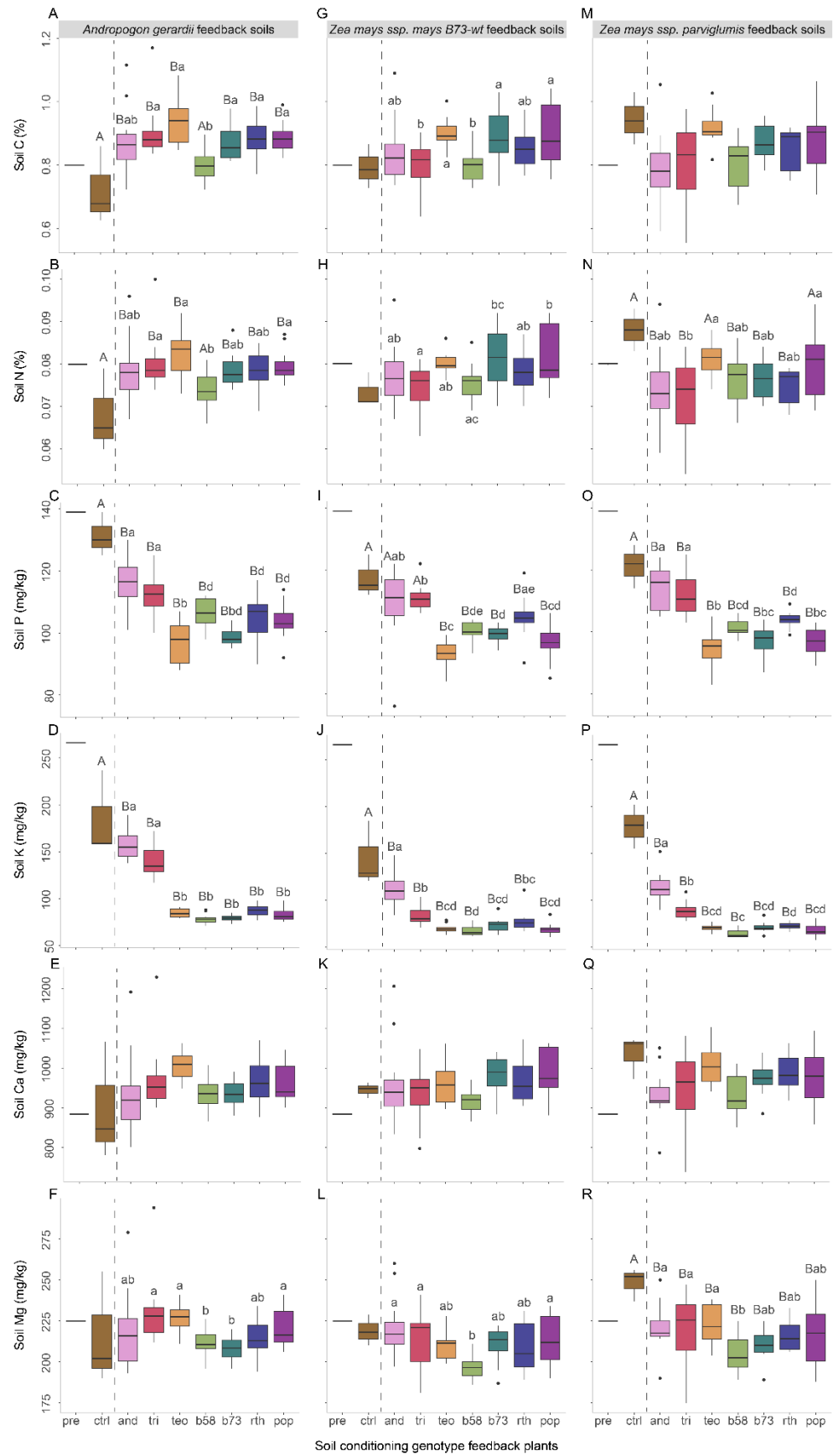


Figure S5. Variation in soil nutrient concentrations in pots of feedback plants among conditioning genotypes, preconditioned soils, and unconditioned control soils. Differences in total soil nutrient concentrations were quantified for conditioning genotype effect using type III analysis of variance (ANOVAs) of separate linear mixed models for soil carbon (A, G, and M), nitrogen (B, H, and N), phosphorus (C, I, and O), potassium (D, J, and P), calcium (E, K, and Q), and magnesium (F, L, and R) in *A. gerardii* (A-F), maize *B73-wt* (G-L), and teosinte feedback plants (M-R). The leftmost two categories are soil samples from a pre-conditioned soil sample (line, “pre”) and from unconditioned control pots that were not conditioned by plants but did have feedback plants growing in them (brown, “ctrl”). Thus, the difference between the plant-conditioned versus the unconditioned soils reflects the effects of plant conditioning. Colors indicate conditioning genotypes and other soil conditioning treatments. The prairie grass species are pink (*Andropogon gerardii*; ‘and’) and red (*Tripsacum dactyloides*; ‘tri’). Maize genotypes of *Z. mays* ssp. *parviglumis* are light orange (teosinte, ‘teo’) and the *Z. mays* ssp. *mays* genotypes are in cooler colors: *b58* is light green, *B73-wt* is dark green, *B73-rth3* (‘rth’) is dark blue, and *HP301* (‘pop’) is purple. Lowercase letters indicate significant differences between conditioning genotypes and uppercase letters indicate significant differences between conditioning and negative controls, from *post-hoc* pairwise comparisons using Benjamini-Hochberg correction. Refer to Table 3 for omnibus tests of conditioning genotype effects on final soil nutrient concentrations.

Appendix S3: Sample analysis code

The R programming code below provides the main code used for each research question.

```
#R version 4.1.2 (2021-11-01); RStudio version 2022-07-01+554

#Packages used for phenotypic analysis
library(vegan)
library(lme4)
library(lmerTest)

#Packages used for microbial analysis
library(tidyverse)
library(phyloseq)
library(factoextra)
library(ranacapa)
library(microbiome)

#packages used for visualization
library(ggplot2)

#datasets provided:

# filtered relative abundances of ASV table (microASV), metadata (microMET),
and taxonomic classifications (microTAX) in a phyloseq object:

#microASV shows relative abundances of each ASV as separate columns, a
biological replicate (pot)as rows, with numeric values as entries. Sample
dataset in comma delimited format:

#microMET has corresponding rows of biological replicates as rows, with each
metadata variable as entries in separate columns, including cond_gt
(conditioning genotype), cond_gt_group, soil_trt (including preconditioned and
negative control soils), with character class descriptions as entries

#microTAX is taxonomy table with ASVs as separate rows and phylum, kingdom,
class, order, family, genus, species in columns, with character class
descriptions as entries

microdat = phyloseq(microASV, microMET, microTAX)

# phenotypic traits data frame, including separate variables for plant
ecophysiological traits, foliar nutrient concentrations, and final soil
nutrient concentrations in columns, biological replicate (pot-level samples) as
rows, with numeric values as entries:

phenodat

#Q1 analysis: rhizosphere community structure
```

```

#taxonomic bar plots:
a <- microdat %>%
  tax_glom(taxrank = "Class", NArm=F) %>%
  transform_sample_counts(function(x) {x/sum(x)} ) %>%
  psmelt() %>%
  arrange(Class)

b = ggplot(a, aes(x = cond_gt, y = Abundance, fill = group)) +
  xlab("Conditioning genotype") +
  geom_bar(position = "fill", stat = "identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1), panel.background
        = element_rect(fill = "white"))

b

#plot composition of rhizosphere conditioning genotype group, initials, and
controls:

c <- phyloseq::ordinate(microdat, method = "PCoA", distance = "jaccard", binary
= T)

d <- plot_ordination(microdat, c, color = "cond_gt_group", shape = "soil_trt")
+
  geom_point(size = 3, alpha = 0.8) +
  stat_ellipse(inherit.aes = TRUE, level = 0.8, size = 2, alpha = 0.8) +
  theme(#panel.grid = element_line(color = 'gray', linetype = 2, size =
0.1),
  panel.background = element_rect(color = 'black', fill = 'transparent'),
  legend.key = element_rect(fill = 'transparent'))

d

#perMANOVA analysis for conditioning genotype nested within conditioning
genotype group:

dat1 <- cbind(microASV, microMET)

e <- adonis(microASV ~ (cond_gt_group/cond_gt),
  data = dat1, permutations=999, method = "jaccard", binary = T)

e$aov.tab

# alpha diversity and ANOVA:

sample_data(microdat)$alpha<- microbiome::alpha(microdat, index = "all")
alphadat <- data.frame(as(sample_dat(microdat), "matrix"))
alphadat $obsrich = as.numeric(alphadat$alpha.obsrich)
anova(lmer(obsrich~cond_gt + (1|bio_replicate), data = alphadat))
summary(lmer(obsrich~cond_gt + (1|bio_replicate), data = alphadat))

```

```

#shared ASVs:

mecodat<- phyloseq2meco(microdat) #microeco package file type conversion
fit <- meco_dataset$merge_samples(use_group = "cond_gt_group")
fit.venn <- trans_venn$new(f.it, ratio = "segratio")
fit.venn$plot_venn()

fit2 <- mecodat$merge_samples(use_group = "cond_gt")
fit2_venn <- trans_venn$new(fit2)

fit_petal <- fit2_venn$plot_venn(petal_plot = TRUE, petal_center_size = 50,
petal_r = 1.5, petal_a = 3, petal_move_xy = 3.8)

#indicator analysis:
abund = microASV
gt = microMET$cond_gt
inv = multipatt(abund, gt, func = "r.g", control = how(nperm=1999))
summary(inv)
inv$sign

#Q2.1 and 2.2 analyses: conditioning gt /group influence on plant performance
and phenotypes

#see Dryad dataset link for more information on phenotypic trait calculations
#omnibus tests of each growth rate for each feedback genotype
landmet = subset.data.frame(dat_min2, feedback_sp=="and")
m1 = lmer( Total_Biomass_Growth ~ cond_ gt + (1| cond_gt), data=landmet)
summary(m2)

m2 = lmer( Total_Biomass_Growth ~ cond_ gt + (1|cond_gt_group:cond_gt),
data=landmet)

summary(m2) #can replace "m2" with "m1" to see results for separate model
anova(m2)

#phenotypic traits and foliar nutrient concentrations add a control for initial
biomass to models within each feedback genotype:

n1 = lmer(rlr ~ cond gt + initial_biomass + (1|cond_gt_group:cond_gt),
data=landmet)

n2 = lmer(rlr ~ cond gt + initial_biomass + (1|cond_gt_group:cond_gt),
data=landmet)

summary(n2)

anova(n2)

#for all omnibus tests:

```

```

p.adjust(p, method = "BH", n = 23) # p = p value resulting from anova(m); n
argument is number of multiple comparisons

#for significant p-adjusted values from omnibus tests:

pairwise.t.test(landmet$rlr, landmet$cond_gt, p.adjust.method = "BH",
alternative = "two.sided")

o<- ggplot(landmet, aes(x = cond_gt, y = rlr, fill = cond_gt, )) +
  geom_boxplot(position=position_dodge(width=1), show.legend = F) +
  theme(axis.text.y = element_text(angle = 90 ),
text=element_text(size=21), plot.background = element_rect(fill =
"white"), panel.background = element_rect(fill = "white"), axis.line.x =
element_line(color = "black"), axis.line.y = element_line(color =
"black"))

o

#Q2.3 analysis: conditioning gt and feedback gt influence on final soil
nutrient concentrations

#omnibus tests for each final soil nutrient for each feedback genotype:

anova(lmer(soil_perc_C ~cond_gt + initial_biomass + (1|bio_rep), data =
phenodat[which(phenodat$feedback_gt == "b73"),]))

#subset for pairwise comparisons

j = subset.data.frame(phenodat, feedback_gt=="b73")

pairwise.t.test(j$soil_perc_C, j$cond_gt, p.adjust.method = "BH")

#NMDS plot of final soil nutrient concentrations across conditioning genotypes,
split by feedback genotype

f = pheno_dat[,c("soil_perc_C", "soil_perc_N", "soil_P_mgperkg",
"soil_K_mgperkg", "soil_Ca_mgperkg", "soil_Mg_mgperkg")] #subsetting soil
nutrient concentrations

g = metaMDS(f, distance = "gower", k=4, trymax = 1000, scale = TRUE)

stressplot(g)

h<- cbind(phenodat[,c("feedback_ID", "feedback_gt", "cond_gt", "soil_trt",
"cond_gt_only", "cond_gt_group")], data.frame(g$points) #adding metadata to
points produced by NMDS

i<-ggplot(h, aes(x=MDS1, y=MDS4, col = cond_gt_only, shape = cond_gt_group))+
  geom_point(alpha = 0.8, size = 3) +
  facet_wrap(~feedback_gt) +
  stat_ellipse(linewidth = 2, inherit.aes = TRUE) +
  theme(panel.background = element_rect(color = 'black',
'transparent'),
  legend.key = element_rect(fill = 'transparent'))

```

i