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Trait-based responses of Gram-positive and Gram-negative soil bacteria to grazing intensity in steppe ecosystems

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Abstract

Background and Aim. Steppe pastures of Central Asia are exposed to long-term grazing pressure that can modify soil properties and belowground microbial communities. Soil bacteria regulate nutrient cycling and ecosystem resilience, yet their responses to grazing intensity in steppe ecosystems remain poorly understood. This study evaluated the effects of grazing intensity on soil bacterial diversity, community composition, and functional structure,with particular emphasis on taxonomic richness and on Gram-positive and Gram-negative bacteria.

Materials and Methods. Soil samples were collected from steppe pastures subjected to light, moderate, and heavy grazing. Bacterial community composition was analyzed using high-throughput sequencing of the 16S rRNA gene. Alpha diversity indices (Chao1, observed species richness, Shannon, Simpson, Pielou's evenness, and Faith's phylogenetic diversity) were calculated. Beta diversity was assessed using Bray-Curtis dissimilarity, principal coordinates analysis (PCoA), and permutational multivariate analysis of variance (PERMANOVA). Homogeneity of multivariate dispersion was evaluated using the betadisper. Bacterial taxa were additionally classified into Gram-positive and Gram-negative groups to assess functional responses to grazing.

Results. Taxonomic richness indices differed significantly among grazing groups, indicating sensitivity of bacterial richness to grazing intensity. In contrast, Shannon diversity, evenness indices, and phylogenetic diversity did not differ significantly, suggesting structural stability of bacterial communities. Beta diversity analysis revealed significant compositional differences among grazing groups, while dispersion did not differ significantly, confirming that the observed differences reflect true shifts in community composition. Functional analysis demonstrated contrasting responses of Gram-positive and Gram-negative bacteria along the grazing gradient.

Conclusion. Grazing intensity in steppe ecosystems primarily affects soil bacterial richness and community composition, whereas diversity evenness and phylogenetic structure remain comparatively stable. Grazing acts as an environmental filter shaping microbial functional structure without causing a pronounced loss of bacterial diversity. These findings highlight the resilience of steppe soil bacterial communities and support the use of microbial indicators in sustainable pasture management.

Keywords: alpha-beta diversity; Gram-negative bacteria; grazing intensity; soil bacteria; steppe pastures.

Introduction

Grazing is one of the most widespread land-use practices in steppe ecosystems and represents a major driver of soil change in arid and semi-arid regions. Long-term grazing alters vegetation cover, soil structure, and nutrient availability through biomass removal and trampling, which can subsequently affect soil moisture retention and erosion processes [1, 2].

Soil bacteria play a central role in ecosystem functioning by regulating carbon and nitrogen cycling, organic matter decomposition, and nutrient availability for plants. Due to their rapid turnover rates and sensitivity to environmental change, bacterial communities respond quickly to grazing disturbances and are increasingly recognized as informative indicators of soil condition in rangeland ecosystems [3, 4].

Among soil bacteria, Gram-positive and Gram-negative groups differ fundamentally in cell wall structure, physiological traits, and ecological strategies. Gram-positive bacteria, characterized by thick peptidoglycan layers, are generally more resistant to desiccation, temperature fluctuations, and physical disturbance, whereas Gram-negative bacteria are often associated with higher nutrient availability and less stressful soil conditions [5, 6]. Consequently, shifts in the relative abundance of these groups may reflect grazing-induced environmental stress.

Previous studies demonstrate that grazing intensity can modify soil bacterial diversity and community composition; however, reported responses vary widely among ecosystems. While heavy grazing has been associated with reduced microbial diversity in some grasslands, other studies report stable or even increased bacterial richness in arid and steppe systems dominated by stress-tolerant taxa [7, 8]. These contrasting results highlight the importance of environmental context and suggest that functional or trait-based approaches may provide additional insight beyond overall diversity metrics.

Steppe ecosystems of Central Asia represent one of the largest continuous pastoral regions worldwide and have experienced centuries of grazing under harsh continental climatic conditions. Despite their ecological and socio-economic importance, these systems remain underrepresented in soil microbiome research, particularly with respect to microbial functional traits related to grazing pressure.

Therefore, the objective of this study was to assess the response of Gram-positive and Gram-negative soil bacterial communities to grazing intensity in steppe pastures. Specifically, we aimed to (i) compare the relative abundance of Gram-positive and Gram-negative bacteria across grazing gradients and (ii) evaluate their potential as microbial indicators of grazing-induced soil stress. Although soil samples were collected across three natural zones, the present study focuses on the steppe ecosystem as a representative system for evaluating microbial responses to grazing intensity, in order to minimize environmental variability and isolate the effects of grazing pressure.

Materials and Methods

Soil samples were collected from pasture ecosystems located in three contrasting natural zones of southeastern Kazakhstan: desert (Bozoy area), steppe (Turgen area), and mountain pastures (Tau-Turgen area). These zones represent a pronounced environmental gradient in terms of climate, vegetation structure, altitude, and grazing regimes typical for Central Asian rangelands [1, 9]. Within each natural zone, pastures were classified according to grazing intensity as lightly grazed, moderately grazed, or heavily grazed, based on distance from settlements, livestock density, and visible signs of grazing pressure [1]. For each combination of natural zone and grazing intensity, five independent soil samples were collected, resulting in a total of 45 samples (3 natural zones × 3 grazing intensities × 5 replicates). For the steppe zone, grazing intensity groups were coded as LGSN (light grazing, steppe zone), MGSN (moderate grazing, steppe zone), and HGSN (heavy grazing, steppe zone), where group designation reflects increasing grazing pressure based on livestock density, distance from settlements, and visible grazing impact and are used consistently in figures and tables. In this study, detailed microbial community analysis was performed for the steppe zone only, while results for the desert and mountain zones will be reported separately.

Soil samples were collected from the topsoil layer (0-15 cm) following the removal of surface litterand plant residues. Each sample was placed in sterile containers, transported on ice, and stored at −20 °C prior to molecular analysis to preserve microbial DNA integrity [10]. Total genomic DNA was extracted from soil samples using standardized protocols for environmental samples. Bacterial community composition was assessed using high-throughput sequencing of the 16S rRNA gene [3].

Library preparation, sequencing, and primary bioinformatic processing were performed by an external commercial sequencing service (GenesCloud, China), following established quality control procedures. Sequencing targeted a commonly used bacterial 16S rRNA gene region suitable for microbial community profiling [10].

Raw sequencing reads were quality-filtered, denoised, and clustered into operational taxonomic units (OTUs) based on sequence similarity thresholds. Operational taxonomic units (OTUs) were generated at a 97% sequence similarity threshold, which remains a widely applied approach for comparative microbial community analyses across environmental gradients. Although amplicon sequence variants (ASVs) have been increasingly used in recent studies, OTU-based clustering is considered appropriate for identifying community-level patterns and relative differences among treatment groups in ecological disturbance studies. Taxonomic assignment was performed using curated reference databases for bacterial 16S rRNA gene sequences, resulting in OTU tables and taxonomic abundance matrices for downstream analyses [3]. Gram-positive and Gram-negative classification was assigned at the phylum level based on dominant cell wall characteristics reported in the literature [4, 3]. Functional heterogeneity may exist within individual phyla; therefore, this classification represents a broad ecological approximation rather than a strict taxonomic assignment.Although OTU-based clustering was applied in this study, it remains suitable, for comparative analyses of microbial community patterns across grazing gradients [11].

Alpha diversity of soil bacterial communities was assessed using several complementary indices reflecting taxonomic richness, diversity, evenness, and phylogenetic structure. These included the Chao1 estimator, observed species richness, Shannon diversity index, Simpson diversity index, Pielou's evenness, Faith's phylogenetic diversity (PD), and Good's coverage [12, 3]. Differences in alpha diversity indices among grazing-environmental groups were tested using one-way analysis of variance (ANOVA) or the Kruskal-Wallis test, depending on data normality as assessed by the Shapiro-Wilk test. Statistical significance was evaluated at $p < 0.05$

Beta diversity was evaluated based on Bray-Curtis dissimilarity matrices calculated from OTU abundance data [13]. Patterns of bacterial community dissimilarity among samples were visualized using principal coordinates analysis (PCoA). Differences in bacterial community composition among grazing-environmental groups were tested using permutational multivariate analysis of variance (PERMANOVA) with 999 permutations [14]. To assess whether PERMANOVA results were influenced by unequal within-group variability, homogeneity of multivariate dispersion was evaluated using the betadisper approach [15]. Distances of individual samples to group centroids in multivariate space were calculated, and differences among groups were tested using both analysis of variance (ANOVA) and permutation tests with 999 permutations. Boxplots of distances to centroids were used to visualize beta dispersion patterns across grazing and environmental groups.

All statistical analyses and data visualization were performed using R software (version 4.5.2). Alpha diversity analyses and statistical testing were conducted using base R and supplementary packages. Multivariate analyses, including Bray-Curtis dissimilarity calculation, PCoA ordination, PERMANOVA, and betadisper analyses, were performed using the vegan package [16]. Statistical significance was assessed at $p < 0.05$ unless stated otherwise.

Results and Discussion

Alpha diversity of soil bacterial communities in the steppe pasture ecosystem varied among grazing intensities (Table 1). Indices describing taxonomic richness showed significant differences among grazing groups, whereas indices reflecting community diversity, evenness, and phylogenetic structure remained comparatively stable. The Chao1 richness estimator differed significantly among grazing intensities (one-way ANOVA, $p < 0.001$), with the highest values observed under heavy grazing (HGSN: 6989.29 ± 694.25) and lower values under light grazing (LGSN: 6120.23 ± 385.44). A similar pattern was observed for observed species richness, which also varied significantly across grazing groups (Kruskal-Wallis test, $p < 0.001$), ranging from 5866.40 ± 343.80 under light grazing to 6534.20 ± 569.68 under heavy grazing.

Table 1 – Alpha diversity indices (mean ± SD) of soil bacterial communities across grazing intensities in the steppe pasture ecosystem

Index	Test	p-value	Shapiro_ min_p	HGSN	LGSN	MGSN
Chao1	ANOVA	0.0001	0.0761	6989.29 ± 694.25	6120.23± 385.44	6565.74 ± 123.14
Good'scoverage	ANOVA	0.0045	0.0768	0.97± 0.01	0.98± 0.00	0.98± 0.00
Simpson	Kruskal-Wallis	0.0555	0.00097	1.00± 0.00	1.00± 0.00	1.00± 0.00
Pielou_e	Kruskal-Wallis	0.0798	0.018	0.90± 0.01	0.91± 0.01	0.91± 0.01
Shannon	ANOVA	0.4070	0.0543	11.36± 0.16	11.55± 0.37	11.65± 0.24
Observed_species	Kruskal-Wallis	0.0005	0.0231	6534.20± 569.68	5866.40± 343.80	6272.60± 93.06
Faith_pd	ANOVA	0.7430	0.0593	457.42± 40.45	459.98± 32.51	460.52± 6.34

The increase in bacterial richness under heavy grazing suggests that, in steppe ecosystems, grazing disturbance does not necessarily lead to taxon loss but may promote the coexistence of multiple stress-tolerant bacterial taxa. Comparable disturbance-mediated richness patterns have been reported in arid and semi-arid grassland soils, where environmental stress favors microbial taxa adapted to low resource availability and physical disturbance [1, 17]. In contrast, diversity and evenness-related indices did not differ significantly among grazing intensities. Shannon diversity ranged from 11.36 ± 0.16 to 11.65 ± 0.24 ($p > 0.05$), while Simpson diversity and Pielou's evenness exhibited consistently high and comparable values across all grazing groups (Simpson ≈ 1.00; Pielou's evenness = 0.90-0.91). Faith's phylogenetic diversity also remained stable across grazing intensities ($p > 0.05$), indicating that grazing pressure did not substantially affect the evolutionary breadth of bacterial communities (Table 1). Together, these results indicate a decoupling between taxonomic richness and community evenness under grazing disturbance. While grazing intensity altered the number of detectable taxa, relative abundance distributions and phylogenetic structure remained conserved, a pattern characteristic of soil microbial communities exhibiting high functional redundancy and resilience to disturbance [18].

Beta diversity analysis based on Bray-Curtis dissimilarity revealed significant differences in bacterial community composition among grazing intensities in steppe pastures. PERMANOVA results indicated that grazing pressure significantly structured bacterial assemblages (F = 1.69, R2 = 0.22, p = 0.006; Table 2).

Table 2 – Results of permutational multivariate analysis of variance (PERMANOVA)

Source	Df	Sum of squares	R^2	F	p-value
Group	2	0.92	0.22	1.69	0.006
Residual	12	3.26	0.78		
Total	14	4.18	1.00		

The moderate R^2 value suggests that grazing intensity explains a meaningful but not dominant proportion of total community variation, indicating that grazing acts alongside strong background controls such as climate and soil type. Similar moderate effect sizes have been reported for grazing impacts on soil bacterial communities in environmentally constrained grassland ecosystems [3, 19]. Importantly, tests of homogeneity of multivariate dispersion (betadisper) revealed no significant differences in within-group variability among grazing intensities (ANOVA p = 0.41; permutation test p = 0.39; Figure 1). This confirms that the observed PERMANOVA results reflect true compositional differences rather than dispersion effects [15].

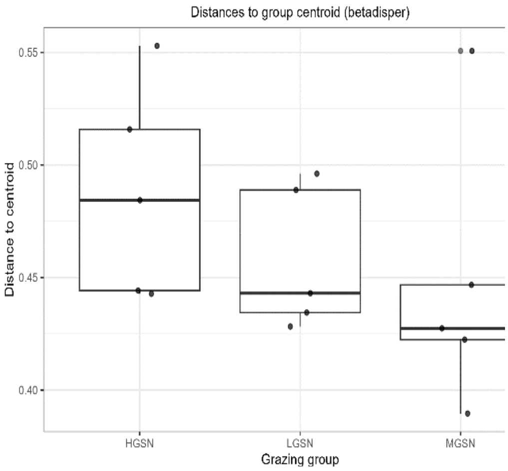

Figure 1 – Beta dispersion of soil bacterial communities across grazing intensities in steppe pastures based on Bray-Curtis dissimilarity

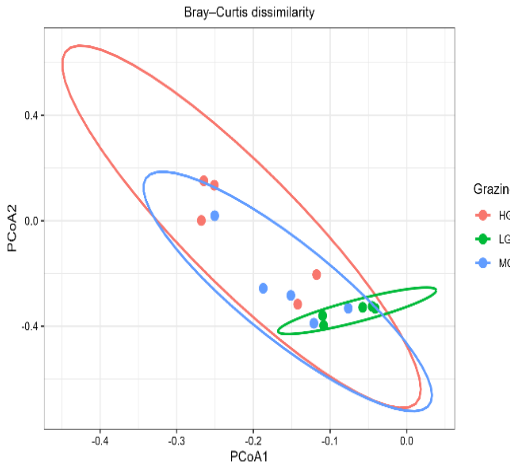

Figure 2 – Principal coordinates analysis (PCoA) of soil bacterial community composition across grazing intensities in steppe pastures based on Bray-Curtis dissimilarity

Ordination patterns from principal coordinates analysis further indicated partial overlap among grazing groups, suggesting that grazing-induced community changes occurred along a continuous gradient rather than as abrupt compositional shifts (Figure 2). Overall, these findings indicate that grazing intensity modifies bacterial community composition without increasing within-group heterogeneity.

Across all grazing intensities, soil bacterial communities in the steppe ecosystem were dominated by members of the phyla *Actinobacteriota, Proteobacteria, Firmicutes, Acidobacteriota,* and *Bacteroidota,* which together accounted for the majority of total sequence abundance (Figure 3).

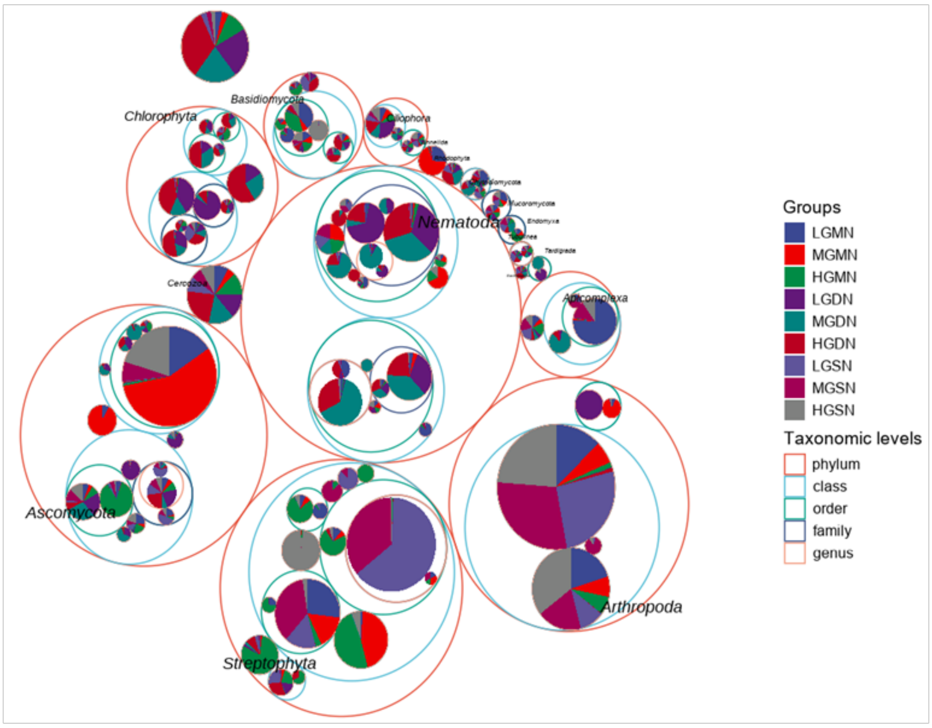

Figure 3 – Taxonomic composition of soil bacterial communities in steppe pastures across grazing intensities

The overall taxonomic structure at the phylum level remained broadly similar across grazing groups, indicating the presence of a shared core bacterial community adapted to steppe environmental conditions. However, variations in the relative abundance of dominant phyla were observed along the grazing gradient, suggesting reorganization of community structure rather than complete taxonomic turnover. Such stability of higher-level taxonomic composition under disturbance has been widely reported for grassland soils [20].

Classification of bacterial taxa according to Gram staining characteristics revealed distinct functional patterns along the grazing gradient (Figure 4).

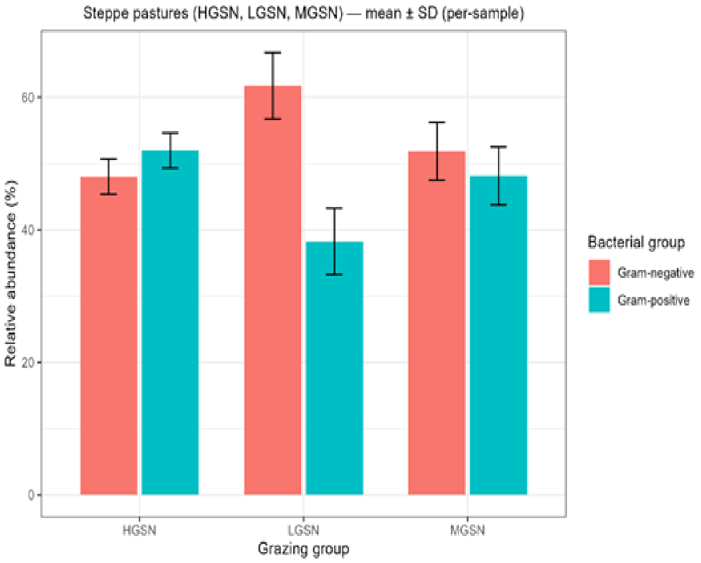

Figure 4 – Relative abundance of Gram-positive and Gram-negative bacterial groups across grazing intensities in steppe pastures, indicating a shift toward stress-tolerant bacterial group
s under increased grazing pressure

Gram-positive bacteria, primarily represented by *Actinobacteriota* and *Firmicutes*, exhibited higher relative abundance under moderate and heavy grazing conditions, whereas Gram-negative bacteria, including *Proteobacteria* and *Bacteroidota*, were relatively more abundant under light grazing. The increased dominance of Gram-positive bacteria under elevated grazing pressure likely reflects their enhanced resistance to environmental stressors such as desiccation, nutrient limitation, and physical disturbance. Traits such as thick cell walls, spore formation, and conservative growth strategies may confer competitive advantages under grazing-induced soil stress [4,5]. These stress-tolerant groups primarily include representatives of *Actinobacteriota* (e.g., *Streptomyces, Nocardia*) and spore-forming *Firmicutes* (e.g., *Bacillus, Clostridium*). In contrast, Gram-negative bacteria are often associated with copiotrophic lifestyles and higher availability of labile organic substrates, conditions more typical of less disturbed soils [3]. The observed shifts in Gram-positive and Gram-negative proportions therefore suggest that trait-based microbial indicators may provide sensitive signals of grazing pressure. Gram classification in this study was assigned at the phylum level and therefore represents a functional approximation rather than a strict taxonomic distinction. Functional heterogeneity may exist within individual phyla, and not all taxa within *Actinobacteriota* or *Firmicutes* necessarily exhibit uniform physiological responses to environmental stress. Consequently, the observed Gram-positive and Gram-negative patterns should be interpreted as indicative of broad community-level functional tendencies rather than precise trait-based classifications at lower taxonomic resolution. Importantly, these functional shifts occurred without substantial loss of overall bacterial diversity, indicating that grazing alters community structure and functional balance rather than causing microbial degradation per se. Similar trait-based microbial responses have been proposed as early indicators of soil disturbance preceding visible changes in vegetation [21].

Despite significant changes in taxonomic richness and community composition, phylogenetic diversity remained stable across grazing intensities, as indicated by Faith's PD values. This suggests that grazing-induced changes occurred primarily within existing evolutionary lineages rather than through the loss of deeply divergent taxa. Phylogenetic patterns further revealed that taxa persisting under higher grazing pressure tended to cluster within specific lineages associated with stress tolerance, particularly within *Actinobacteriota* (Figure 5).

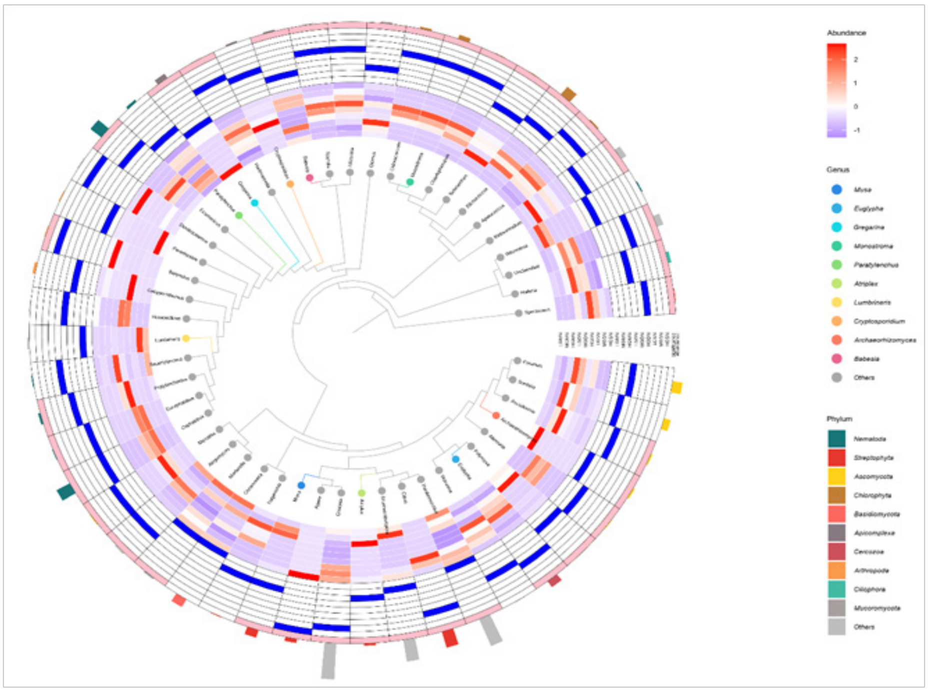

Figure 5 – Phylogenetic relationships of dominant soil bacterial taxa across pasture ecosystems

Such patterns support the concept of phylogenetic conservatism, whereby closely related taxa share adaptive traits that confer resilience to environmental disturbance [22]. Overall, the results indicate that grazing acts as an environmental filter, reshaping bacterial communities through lineage-level reorganization while preserving overall evolutionary structure. The combined alpha and beta diversity results demonstrate that soil bacterial communities in steppe pastures exhibit a high degree of resilience to grazing disturbance, highlighting the importance of ecosystem-specific and trait-based approaches when assessing grazing impacts on soil microbial diversity and pasture sustainability [20].

A limitation of this study is the absence of direct measurements of key abiotic soil properties, such as soil moisture, organic carbon content, and nutrient availability, which are known to strongly influence microbial community composition. Incorporating these environmental parameters in future studies would improve the mechanistic interpretation of grazing-induced microbial responses. It should also be noted that functional interpretations in this study are based on taxonomic inference derived from 16S rRNA gene sequencing rather than direct measurements of microbial metabolic potential. Consequently, the trait-based patterns observed here should be interpreted as indirect indicators of functional shifts within the microbial community.

Conclusion

This study provides a comprehensive assessment of soil bacterial community responses to grazing pressure within steppe pasture ecosystems of Central Asia. By integrating taxonomic, phylogenetic, and compositional analyses based on high-throughput 16S rRNA gene sequencing, we demonstrate that grazing influences bacterial communities in a selective and context-dependent manner rather than causing uniform degradation.

Our results show that grazing pressure significantly affected bacterial taxonomic richness, as reflected by changes in Chao1 and observed species richness indices. Richness responses to grazing were ecosystem-specific, with the steppe zone exhibiting elevated richness under heavy grazing. In contrast, diversity indices incorporating community evenness, including Shannon diversity, Simpson index, and Pielou's evenness, remained relatively stable across grazing regimes. These findings indicate that grazing primarily alters the number of taxa present rather than the relative distribution of abundances among dominant bacterial groups.

Beta diversity analyses further revealed significant differences in bacterial community composition among grazing groups, suggesting that grazing pressure reshapes community structure through gradual compositional shifts. The absence of significant differences in multivariate dispersion confirms that these patterns reflect genuine changes in community composition rather than increased variability within grazing groups. Together, these results indicate that grazing modifies bacterial assemblages along a continuum, without inducing abrupt community reorganization.

Analysis of Gram-positive and Gram-negative bacterial groups revealed contrasting responses to grazing intensity. Gram-positive bacteria, particularly representatives of Actinobacteriota and Firmicutes, increased in relative abundance under moderate grazing, whereas Gram-negative bacteria were more prevalent under lighter grazing conditions. This shift suggests that grazing favors stress-tolerant bacterial lineages with traits adapted to resource limitation and physical disturbance.

Despite observable changes in taxonomic composition and richness, phylogenetic diversity remained relatively conserved across grazing regimes. This indicates that grazing-induced shifts occur primarily within existing evolutionary lineages, supporting the concept of environmental filtering acting on phylogenetically conserved traits rather than eliminating broad evolutionary groups.

Overall, the findings highlight the resilience of steppe soil bacterial communities to grazing disturbance and emphasize that grazing effects on microbial diversity cannot be generalized across ecosystems. Instead, microbial responses are shaped by interactions between grazing pressure, environmental constraints, and long-term adaptation to arid and semi-arid conditions. These results underscore the importance of ecosystem-specific assessments when evaluating grazing impacts on belowground biodiversity and provide a foundation for integrating microbial indicators into sustainable rangeland management strategies in Central Asian pastures.

Authors' contributions

MT, DW and AK: conceptualized and designed the study, conducted a comprehensive literature search, analyzed the collected data, and drafted the manuscript. KK, AK and AS: conducted the literature search and proofread the manuscript. All authors read, reviewed, and approved the final version of the manuscript.

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Trait-based (основанные на функциональных признаках) реакции грамположительных и грамотрицательных почвенных бактерий на интенсивность выпаса в степных экосистемах

Тастыбай М.Б., Дели Ванг, Канаев А.Т., Кушенов К.И., Сейтбатталова А.И.

Аннотация

Предпосылки и цель. Степные пастбища Центральной Азии подвергаются длительному пастбищному воздействию, которое может изменять почвенные свойства и структуру подземных микробных сообществ. Почвенные бактерии играют ключевую роль в круговороте питательных веществ и устойчивости экосистем, однако их реакции на интенсивность выпаса в степных экосистемах остаются недостаточно изученными. Целью настоящего исследования была оценка влияния интенсивности выпаса на разнообразие почвенных бактерий, состав сообществ и функциональную структуру с особым акцентом на таксономическое богатство и группы грамположительных и грамотрицательных бактерий.

Материалы и методы. Почвенные образцы были отобраны на степных пастбищах с лёгкой, умеренной и сильной степенью выпаса. Состав бактериальных сообществ анализировали методом высокопроизводительного секвенирования гена 16S рРНК. Рассчитывали показатели альфа-разнообразия (Chao1, наблюдаемое видовое богатство, индексы Шеннона, Симпсона, равномерности Пиелу и филогенетического разнообразия Фейта). Бета-разнообразие оценивали с использованием расстояния Брея–Кёртиса, анализа главных координат (PCoA) и пермутационного многомерного дисперсионного анализа (PERMANOVA). Однородность многомерной дисперсии оценивали методом betadisper. Таксоны бактерий дополнительно классифицировали на грамположительные и грамотрицательные группы для оценки функциональных реакций на выпас.

Результаты. Показатели таксономического богатства достоверно различались между группами интенсивности выпаса, что свидетельствует о чувствительности бактериального богатства к пастбищному воздействию. В то же время индексы Шеннона, равномерности и филогенетического разнообразия не выявили значимых различий, указывая на структурную стабильность бактериальных сообществ. Анализ бета-разнообразия показал достоверные различия в составе сообществ между группами выпаса при отсутствии различий в дисперсии, что подтверждает реальные сдвиги в составе сообществ. Функциональный анализ выявил контрастные реакции грамположительных и грамотрицательных бактерий вдоль градиента выпаса.

Заключение. Интенсивность выпаса в степных экосистемах в первую очередь влияет на таксономическое богатство и состав почвенных бактериальных сообществ, тогда как равномерность разнообразия и филогенетическая структура остаются относительно стабильными. Выпас выступает в роли экологического фильтра, формируя функциональную структуру микробных сообществ без выраженной потери бактериального разнообразия. Полученные результаты подчёркивают устойчивость почвенных бактериальных сообществ степей и подтверждают целесообразность использования микробных индикаторов в устойчивом управлении пастбищами.

Ключевые слова: альфа-бета разнообразие; грамположительные бактерии; грамотрицательные бактерии; интенсивность выпаса; почвенные бактерии; степные пастбища.

Далалық экожүйелерде жайылым қарқындылығына жауап ретінде грам-оң және грам-теріс топырақ бактерияларының функционалдық белгілерге негізделген (trait-based) реакциясы

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Түйін

Алғышарттар және мақсат. Орталық Азияның далалық жайылымдары ұзақ мерзімді жайылым әсеріне ұшырап, топырақ қасиеттері мен жерасты микробтық қауымдастықтарының құрылымын өзгертуі мүмкін. Топырақ бактериялары қоректік элементтердің айналымында және экожүйелердің тұрақтылығында маңызды рөл атқарады, алайда олардың жайылым қарқындылығына реакциясы далалық экожүйелерде жеткілікті деңгейде зерттелмеген. Осы зерттеудің мақсаты – жайылым қарқындылығының топырақ бактерияларының әртүрлілігіне, қауымдастық құрамына және функционалдық құрылымына әсерін, әсіресе таксономиялық байлық пен грамоң және грамтеріс бактериялар топтарына баса назар аудара отырып, бағалау.

Материалдар мен әдістер. Топырақ үлгілері жеңіл, орташа және күшті жайылым жағдайындағы далалық жайылымдардан алынды. Бактериялық қауымдастықтардың құрамы 16S рРНҚ генін жоғары өнімді секвенирлеу әдісімен анықталды. Альфа-әртүрлілік көрсеткіштері (Chao1, байқалған түрлік байлық, Шеннон, Симпсон индекстері, Пиелу теңдестігі және Фейттің филогенетикалық әртүрлілігі) есептелді. Бета-әртүрлілік Брей-Кёртис қашықтығы, негізгі координаталар талдауы (PCoA) және пермутациялық көпөлшемді дисперсиялық талдау (PERMANOVA) арқылы бағаланды. Көпөлшемді дисперсияның біртектілігі betadisper әдісімен тексерілді. Функционалдық жауаптарды бағалау үшін бактериялық таксондар грамоң және грамтеріс топтарға жіктелді.

Нәтижелер. Таксономиялық байлық көрсеткіштері жайылым қарқындылығы бойынша айтарлықтай айырмашылық көрсетті, бұл бактериялық байлықтың жайылым әсеріне сезімтал екенін дәлелдейді. Ал Шеннон индексі, теңдестік көрсеткіштері және филогенетикалық әртүрлілік бойынша мәнді айырмашылықтар байқалмады, бұл бактериялық қауымдастықтардың құрылымдық тұрақтылығын көрсетеді. Бета-әртүрлілік талдауы жайылым топтары арасында қауымдастық құрамында елеулі айырмашылықтарды анықтады, ал дисперсияның айырмашылығы болмауы нақты құрамдық өзгерістердің бар екенін растады. Функционалдық талдау жайылым градиенті бойында грамоң және грамтеріс бактериялардың қарама-қарсы жауаптарын көрсетті.

Қорытынды. Далалық экожүйелерде жайылым қарқындылығы топырақ бактерияларының таксономиялық байлығы мен қауымдастық құрамына негізінен әсер етеді, ал әртүрліліктің теңдестігі мен филогенетикалық құрылымы салыстырмалы түрде тұрақты болып қалады. Жайылым микробтық функционалдық құрылымды қалыптастыратын экологиялық сүзгі ретінде әрекет етеді және бактериялық әртүрліліктің айқын төмендеуіне әкелмейді. Алынған нәтижелер далалық топырақ бактериялық қауымдастықтарының тұрақтылығын көрсетіп, тұрақты жайылым басқаруында микробтық индикаторларды қолданудың маңыздылығын дәлелдейді.

Кілт сөздер: альфа-бета әртүрлілік; грамоң бактериялар; грамтеріс бактериялар; жайылым қарқындылығы; топырақ бактериялары; далалық жайылымдар.