Plant property regulates soil bacterial community structure under altered precipitation regimes in a semi-arid desert grassland, China postprint

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Abstract

Variations in precipitation profoundly impact soil carbon cycling and organic matter decomposition. Soil bacteria play crucial roles in regulating these ecological processes and are highly vulnerable to altered precipitation regimes. Investigating how precipitation changes affect soil bacterial community structure can provide novel insights into the potential consequences for soil carbon cycling and carbon storage in grassland ecosystems. Therefore, we examined soil bacterial community structure under a precipitation manipulation experiment in a semi-arid desert grassland on the Chinese Loess Plateau. Five precipitation levels were established: control, 40% and 20% precipitation reduction, and 20% and 40% precipitation increase (designated CK, DP40, DP20, IP20, and IP40). Results showed that soil bacterial alpha diversity and rare bacterial taxa changed significantly with altered precipitation, whereas dominant bacteria and beta diversity remained unchanged, likely reflecting the ecological strategies of soil bacteria.

Full Text

Preamble

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Plant Property Regulates Soil Bacterial Community Structure Under Altered Precipitation Regimes in a Semi-Arid Desert Grassland, China

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Abstract: Variations in precipitation profoundly impact soil carbon cycling and organic matter decomposition. Soil bacteria play crucial roles in regulating these ecological processes and are highly vulnerable to altered precipitation regimes. Investigating how precipitation changes affect soil bacterial community structure can provide novel insights into the potential consequences for soil carbon cycling and carbon storage in grassland ecosystems. Therefore, we examined soil bacterial community structure under a precipitation manipulation experiment in a semi-arid desert grassland on the Chinese Loess Plateau. Five precipitation levels were established: control, 40% and 20% precipitation reduction, and 20% and 40% precipitation increase (designated CK, DP40, DP20, IP20, and IP40). Results showed that soil bacterial alpha diversity and rare bacterial taxa changed significantly with altered precipitation, whereas dominant bacteria and beta diversity remained unchanged, likely reflecting the ecological strategies of soil bacteria.

Linear discriminant analysis effect size (LEfSe) revealed that the primary response patterns of soil bacteria to altered precipitation involved resource-limited and drought-tolerant populations. Additionally, increased precipitation strongly promoted interspecies competition, while decreased precipitation facilitated interspecies cooperation. These shifts in species interactions may drive different distribution patterns of bacterial populations under varying precipitation conditions. Structural equation modeling (SEM) indicated that changes in plant growth characteristics, rather than soil properties, were the primary drivers of soil bacterial community composition under altered precipitation. In conclusion, our results demonstrate that in desert grassland ecosystems, rare bacterial taxa are more sensitive to precipitation changes than dominant taxa, possibly due to bacterial ecological strategies, species interactions, and precipitation-induced variations in plant growth characteristics.

Keywords: plant-microbe interactions; bacterial community diversity; bacterial community composition; bacterial interactions; precipitation gradients

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1 Introduction

Global warming affects the global hydrological cycle, leading to shifts in precipitation regimes, including increased inter-annual precipitation variability and more frequent extreme precipitation events [?, ?]. Arid and semi-arid regions, characterized by low precipitation and limited nutrients [?], are particularly sensitive to these changes. Precipitation variations significantly influence soil carbon cycling and organic matter decomposition in semi-arid grasslands [?, ?]. Soil microorganisms are key regulators of these ecosystem processes [?, ?] and are highly susceptible to abiotic and biotic changes induced by altered precipitation [?, ?, ?, ?]. Consequently, precipitation-driven changes in soil microbes can affect soil carbon cycling and regulate carbon storage through organic carbon decomposition and heterotrophic respiration [?, ?]. Understanding how precipitation changes influence soil microbial community structure is therefore essential for predicting impacts on soil carbon dynamics and storage.

Soil bacteria are more sensitive to precipitation changes than fungi [?] because bacterial movement and substrate diffusion are constrained by soil moisture fluctuations [?]. Additionally, bacteria constitute the largest proportion of soil microorganisms [?]. Previous studies have identified Actinobacteria, Acidobacteria, and Proteobacteria as dominant soil bacterial phyla in grasslands under altered precipitation [?, ?, ?, ?]. However, the sensitivity of dominant versus rare bacterial taxa to precipitation changes remains inconsistent. Some studies report significant effects on dominant phyla [?, ?], while others find that only rare phyla respond significantly [?, ?]. These discrepancies may reflect ecosystem-specific conditions, bacterial survival strategies, or adaptive capacity to precipitation changes.

High-throughput sequencing has revealed diverse responses of soil microbial diversity to precipitation. Increased precipitation improves soil moisture, promoting bacterial diversity in desert steppes [?, ?], whereas precipitation reduction decreases diversity [?]. However, some desert steppe studies show no significant changes [?, ?], likely due to microbial survival strategies. For instance, bacterial diversity increased under drought in soils with historical drought exposure [?], confirming that survival strategies drive diversity changes under altered precipitation. These inconsistent results likely stem from ecosystem background, precipitation history, or bacterial adaptive strategies [?].

Precipitation changes affect soil microbial communities by altering plant growth characteristics and soil physicochemical properties [?, ?]. First, plant species changes enhance environmental heterogeneity through variations in residue quantity and quality (e.g., root exudates, litter) and nutrient availability, thereby shaping microbial communities [?]. While some studies identify plant diversity as a key driver of bacterial communities [?, ?], others find no significant effects [?]. Aboveground biomass (AGB), as a major resource input, influences bacterial composition in SEM analyses [?]. Second, precipitation directly regulates bacterial communities through soil properties like water content (SWC), total phosphorus (TP), soil organic carbon (SOC), and pH [?, ?, ?]. Increased precipitation generally enhances nutrient availability, promoting copiotrophic growth and bacterial diversity [?]. However, SWC effects on bacterial communities vary across ecosystems [?, ?]. Few studies have examined these mechanisms in the fragile ecosystems of Northwest China [?], highlighting the need for deeper understanding to predict climate change feedbacks on soil carbon cycling in desert grasslands.

To assess potential impacts of altered precipitation on soil bacterial communities in desert grasslands of the northwestern Chinese Loess Plateau, we conducted a field manipulation experiment with five precipitation gradients. Our hypotheses were: (1) precipitation changes significantly affect soil bacterial community diversity and composition, and (2) these effects are mediated through changes in plant and soil properties.

2.1 Study Area

This study was conducted at the Gaolan Experiment Station for Ecology and Agriculture Research (36°13″N, 103°47″E; 1780 m a.s.l.), Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, located in the northwestern Chinese Loess Plateau. The climate is drought-prone, semi-arid, and continental, with mean annual precipitation of 263 mm concentrated in summer (May–September). Mean annual temperature is 8.4°C, ranging from −9.1°C in January to 20.7°C in July [?]. Mean annual evaporation is 1786.0 mm. Average SOC and total nitrogen (TN) are 0.8% and 0.1%, respectively, with soil pH of 8.5 [?]. The soil is classified as Haplic Calcisol, developed from wind-accumulated loess parent material with uniform silt loam texture [?]. Vegetation is typical desert steppe dominated by *Ajania fruticulosa* (Gramineae), accompanied by *Peganum harmala* L. (Zygophyllaceae), *Zygophyllum mucronatum* Maxim. (Zygophyllaceae), *Artemisia capillaris* Thunb. (Compositae), *Cleistogenes squarrosa* (Trin.) Keng (Gramineae), and *Salsola ruthenica* Iljin (Chenopodiaceae).

2.2 Experimental Design

Based on 50-year precipitation variability (−41% to +40%), we established a randomized complete block design with five precipitation gradients: 40% and 20% reduction (DP40, DP20), natural precipitation as control (CK), and 20% and 40% increase (IP20, IP40). Precipitation timing and frequency were held constant. Three replicate plots (2.5 m × 2.5 m) were established in a relatively homogeneous grassland area. Manipulations were conducted from May to September in 2013, 2014, and 2015.

Rainout shelters reduced precipitation by 20% and 40% for drought treatments. Shelters consisted of steel frames with transparent acrylic bands (V-shaped, 10 cm wide) covering 20% or 40% of plot area, with average height of 0.5 m. Gutters channeled intercepted water to enclosed containers. Acrylic provides higher light transmittance than plastic or PVC, minimizing photosynthetic active radiation interception. Side openings maximized air flow and minimized temperature and humidity artifacts. Intercepted water was manually applied to corresponding increased precipitation plots (IP20, IP40) within 8 h of each event.

2.3 Plant Community Investigation

Plant species composition was recorded in a central 1 m × 1 m subplot in each plot. Species richness, density, coverage, and height were measured monthly from late May to late September 2019. Richness was calculated as species count per subplot. Density was the sum of individual plants. Coverage was estimated using a 1 m × 1 m frame with 100 grids. Height was averaged across individuals.

Aboveground biomass (AGB) was harvested at peak biomass (early September 2019). All plants were clipped to soil surface by species in two random 0.5 m × 0.5 m subplots per plot, dried at 65°C for 48 h, and weighed (g/m^2). Community AGB was the sum across species. Plant community diversity was calculated using Shannon's index (H′):

$$H' = -\sum_{i=1}^{S} P_i \ln(P_i)$$

where P_i is the proportion of individuals of species i and S is total species number.

2.4 Soil Sampling and Property Analysis

In August 2019, three soil cores (5 cm diameter, 0–10 cm depth) were collected along plot diagonals and composited per plot. Samples were placed on ice, transported to the laboratory, sieved (2 mm), and split: half air-dried for physicochemical analysis, half stored at −80°C for DNA extraction and microbial biomass carbon (MBC) analysis.

SWC was determined by oven-drying. MBC was measured via fumigation-extraction [?]. SOC, TN, and TP were analyzed by UT-1810PC spectrophotometry, Kjeldahl digestion, and $K_2Cr_2O_7$-H_2SO_4 oxidation, respectively [?]. Soil available phosphorus (SAP) was measured by the Bray method [?]. Soil available nitrogen (SAN) was analyzed by flow analyzer (Skalar 8505). Soil available potassium (SAK) was determined by ammonium acetate extraction and flame spectrophotometry [?]. Soil pH and electrical conductivity (EC) were measured at 1:2.5 soil:water ratio [?].

2.5 Analysis of Soil Microbial Community

Microbial genomic DNA was extracted from replicate samples (n=3) using the MP FastDNA SPIN Kit following manufacturer instructions. DNA concentration and purity were assessed via NanoDrop 2000 UV-vis spectrophotometer. The V3-V4 hypervariable region of bacterial 16S rRNA gene was amplified using 338F/806R primers. PCR amplification followed [?], and amplicons were sequenced on the Illumina MiSeq platform (Majorbio Bio-Pharm Technology, Shanghai). Mean sequencing depth in 2019 was 43,705 clean reads (range: 32,794–54,938). Sequence data are archived in NCBI SRA (accession: SRP405290).

Paired reads were merged using FLASH v.1.2.7 [?]. Sequences were analyzed in QIIME [?] and UPARSE v.7.1 [?]. Operational taxonomic units (OTUs) were clustered at 97% similarity [?]. Taxonomy was assigned using RDP Classifier v.2.2 [?] against the 16S rRNA database (confidence threshold: 0.7).

2.6 Statistical Analysis

One-way ANOVA followed by least significant difference (LSD) test assessed differences in plant characteristics (species richness, Shannon's index, coverage, density, height, AGB), soil properties (SWC, MBC, SOC, TN, TP, SAN, SAP, SAK, pH, EC), and bacterial diversity across treatments. LEfSe identified statistically and biologically significant differences in bacterial composition at phylum through genus levels. Principal coordinates analysis (PCoA) based on weighted UniFrac distance evaluated compositional variation, with significance tested by ANOSIM [?].

Network analysis examined OTU interactions. To avoid spurious correlations, only the top 50 most abundant OTUs were included [?]. Spearman's correlation (coefficient >0.5, P<0.05) defined robust correlations. Cytoscape v.3.5.0 visualized networks and calculated topological properties (nodes, edges, average degree, average distance). Spearman's correlation also linked bacterial diversity/composition with plant and soil properties. Structural equation modeling (SEM) in Amos v.22.0 assessed direct and indirect precipitation effects. Principal component analysis (PCA) reduced plant and soil property variables before SEM. Models were fitted by maximum likelihood and simplified by removing non-significant paths. Model fit was evaluated using non-significant ^{2} test, RMSEA, and goodness-of-fit index (GFI).

3.1 Variation in Plant Communities and Soil Properties Under Altered Precipitation

Plant AGB, coverage, density, and height increased significantly with precipitation ($P<0.05$, Table 1). IP40 treatment significantly increased AGB compared to DP20. DP40 coverage was significantly lower than IP20. DP40 significantly reduced plant height and density compared to CK and increased precipitation treatments. Species richness and Shannon's diversity trended upward with precipitation ($P>0.05$, Table 1).

SWC, MBC, SOC, TN, TP, SAN, and pH were unaffected by precipitation treatments ($P>0.05$), while SAP, SAK, and EC changed significantly ($P<0.05$, Table 1). SAP and EC increased with decreasing precipitation, peaking under DP40. SAK was significantly higher under IP40 than IP20. SWC, MBC, and SOC reached maximum values under IP40 ($P>0.05$). pH was highest under CK ($P>0.05$), while TN, TP, and SAN peaked under DP40 ($P>0.05$, Table 1).

3.2.1 Changes in Soil Bacterial Community Diversity

Precipitation treatments significantly affected bacterial alpha diversity indices (Fig. 1a–d [Figure 1: see original paper]). ACE index under IP20 was significantly higher than under DP40 ($P<0.05$). Shannon's index increased significantly across all precipitation treatments compared to CK ($P<0.05$). Both decreased and increased precipitation significantly elevated the Smith-Wilson index relative to CK, with DP40 showing the highest value ($P<0.05$).

PCoA of bacterial beta diversity showed that the first two axes explained 34.15% and 28.43% of variance, respectively (Fig. 1e [Figure 1: see original paper]). However, community differences among treatments were marginal ($R^2=0.1674$, $0.05<P<0.06$). PC1 separated DP20 from IP20, while PC2 distinguished IP20 from IP40 and DP40.

3.2.2 Changes in Soil Bacterial Community Composition

At the phylum level, bacterial communities were dominated by Actinobacteria (26.7%–36.0%), Acidobacteria (17.2%–26.1%), Proteobacteria (15.1%–19.3%), and Chloroflexi (12.5%–18.6%), collectively accounting for 83.9% of sequences (Fig. 2a [Figure 2: see original paper]). No significant differences in these phyla were observed among treatments ($P>0.10$). Abundances of Actinobacteria, Acidobacteria, Proteobacteria, and Chloroflexi peaked under IP40, IP20, CK, and DP40, respectively. Minor differences were detected in Acidobacteria, Patescibacteria, and Rokubacteria ($0.05<P<0.10$).

Eighteen dominant classes (>1% abundance) comprised 95.8%–96.8% of sequences (Fig. 2b [Figure 2: see original paper]). Actinobacteria was most abundant (26.7%–36.0%) and enriched under IP40. Among high-abundance groups, Alphaproteobacteria and Deltaproteobacteria were enriched under CK (12.80% and 3.04%), while Gammaproteobacteria was enriched under IP40 (4.30%). In Acidobacteria, Blastocatellia_{subgroup}4 and subgroup_6 were more abundant under IP20 (12.20% and 11.20%). In Chloroflexi, Chloroflexia class (5.30%–7.20%) was relatively abundant under DP40, while TK10 class was abundant under IP40 (2.10%).

A hierarchically clustered heatmap of the top 50 genera revealed strongest similarities among CK, DP20, and IP20, and between IP40 and DP40 (Fig. 2c [Figure 2: see original paper]). These genera accounted for 74.80%–76.90% of sequences, though most differentially abundant genera had <1.00% relative abundance, peaking in precipitation addition treatments (IP20, IP40). Representative genera included norank_c_{subgroup}6, RB41, and norank_c_{Actinobacteria}. Norank_c_{subgroup}6 and RB41 (Acidobacteria) were abundant under IP20, while norank_c_{Actinobacteria} was abundant under DP40.

LEfSe identified 23 bacterial populations with significant differences (LDA scores >3.0) among treatments (Fig. 3 [Figure 3: see original paper]). Most differential groups were enriched under increased precipitation, while only four were enriched under decreased precipitation (Fig. 3b [Figure 3: see original paper]). Two major response patterns emerged: resource-limited populations (e.g., Thermoanaerobaculia class, Microtrichales order, Xanthomonadales order, Nitrosomonadaceae family) increased with precipitation and peaked under IP40 (Fig. 3c [Figure 3: see original paper]). In contrast, drought-tolerant populations (e.g., Kallotenuales order, AKIW781 family, Hymenobacteraceae family) were more abundant under decreased precipitation, particularly DP40 (Fig. 3c [Figure 3: see original paper]).

3.2.3 Interaction of Soil Dominant Bacteria Under Different Precipitation Treatments

Network analysis revealed that CK treatment had the most complex network, with more edges (1012) and higher average degree (20.24) than altered precipitation treatments (Fig. 4 [Figure 4: see original paper]). Negative interactions among OTUs increased with precipitation (Table 2), indicating that drought promoted cooperation while increased precipitation intensified competition. Average network distance was shorter under altered precipitation than CK (Table 2), suggesting that precipitation changes shortened interspecies distances, enhancing material, energy, and information transfer.

3.3 Driving Factors of Bacterial Community Structure Under Altered Precipitation

Correlation analysis showed bacterial diversity was significantly associated with precipitation, TN, TP, SAN, SAP, pH, EC, SWC, AGB, Shannon's index, and coverage ($P<0.05$, Table 3). Alpha diversity (ACE index) correlated with precipitation, plant coverage, SAP, and EC ($P<0.05$). The Smith-Wilson index correlated with AGB, TN, and pH ($P<0.05$). Beta diversity (PCoA) relationships depended on UniFrac distance weighting: unweighted distances correlated with precipitation, coverage, SAP, EC, and SWC ($P<0.05$), while weighted distances correlated with plant Shannon's diversity, SAN, and TP ($P<0.05$).

Bacterial community composition at the phylum level was significantly related to plant Shannon's index, richness, coverage, and density ($P<0.05$; Fig. 5 [Figure 5: see original paper]). Plant Shannon's index was the dominant factor, significantly affecting seven phyla (Actinobacteria, Chloroflexi, Cyanobacteria, Dependentiae, Fibrobacteres, Gemmatimonadetes, and Patescibacteria). Soil factors significantly affecting composition included SAP, EC, MBC, TN, TP, and SWC, with SAP as the dominant factor influencing five phyla (Acidobacteria, Chlamydiae, Elusimicrobia, Patescibacteria, and WS2).

SEM analysis revealed that altered precipitation directly affected plant community properties, particularly AGB, which significantly influenced bacterial community composition ($P<0.05$; Fig. 6 [Figure 6: see original paper]). However, precipitation did not significantly affect soil properties ($P>0.05$), and soil property changes did not alter plant properties or bacterial composition. The final model fit well (^{2}=5.864, df=15, $P=0.982$, RMSEA<0.001) and explained 81% of variation in plant properties, 20% in soil properties, and 73% in bacterial community composition.

4.1 Responses of Soil Bacterial Community Composition and Diversity to Altered Precipitation

Our results demonstrate that soil bacterial alpha diversity and rare taxa changed significantly with altered precipitation, while beta diversity and dominant groups remained stable (Figs. 1 and 3 [Figure 1: see original paper] [Figure 3: see original paper]). Desert grassland bacterial communities were dominated by Actinobacteria, Acidobacteria, Proteobacteria, and Chloroflexi (Fig. 2a [Figure 2: see original paper]), consistent with similar ecosystems [**?**, **?**]. Low-abundance groups (<1% relative abundance) rather than dominant taxa differed significantly among treatments (Fig. 3 [Figure 3: see original paper]), suggesting stronger precipitation effects on rare taxa, consistent with [**?**, **?**] but contrasting with [**?**]. This inconsistency may arise from methodological differences: our field manipulation versus natural precipitation gradients in [**?**], where greater environmental variation (precipitation, temperature, evaporation, vegetation, soil properties) could amplify differences in dominant taxa.

The lack of correlation between precipitation and weighted UniFrac distance (Table 3) confirms low sensitivity of dominant species to precipitation changes [?], as weighted UniFrac emphasizes common taxa. Small precipitation events (<10 mm) and long dry intervals in our study area [?] may cause rapid soil water evaporation, weakening dominant taxa responses. In contrast, rare taxa are more susceptible to disturbances like precipitation changes [?]. The strong correlation between precipitation and unweighted UniFrac distance (Table 3) further confirms rare taxa sensitivity [?]. Rare taxa also contribute substantially to genetic and functional diversity [?]. Increased alpha diversity (ACE and Shannon's indices) with precipitation (Fig. 1 [Figure 1: see original paper]) reflects rare taxa contributions under favorable conditions [?, ?].

The stability of dominant phyla across treatments (Figs. 1 and 3 [Figure 1: see original paper] [Figure 3: see original paper]) suggests adaptation to local climate variability through long-term selection [?], conferring community stability [?]. Actinobacteria, Chloroflexi, and Acidobacteria can tolerate drought or moisture through osmotic adjustment and stress tolerance mechanisms associated with thicker cell walls [?]. This tolerance may underlie the unchanged community composition across treatments.

4.2 Ecological Strategies of Soil Bacterial Populations in Response to Altered Precipitation

LEfSe analysis identified two response patterns: resource-limited and drought-tolerant populations (Fig. 3 [Figure 3: see original paper]). Resource-limited populations enriched under IP40 treatment primarily belonged to Actinobacteria and Proteobacteria, predicted as copiotrophic groups [?]. For example, Microtrichales order (Actinobacteria) was enriched under IP40, and Actinobacteria abundance correlated positively with plant species richness and Shannon's index (Fig. 5 [Figure 5: see original paper]). Enhanced plant growth under increased precipitation raises nutrient inputs and availability, promoting these populations [?]. Conversely, drought-tolerant populations enriched under DP40 primarily belonged to Chloroflexi, an oligotrophic/drought-tolerant phylum [?] whose abundance correlated negatively with plant diversity (Fig. 5 [Figure 5: see original paper]). Mycelial production by some Chloroflexi members may enhance growth under drought by improving nutrient absorption [?].

Bacterial interactions shape population distributions under different precipitation regimes [?]. IP40 promoted competitive relationships, while DP40 facilitated cooperation (Fig. 4 [Figure 4: see original paper]), consistent with [?]. Increased precipitation enhances bacterial activity and growth, intensifying competition for aggregated resources [?, ?]. Network analysis showed negative correlations between Chloroflexi and Actinobacteria under IP40, reflecting competitive exclusion of Chloroflexi. Positive correlations between Acidobacteria and Chloroflexi under DP40 indicated cooperative resource use in nutrient-poor conditions. Thus, precipitation-mediated interactions influence bacterial group patterns.

4.3 Relations Among Soil Bacterial Community, Vegetation Characteristics, and Soil Environment

Altered precipitation affected bacterial communities primarily through plant community changes rather than soil properties (Figs. 5 and 6 [Figure 5: see original paper] [Figure 6: see original paper]; Table 3), consistent with [?, ?] but contrasting with [?] who found indirect effects via plant AGB regulation of soil properties. In our study, plant AGB contributed more substantially to bacterial composition changes under altered precipitation (Fig. 6 [Figure 6: see original paper]). Plant AGB, coverage, height, and density increased significantly with precipitation (Table 1), enhancing litter and root exudates [?, ?, ?] and altering microbial resource use and metabolism [?, ?]. Dominant decomposer phyla (Actinobacteria, Chloroflexi, Acidobacteria) were directly affected by plant residue quality and secondary metabolite concentrations [?, ?, ?], leading to community differences across treatments. Our previous work showed that three-year extreme drought reduced plant density, height, and coverage, simplified community structure, and affected plant diversity [?], highlighting the strong sensitivity of plant communities to precipitation changes in desert grasslands.

Soil properties did not significantly affect bacterial composition under altered precipitation (Fig. 6 [Figure 6: see original paper]), likely because manipulation only significantly changed EC, SAP, and SAK (Table 1), with minimal impact on overall nutrient status. Oligotrophic phyla (Chloroflexi, Acidobacteria) can exploit nutrient-poor environments and respond weakly to resource changes [?, ?]. Additionally, increased precipitation may cause nutrient loss via runoff and disrupt soil aggregates through raindrop impact and shear forces, inhibiting bacterial growth [?, ?, ?]. Consequently, soil property variations contributed little to bacterial composition changes in this desert grassland.

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5 Conclusions

This study demonstrates that soil bacterial alpha diversity and rare taxa responded significantly to altered precipitation, while dominant bacteria and beta diversity remained stable. Increased precipitation promoted species competition, whereas decreased precipitation strengthened cooperation. Bacterial response patterns involved resource-limited and drought-tolerant populations. SEM analysis revealed that precipitation changes influenced bacterial communities primarily through plant community modifications, particularly plant AGB.

These findings illuminate the dynamics and drivers of soil bacterial diversity and composition under altered precipitation in desert grasslands. Future research should examine plant root dynamics, exudates, and root-microbe relationships to accurately assess soil carbon pool trends under global climate change.

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Note: Figure translations are in progress. See original paper for figures.