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Effects of Enclosure on Plant and Soil Restoration in the Junggar Desert

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Abstract: Enclosure is commonly used in the restoration of degraded grasslands. However, the effects of enclosure on grassland plant and soil restoration remain controversial, particularly in deserts. To assess the effects of enclosure on desert plants and soil properties, using high throughput sequencing, the differences between plants and soil were systematically analyzed before and after enclosure construction. The soil organic carbon, total nitrogen and total phosphorus contents of the three desert flora increased and decreased, but the difference was not significant; enclosure increased plant height, coverage, aboveground biomass, and species richness by 58.99%, 59.35%, 33.29%, and 51.21%, respectively, in a *Seriphidium transiliense* formation; by 15.49%, 33.52%, 20.85%, and 5.13%, respectively, in a *Haloxylon persicum* formation; and by 83.80%, 31.51%, 76.66% and 33.33%, respectively, in an *Anabasis salsa* formation. For soil bacteria, enclosure significantly increased the average number of operational taxonomic units and Shannon-Wiener index by 12.74% and 2.92%, respectively, under *S. transiliense* formation and by 17.08% and 3.17%, respectively, under *H. persicum* formation. However, enclosure had no significant effect on the average number of operational taxonomic units or Shannon-Wiener index under *A. salsa* formation. Enclosure significantly increased desert plants, soil bacterial diversity, and desert plant community productivity; however, the increase in soil nutrient content was not significant. These results demonstrate that enclosure is effective for restoring desert ecosystems but may have little effect on the soil nutrient content.

Key words: diversity; plant community; soil bacteria; soil nutrient; Junggar Desert

1 Introduction

Deserts are important terrestrial ecosystems (Liang et al., 2019) and are dry with low precipitation levels; therefore, vegetation is sparse, and the structure and nutrition levels are simple. Consequently, the desert ecosystems are extremely fragile; once destroyed, recovery of desert ecosystems is difficult. Desert ecosystems are key areas for biodiversity conservation and are sensitive to climate change (Zhang, 2019). Therefore, maintaining their stability is important.

Xinjiang Uygur Autonomous Region with the largest desert grassland distribution area in China, accounting for 46.9% of the total grassland area in the Autonomous Region (Xu, 1993). It is an important grazing land in spring, autumn, and winter, giving it an important ecological, economic, and social status (Xun, 2017; Wei et al., 2020). However, in recent years, because of fluctuations in climate and population growth and a lack of scientific knowledge, deserts are subjected to overgrazing and other detrimental activities, altering the growth and development of desert vegetation. The production and ecological functions of desert grasslands have been weakened, the community stability and recovery ability have been reduced, and the system balance has been disrupted, seriously affecting the health and sustainable development of desert grasslands (Gao, 2007; Li, 2016). Therefore, the restoration and management of degraded de-

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sert vegetation are required.

Enclosure plays an important role in the restoration and management of degraded desert grasslands in Xinjiang (Zhang, 2010; Yang et al., 2015). The purpose of enclosure is to ensure the self-repair and renewal of grassland plants by regulating the relationship between herbivores and plants in the ecosystem. Enclosure promotes the succession of grassland plants and results in the gradual recovery of degraded grasslands. To date, studies of the restoration of desert grasslands using enclosure have mainly focused on grassland productivity, plant diversity, community coverage, and soil nutrient changes after enclosure construction (Taddese et al., 2002; Guo et al., 2016; Yang, 2017). Only a few studies have focused on soil microbial changes after enclosure construction (Yu et al., 2010); therefore, further research is required.

In this study, three typical plant formations of the Junggar Desert (*Seriphidium transiliense* formation from the southern margin, *Haloxylon persicum* formation from the heartland, and *Anabasis salsa* formation from the northern margin) were studied. The objectives of the study were to determine the: 1) Changes in soil nutrients under different desert plant formations after enclosure construction; 2) Ef-fects of enclosure on the community characteristics of desert plants, and 3) Effects of enclosure on bacterial diversity and community structure in desert soil.

2 Materials and methods

2.1 Study area

The study area is in the Junggar Basin (43°57′–47°01′N, 85°52′–88°12′E, elevation 350–1215 m). The area has a typical moderate temperate desert climate, climate change is strong, the day length differs substantially throughout the year, the average annual temperature is 5–9 ℃, the average annual precipitation is 50–100 mm, and the foothills generally do not exceed 200 mm. The zonal soil types are calcareous soil, brown calcareous soil, gray desert soil, and gray–brown desert soil. The zonal vegetation is mainly composed of small trees and shrubs, and the middle section of the basin is a quaternary alluvial wind desert.

The following three typical desert plant formations in the Junggar Basin were selected: *Seriphidium transiliense* formation in the southern margin, *Haloxylon persicum* formation in the heartland, and *Anabasis salsa* formation in the northern margin. An experimental site was established in each plant formation. The details of these three sites are presented in Table 1.

Table 1 Details of experimental sites in the Junggar Basin

Formation type	Plot	Dominant species	Location	MAT (℃)	MAP (mm)	Altitude (m)
Seriphidium transiliense	EN FG	*S. transiliense* *Petrosimonia sibirica* *Carex turkestanica* *Ceratocarpus arenarius*	46°58′N, 88°09′E	6.49	114.54	1015
Haloxylon persicum	EN FG	*H. persicum*, *C. arenarius* *Seriphidium terrae-albae* *Salsola collina*	44°23′N, 88°08′E	8.20	65.94	358
Anabasis salsa	EN FG	*Salsa C. arenarius* *S. terrae-albae*, *Salsola arbuscula*	44°01′N, 86°09′E	4.94	166.88	667

Note: MAT: Mean annual temperature; MAP: Mean annual precipitation; EN: Enclosure plot; FG: Free grazing plot.

2.2 Experimental design

Samples were collected at the beginning of September 2018, whi ch was close to the peak growing season of desert plants according to the Vegetation Map of the People's Republic of China (1:1000000) (China Vegetation Map Committee of Chinese Academy of Sciences, 2007) and "Vegetation and Utilization in Xinjiang" (Xinjiang Comprehensive Investigation Team, The Chinese Academy of Sciences, 1978). Two plots were established in each of the three plant formations; one was a national grassland fixed monitoring point (enclosure area) and the other was a free grazing area adjacent to the enclosed area. Hereinafter, these plots are referred to as enclosure (EN) plots and free grazing (FG) plots. Grazing was excluded from the EN plots at *S. transiliense*, *H. persicum*, and *A. salsa* formations using fencing in 2015, 2011, and 2012, respectively. Therefore, the duration of enclosure at the time of sampling (2018) was 3, 7, and 6 years, respectively. Species composition, structure, topography, and geomorphology of grassland before and after fencing were similar.

Five subplots were randomly established in each plot at least 50 m apart. Within each subplot, three quadrats (1 m × 1 m) were used to sample typical plants. Additionally, five soil samples were collected from each quadrat to a depth of 0–20 cm using a soil drill (diameter 2.5 cm). The 15 soil samples from each subplot (i.e., five samples from each of the three quadrats) were pooled into one composite sample, resulting in 30 soil samples [three sites (plant formations) × two plots (EN and FG) × five subplots]. Additionally, in *H. persicum* plots, a 10 m × 10 m survey area was established to examine small arbor.

2.3 Field sampling and laboratory analysis

2.3.1 Investigation of aboveground plant characteristics

In each quadrat, the species composition, species number, height (plant cluster natural growth height), coverage (acupuncture method), density (plant cluster number of each

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species per unit area), and aboveground biomass were recorded. All plants in each quadrat were collected and stored in paper bags.

In the 10 m ×10 m survey areas, species composition, density, crown width (north–south and east–west direction), height, and aboveground biomass (standard branch biomass × number of branches) were recorded. Standard branches were collected and stored in paper bags.

All plant samples were transported to the laboratory and dried at 105℃ for 30 min, followed by 80℃ for 24 h, and the dry weights were determined.

2.3.2 Soil sample preparation

Roots, stones, and other large objects were removed from soil samples, which were then passed through a 2-mm sieve. Mixed soil samples were divided into two parts: One was placed in an aseptic sealed bag and stored at –20℃ for molecular analyses, and the other was placed in a cloth bag and stored at room temperature for soil nutrient determination.

2.3.3 Soil nutrient determination

Soil organic carbon (SOC), total nitrogen (STN), and total phosphorus (STP) were measured as described by Bao (2000).

2.3.4 Bacterial DNA extraction, amplification, and sequencing

Soil DNA extraction was conducted as described by Zhou et al. (1996). DNA was extracted using a soil genome DNA extraction kit. Next, 0.8% low-melting-point agarose gel was used for DNA purification, and the DNA was quantified using an ultraviolet spectrophotometer (NanoDrop ND-1000; Thermo Fisher Scientific, Waltham, MA, USA).

For the bacterial analysis, PCR was conducted to amplify a highly variable V4 region of the 16S rRNA gene with a length of approximately 250 bp. The specific primers used were 520F (5′-barcode AYTGGGYDTAAAGNG-3′) and 802R (5′-TACNVGGTATATAATCC-3′).

An Illumina TruSeq Nano DNA LT Library Prep Kit (San Diego, CA, USA) was used to prepare the sequencing library. Next, an Illumina MiSeq was used with MiSeq Reagent Kit V3 (600 cycles) to carry out 2 × 300 bp double-terminal sequencing. Reads were processed using QIIME. This included filtering of tags, removal of chimeras, and validation of data. Sequences were then clustered at 97% similarity into operational taxonomic units (OTUs) using the Silva database for species classification.

2.3.5 Meteorological data acquisition

The distribution of meteorological stations in the Junggar Basin is uneven. Therefore, the average annual temperature and annual precipitation data of each plot were obtained by ANUSPLINE interpolation using meteorological data from the Junggar Basin Meteorological Station (2014–2018) provided by the National Meteorological Science Data Center website.

2.4 Data analysis

2.4.1 Plant diversity parameters

Plant α-diversity was characterized using the Patrick (R), Shannon-Wiener (H), Pielou (P), and Simpson (D) indices as follows:

$$R=S \tag{1}$$

$$H=-\sum_{i=1}^{S} P_i \ln P_i \tag{2}$$

$$P=H/\ln S \tag{3}$$

$$D=-\sum_{i=1}^{S} P_i^2 \tag{4}$$

where, S is the number of species and P_i is the importance value of species i.

2.4.2 Soil bacterial parameters

Bacterial α-diversity was characterized using the Chao1 richness, ACE, and Shannon-Wiener indices. The Chao1 index is commonly used in ecology to estimate the total number of species, was determined using the following equation:

$$Chao1=S_{obs}+\frac{F_1(F_1-1)}{2(F_2+1)} \tag{5}$$

where, S_{obs} is the actual number of OTUs observed, F_1 is the number of OTUs containing only one sequence, and F_2 is the number of OTUs containing only two sequences. The ACE index is used to estimate the index of the number of OTUs in a community. The formula for the ACE index is as follows:

$$ACE=S_{\text{abund}}+\frac{S_{\text{rare}}}{C_{\text{ace}}}+\frac{F_1}{C_{\text{ace}}}\gamma^2{}_{\text{ace}} \tag{6}$$

$$N_{\text{rare}}=\sum_{i=1}^{\text{abund}} i\times n_i \tag{7}$$

$$C_{\text{ace}}=\frac{n_i}{N_{\text{rare}}} \tag{8}$$

$$\gamma^2{}_{\text{ace}}=\max\left(\frac{S_{\text{rare}}}{C_{\text{ace}}}\times\frac{\sum_{i=1}^{10} i(i-1)F_i}{N_{\text{rare}}(N_{\text{rare}}-1)}-1,0\right) \tag{9}$$

where, S_{abund} is more than the OTU number of "abund" sequences, S_{rare} is the number of OTUs containing "abund" sequences or fewer, C_{ace} is the sample abundance coverage estimator, F_i is the frequency of singletons, and $\gamma^2{}_{\text{ace}}$ is the estimated coefficient of variation for rare OTUs, n_i is the number of OTUs containing i sequences, N_{rare} refers to the total number of sequence.

2.4.3 Statistical analyses

Soil bacterial diversity was calculated using QIIME software, including OTU number, Shannon-Wiener index, ACE index, and Chao1 index. SPSS22.0 software (SPSS, Inc., Chicago, IL, USA) was used to analyze environmental factors by single-factor and multi-factor analyses of variance, Duncan's significance test, and Pearson correlation analysis.

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Non-metric multidimensional scaling was conducted using R software (R Project for Statistical Computing, Vienna, Austria).

3 Results

3.1 Effects of enclosure on SOC, STN, and STP under different desert plant formations

The responses of the SOC, STN, and STP content to enclosure in each of the three desert plant formations are shown in Table 2. In *S. transiliense* formation, the SOC content was 9.2% lower in the EN plot than in the FG plot, but the difference was not significant ($P > 0.05$). In *H. persicum* and *A. salsa* formations, the SOC content was 12.27% and 0.5% higher in the EN plot than in the FG plot, respectively ($P > 0.05$). In *S. transiliense* and *A. salsa* formations, the STN content was 14.50% and 2.06% lower in the EN plot than in the FG plot, respectively ($P > 0.05$), whereas in *H. persicum* formation, the STN content was 7.32% higher in the EN plot than in the FG plot ($P > 0.05$). The STP content in *S. transiliense*, *H. persicum*, and *A. salsa* formations was 2.08%, 10%, and 2.13% higher in the EN plot than in the FG plot, respectively.

Table 2 Effects of enclosure on soil nutrients in three desert plant formations (Unit: g kg^{-1})

Formation type	SOC	STN	STP
Seriphidium transiliense			
EN	16.65 ± 0.33^a	1.12 ± 0.03^a	0.49 ± 0.04^a
FG	18.34 ± 0.64^a	1.31 ± 0.04^a	0.48 ± 0.03^a
Haloxylon persicum			
EN	3.66 ± 0.10^a	0.88 ± 0.02^a	0.33 ± 0.02^a
FG	3.26 ± 0.09^a	0.82 ± 0.02^a	0.30 ± 0.01^a
Anabasis salsa			
EN	13.44 ± 0.54^a	0.95 ± 0.02^a	0.48 ± 0.03^a
FG	13.37 ± 0.62^a	0.97 ± 0.03^a	0.47 ± 0.05^a

Note: EN: Enclosure plot; FG: Free grazing plot; SOC: Soil organic carbon; STN: Soil total nitrogen; STP: Soil total phosphorus. The letter "a" indicates no significant differences within plant formations between the EN and FG plots ($P > 0.05$).

3.2 Effects of enclosure on the quantitative characteristics of different desert plant formations

Figure 1 shows the responses of plant height, density, coverage, and biomass of the three desert plant formations in the Junggar Basin to enclosure. In all three plant formations, plant height, coverage, and biomass were significantly higher in the EN plot than in the FG plot ($P < 0.05$). In *S. transiliense* and *H. persicum* formations, community density was significantly higher in the EN plot than in the FG plot ($P < 0.05$). In contrast, in *A. salsa* formation, community density was higher in the EN plot than in the FG plot, but the difference was not significant ($P > 0.05$).

3.3 Effects of enclosure on plant community α diversity in different desert plant formations

The results in Fig. 2 show that enclosure affected the α-diversity of the three desert plant formations. In *S. transiliense*, *H. persicum*, and *A. salsa* formations, the Shannon-Wiener diversity index was 19.8%, 7.7%, and 21.3% lower in the FG plot than in the EN plot, respectively ($P < 0.05$) (Fig. 2a).

In *S. transiliense* and *A. salsa* formations, the Simpson index was significantly higher ($P < 0.05$) by 19.3% and 15.8%, respectively, in the EN plot than in the FG plot; however, in *H. persicum* formation, the Simpson index was

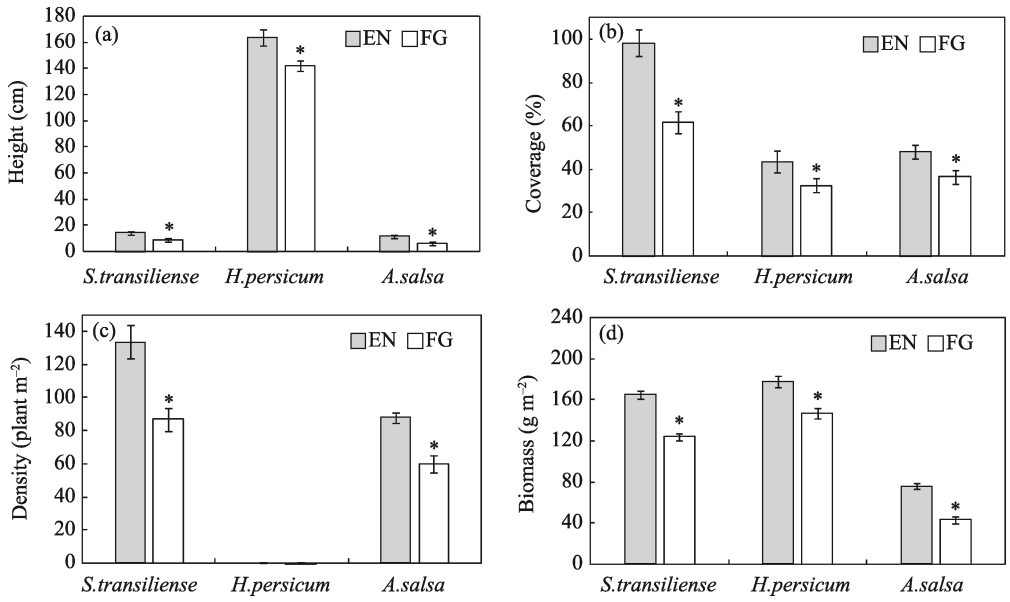


Fig. 1 Effects of enclosure on community characteristics of different desert plant formations.
Note: EN: Enclosure plot; FG: Free grazing plot. *S. transiliense*: *Seriphidium transiliense*; *H. persicum*: *Haloxylon persicum*; *A. salsa*: *Anabasis salsa*.
* indicates significant difference between plots at $P < 0.05$.

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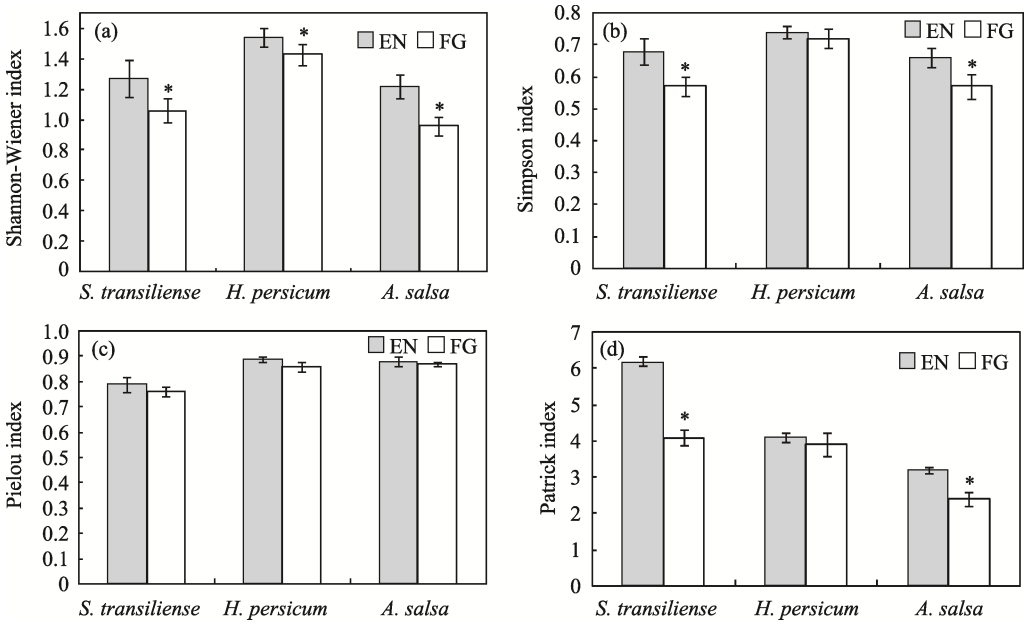


Fig. 2 Effects of enclosure on the α-diversity of different desert plant formations

Note: EN: Enclosure plot; FG: Free grazing plot. *S. transiliense*: *Seriphidium transiliense*; *H. persicum*: *Haloxylon persicum*; *A. salsa*: *Anabasis salsa*. * indicates significant difference between plots at $P < 0.05$.

only 2.8% higher in the EN plot than in the FG plot and the difference was not significant ($P > 0.05$) (Fig. 2b).

The Pielou index, which describes community evenness, was 3.9%, 2.3%, and 1.1% higher in the EN plot than in the FG plot of *S. transiliense*, *H. persicum*, and *A. salsa* formations, respectively, but the differences were not significant ($P > 0.05$) (Fig. 2c).

The Patrick index was 33.8% and 25% higher in the EN plot than the FG plots in *S. transiliense* and *A. salsa* formations, respectively ($P < 0.05$). In contrast, in *H. persicum* formation, the Patrick index was only 4.8% higher in the EN plot than in the FG plot, and the difference was not significant ($P > 0.05$) (Fig. 2d).

3.4 Effects of enclosure on soil bacterial diversity under different plant formations

For bacteria, the OTU number, Chao1 index, ACE index, and Shannon-Wiener index in each plant formation are shown in Table 3. In *S. transiliense* formation, the average OTU number, Chao1 index, ACE index, and Shannon-Wiener index were all higher in the EN plot than in the FG plot, among which the OTU number and Shannon-Wiener index were significantly higher by 12.74% and 2.92%, respectively ($P < 0.05$). In *H. persicum* formation, the average OTU number, Chao1 index, ACE index, and Shannon-Wiener index were 17.08%, 16.70%, 23.86%, and 3.17% higher in the EN plot than in the FG plot, respectively ($P < 0.05$). In *A. salsa* formation, the average OTU number, Chao1 index, ACE index, and Shannon-Wiener index differed between the EN and FG plots, but not significantly ($P > 0.05$).

3.5 Effects of enclosure on soil bacterial β diversity under different desert plant formations

Non-metric multidimensional scaling (NMDS) analysis based on UniFrac distance showed that for each site, the soil bacterial community structure was significantly different between the EN and FG plots (Fig. 3).

Table 3 Response of bacterial diversity to enclosures in three desert plant formations

Formation type	Plot	Number of OTUs	Chao 1 index	ACE index	Shannon-Wiener index
Seriphidium transiliense	EN	3309.40 ± 267.07^{a}	3586.51 ± 526.54^{a}	3770.91 ± 669.77^{a}	10.56 ± 0.11^{a}
	FG	2935.40 ± 166.31^{b}	3214.72 ± 463.41^{a}	3284.09 ± 478.19^{a}	10.26 ± 0.15^{b}
Haloxylon persicum	EN	3341.60 ± 172.30^{a}	3884.64 ± 242.39^{a}	4229.17 ± 297.79^{a}	10.41 ± 0.08^{a}
	FG	2854.20 ± 182.94^{b}	3328.67 ± 543.53^{b}	3414.22 ± 558.59^{b}	10.09 ± 0.14^{b}
Anabasissalsa	EN	3127.80 ± 229.31^{a}	3692.70 ± 355.15^{a}	3997.36 ± 424.69^{a}	10.19 ± 0.29^{a}
	FG	2917.00 ± 250.42^{a}	3400.84 ± 554.56^{a}	3534.98 ± 555.67^{a}	10.26 ± 0.16^{a}

Note: EN: Enclosure plot; FG: Free grazing plot. Letters indicate significant differences within plant formations between the EN and FG plots at $P < 0.05$.

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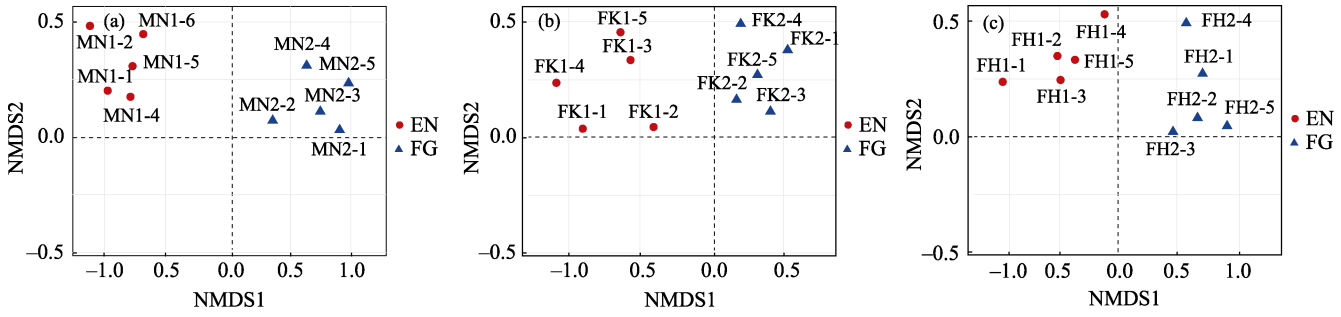


Fig. 3 Effects of enclosure on bacterial β-diversity under different desert plant formations

Note: (a) MN: *Seriphidium transiliense* formation; (b) FK: *Haloxylon persicum* formation; (c) FH: *Anabasis salsa* formation. EN: Enclosure plot; FG: Free grazing plot.

3.6 Effects of enclosure on soil bacterial community structure under different desert plant formations

The relative abundances of several dominant bacterial taxa in the three plant formations differed between the EN and FG plots (Fig. 4). Actinobacteria, Proteobacteria, and Acidobacteria were the dominant taxa in *S. transiliense* formation (>10%). In this formation, the relative abundances of Actinobacteria and Acidobacteria were 9.73% and 10.61% higher in the EN plot than in the FG plot, respectively. In contrast, the relative abundances of Proteobacteria, Chloroflexi, and Gemmatimonadetes were 6.42%, 17.01%, and 25.29% lower in the EN plot than in the FG plot, respectively. The dominant taxa in *H. persicum* formation were Actinobacteria, Proteobacteria, and Chloroflexi (>10%). In this formation, the relative abundance of Actinobacteria was 14.19% higher in the EN plot than in the FG plot, whereas the relative abundances of Proteobacteria and Chloroflexi were lower in the EN plot than in the FG plot. In *A. salsa* formation, the dominant taxa were Actinobacteria, Proteobacteria, and Chloroflexi (>10%). In this formation, the relative abundances of Actinobacteria and Chloroflexi were 11.11% and 15.13% lower in the EN plot than in the FG plot, respectively, whereas the relative abundances of Proteobacteria, Acidobacteria, and Bacteroidetes were higher in the EN plot than in the FG plot. Particularly, the relative abundance of Proteobacteria was 33.61% higher in the EN plot than in the FG plot.

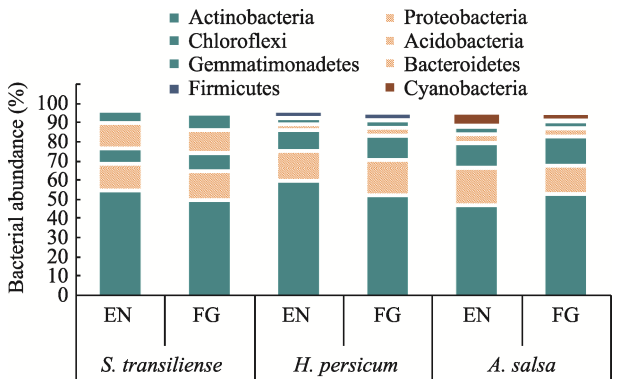


Fig. 4 Effects of enclosure on soil bacterial community structure in different desert plant communities

Note: EN: Enclosure plot; FG: Free grazing plot. *S. transiliense*: *Seriphidium transiliense*; *H. persicum*: *Haloxylon persicum*; *A. salsa*: *Anabasis salsa*.

4 Discussion

4.1 Effects of enclosure on soil nutrients

Enclosure construction is an important management practice for grassland restoration, and it can result in the restoration of soil carbon and ability of grassland soil to fix nitrogen. It can also result in the restoration of the multi-functionality of grassland ecosystems (Dong et al., 2018). Several studies have shown that enclosure significantly reduces the SOC and STN content. For example, Shi et al. (2013) reported that the SOC content in the Qinghai–Tibet Plateau decreased significantly ($P < 0.05$), resulting in an increase in plant aboveground biomass and surface litter. This resulted in a slower nutrient cycle and flow from aboveground to belowground. In contrast, grazing led to the return of livestock manure to the soil, resulting in a significant decrease in the SOC and STN content. However, other studies showed that grazing exclusion has little effect on the SOC and STN content (Sigcha et al., 2018). In the present study, in *S. transiliense* formation, enclosure decreased the SOC and STN content but slightly increased the STP content. In contrast, in *H. persicum* and *A. salsa* formations, enclosure increased the content of SOC, STN, and STP to different degrees. The reasons for these differences can be as attributed to the following: 1) Plant nutrient uptake from soil and litter decomposition are basically equal, resulting in a balanced input and output of soil nutrients; 2) The sites differed in terms of the number of years of enclosure, climate, soil texture, and vegetation type.

4.2 Effects of enclosure on plant community characteristics and diversity in different desert plant formations

The quantitative characteristics and diversity of plant communities can reflect the health status of degraded grasslands after enclosure construction (Xiong et al., 2014), and the

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responses of plant community structure and diversity to enclosure in different environments and grassland types are different (Guo, 2007; Semmartin et al., 2008). We found that plant height, density, coverage, and biomass of the three desert plant formations in the Junggar Basin were not consistent in their response to enclosure. Enclosure increased plant height, coverage, and biomass of all three desert plant formations. Enclosure significantly increased density in *S. transiliense* and *A. salsa* formations. It also increased density in *H. persicum* formation, but not significantly. These results are similar to those of Jing et al. (2014). Desert grasslands in Xinjiang are grazed in spring and autumn. Overgrazing inhibits the renewal of grassland and expansion of fine forage. When grazing is excluded, the previously inhibited forage can grow rapidly, resulting in an increase in biomass and coverage. Additionally, germination of the soil seed bank is promoted, accelerating the self-repair ability of grasslands. The effects of grazing on *H. persicum* formation may be different because *H. persicum* is small arbor, and the propagation of small trees is slower than that of herbaceous and semi-herbaceous shrubs.

Several studies have shown that the diversity of grassland plants significantly increases after enclosure construction (Jeddi and Chaieb, 2010), whereas other studies showed no effect or even a negative effect on plant diversity (Shaltout et al, 1996). In this study, the Simpson and Shannon-Wiener indices of *S. transiliense* and *A. salsa* formations significantly increased after enclosure construction; however, the response of the Simpson index to enclosure was not obvious in *H. persicum* formation. The Pielou index of the three desert plant formations did not significantly respond to enclosure (Fig. 2). This may be because the climate and soil conditions of *S. transiliense* and *A. salsa* formations were relatively good; after enclosure construction, the species richness, height, and biomass increased rapidly, which increased the Simpson and Shannon-Wiener indices. However, the climatic conditions of *H. persicum* formation were poor, and species recovery was relatively slow in the short-term after enclosure construction. The changes in community characteristics, such as plant cover and biomass, were small; however, the Pielou index of the three desert plant formations did not significantly respond to germination of the soil seed bank.

4.3 Effects of enclosure on soil bacterial diversity and community structure under different desert plant formations

Soil bacterial community structure and diversity are sensitive indicators of soil remediation and soil biological activity (Wang, 2017). In this study, the soil bacterial richness under the desert plant formations increased after enclosure construction. This is likely because the plant diversity increased, promoting the accumulation of litter, thus increasing soil nutrients, stabilizing the soil environment, and promoting soil bacterial richness. However, the responses of the number of OTUs, Chao1 index, ACE index, and Shannon-Wiener index were not consistent. Enclosure increased all indices in *H. persicum* formation. Additionally, enclosure increased the number of bacterial OTUs and Shannon-Wiener index in *S. transiliense* formation; however, it had no effect on the other two indices. Moreover, enclosure had no effect on the number of OTUs, Chao1 index, ACE index, or Shannon-Wiener index in *A. salsa* formation. This is not consistent with the results of a previous study (Yin et al., 2019). The main reasons for this difference may be related to the grassland type and number of years since enclosure construction.

The dominant soil bacterial phyla across all sites in the Junggar Desert were Actinobacteria and Proteobacteria, among which the relative abundance of Actinobacteria was the highest (>45%). This is consistent with the finding of Wang (2015) and indicates that Actinobacteria have an advantage in the Junggar Desert. However, there were differences in the soil bacterial communities among the different plant formations, indicating that plant formations affect bacterial communities. According to non-metric multidimensional scaling analysis, enclosure changed the soil bacterial community composition under the three plant formations in the Junggar Desert. Enclosures increased the relative abundances of Actinobacteria and Proteobacteria in *S. transiliense* and *H. persicum* formations, whereas in *A. salsa* formation, the relative abundance of Actinobacteria decreased and that of Proteobacteria increased. The responses of other phyla to enclosure also differed under different plant formations, which may be related to soil type, climatic conditions, or other factors.

5 Conclusions

In general, enclosure had different effects on plant communities and soil microbial communities. Enclosure increased the plant height, coverage, aboveground biomass, and diversity of different desert plant formations in the Junggar Desert; however, it did not significantly affect the SOC, STN, or STP content. For soil bacteria, enclosure increased the number of OTUs, Chao1 index, ACE index, and Shannon-Wiener index under the three plant formations. The bacterial community structure was also significantly affected by enclosure. These findings suggest that enclosure construction is an effective method for restoring desert productivity and biodiversity but has no obvious effect on soil nutrient content. Therefore, we suggest that desert ecosystem restoration should be carried out in combination with other methods, such as moderate grazing and fertilization.

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围封对准噶尔荒漠植物和土壤恢复的影响

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摘 要：封育是恢复退化草地最常用的方法之一，然而封育在草地植物及土壤恢复中的作用尚存争议，尤其在荒漠中，为了进一步评估封育对荒漠植物和土壤性质的影响，本研究以准噶尔荒漠 3 种典型的植物群系为研究对象，应用高通量测序技术，系统分析了封育前后植物、土壤的差异。结果表明，3 种荒漠植物群系的土壤有机碳、全氮和全磷含量封育后有一定的增降变化，但差异不显著；封育后伊犁绢蒿群系植物高度、盖度、地上生物量和物种丰富度分别提高了 58.99%、59.35%、33.29% 和 51.21%；白梭梭群系分别提高了 15.49%、33.52%、20.85% 和 5.13%；盐生假木贼群系分别提高了 83.80%、31.51%、76.66% 和 33.33%。封育后 3 种植物群系细菌多样性也存在差异，其中伊犁绢蒿群系平均 OTU 数量和 Shannon-Wiener 指数显著增加了 12.74%和 2.92%；白梭梭群系平均 OTU 数量和 Shannon-Wiener 指数均显著升高了 17.08% 和 3.17%；盐生假木贼群系平均 OTU 数量和 Shannon-Wiener 指数均封育后虽有高低变化，但差异不显著。封育显著增加了荒漠植物、土壤微生物多样性以及荒漠植物群系群落生产力，但封育后荒漠土壤养分含量有一定的增加，但差异不显著。这些研究表明，封育是恢复荒漠生态的有效方法，但可能对土壤养分的固存意义不大。

关键词：多样性；植物群落；土壤细菌；土壤养分；准噶尔沙漠

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