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Article

Ecological Responses of Soil Properties and Microbial Diversity to Elevational Gradients and Human Activities in the Bogda Mountains, Xinjiang

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Abstract

This study explored the combined effects of elevational gradients and anthropogenic activities on soil physicochemical properties and microbial communities in the northern slope of the eastern foot of the Bogda Mountains, Xinjiang. The key objectives were to identify the dominant driving factors of soil microbial community variation and provide scientific and actionable implications for regional environmental management and ecological sustainability in arid-semiarid mountain ecosystems. Soil samples were collected from 10 sampling sites (8 distributed along the elevational gradient and 2 in human-disturbed areas) using the five-point sampling method. One-way analysis of variance (ANOVA) and redundancy analysis (RDA) were applied to quantify the variations in soil properties (moisture, pH, total nitrogen, etc.) and microbial characteristics (abundance, species richness and diversity). The results showed that soil physicochemical properties presented obvious vertical distribution patterns along the elevational gradient: the mid-altitude spruce forest zone had significantly higher soil moisture and organic matter contents, whereas the high-altitude zone exhibited extremely low levels of these two indicators; the agricultural area had a notably elevated available phosphorus content compared with natural habitats. Soil microbial communities showed distinct spatial heterogeneity: the low-altitude desert zone had the highest bacterial abundance, the mid-altitude spruce forest zone maintained the highest microbial diversity, and the high-altitude meadow/cold desert zone was characterized by the impoverishment of microbial abundance and diversity. Anthropogenic agricultural activities significantly increased soil bacterial abundance but reduced the overall microbial diversity in the affected areas. RDA further revealed that soil organic matter, total nitrogen and moisture were the core driving factors regulating the structure and diversity of soil microbial communities. In conclusion, elevational gradients and anthropogenic activities shape the distribution and variation of soil microbial communities by altering soil physicochemical properties, and irrational human disturbances would disrupt the synergistic interaction between soil properties and microbial communities. These findings provide a solid scientific basis for optimizing regional ecological protection measures, formulating sustainable agricultural practices, and constructing adaptive environmental management strategies for arid-semiarid mountainous regions.

Keywords

Bogda mountains, Elevational gradient, Anthropogenic activity, Soil microbial diversity, Soil physicochemical property, Environmental sustainability

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1. Introduction

The Bogda Mountains, a core segment of the Tianshan Mountains, boast diverse ecosystems and high biodiversity shaped by distinct vertical zonality [1], with rich biological resources and strategic natural reserves [2]. As a sentinel region for studying ecosystem responses to climate change and anthropogenic disturbances, it plays a pivotal role in balancing environmental conservation and sustainable resource utilization [3]. The soil-microbe system, a linchpin of material cycling and energy flow in alpine ecosystems, directly modulates ecological stability and service functions through its adaptive responses to environmental shifts [4]. Investigating how soil physicochemical properties and microbial communities respond to elevational gradients and human activities here not only enhances understanding of arid-semiarid mountain ecosystem vulnerability but also provides actionable insights for designing adaptive conservation strategies, predicting anthropogenic impact thresholds, and guiding regional sustainable development-thus bridging ecological research with practical environmental management [5].

Recent studies on elevational gradients have demonstrated their profound influence on microbial community structure and diversity, primarily via modifications to temperature, precipitation, and vegetation-driven environmental filters [6,7]. Concurrently, research on anthropogenic activities (e.g., agricultural cultivation) highlights that tillage practices alter soil organic matter dynamics, aggregate stability, and nutrient cycling, thereby reshaping microbial biomass and community composition [8,9]. Moreover, strong correlations between microbial biomass and soil organic matter have been documented across ecosystems [10,11]. However, critical knowledge gaps remain: quantitative analyses of how key soil factors (e.g., moisture, total nitrogen, pH) drive microbial communities (bacteria, fungi, actinomycetes) under combined natural elevational gradients and human disturbances are scarce [12,13], particularly in arid-semiarid high-altitude regions where such interactions directly impact land-use sustainability [14].

To address this deficit in understanding microbial regulatory mechanisms under synergistic natural and anthropogenic pressures [15], this study focuses on the northern slope of the eastern Bogda Mountains (Jimusaer County)-a region with pronounced elevational stratification and agricultural activity, making it a model system for studying human-nature interactions [16]. This region, characterized by distinct altitude gradients and agricultural disturbances, provides a typical case for studying interactions between natural and human factors [17]. We aim to explore the combined effects of altitude gradients and human activities (agricultural planting) on soil physicochemical properties and microbial communities, quantify the driving intensity of key factors (e.g., moisture content, total nitrogen, pH) on bacterial, fungal, and actinomycete communities via redundancy analysis (RDA), and thus reveal the synergistic regulatory pathways of natural environmental factors and anthropogenic disturbances on soil microbial communities, filling the research gap in this region.

The aim of the present study is to: (1) clarify the spatial differentiation characteristics of soil physicochemical properties (e.g., moisture content, total nitrogen, pH) across different altitude gradients and human activity-affected (agricultural planting) areas on the northern slope of the eastern foot of the Bogda Mountain Range; (2) clarify the variation patterns of soil bacterial, fungal, and actinomycete communities under the combined effects of altitude gradients and human activities; (3) quantify the driving intensity of key soil physicochemical factors on microbial community structure and distinguish the contribution differences between natural and anthropogenic factors; and (4) reveal the synergistic regulatory mechanisms of natural and anthropogenic factors on soil microbial communities, providing clear scientific insights into the responses of soil-microbe systems to environmental changes in arid-semiarid high-altitude mountainous areas [18].

2. Materials and Methods

2.1 Study Site Description

The experiment was conducted from June to July 2025 in the southern mountainous area of Jimusaer County, Changji Prefecture, Xinjiang (89°03′E, 43°57′N), located on the northern slope of the eastern foot of the Bogda Mountain Range(Here,the grass is abundant in June and July,and the scenery is beautiful.It is a great place for summer. The seasonal pastures,which are also the peak tourist season and the busy farming period each year,are most affected by human activities. Accordingly, this seasonal window and study area were chosen to reflect the peak of human activity in the region. The climate in this region shows significant vertical variation with elevation: Low-altitude areas have an annual evaporation of 1800-2200 mm and annual precipitation of 150-200 mm; Mid-to-high altitude areas have decreasing annual evaporation (800-1200 mm) and increasing annual precipitation (300-500 mm), with a mean annual temperature of 2.5-7.8 °C and a frost-free period of 120-180 days [19].

2.2 Chemicals and Media

Chemicals used in the experiment included sodium hydroxide, sodium hypochlorite, potassium dichromate solution, silver sulfate, o-phenanthroline solution, ammonium ferrous sulfate solution, $NaHCO_3$ solution, potassium sulfate, copper sulfate, concentrated sulfuric acid, and boric acid solution (all analytical grade, Sinopharm Chemical Reagent Co., Ltd.). Media included nutrient agar (beef extract-peptone medium), modified Gao’s No. 1 medium, and rose bengal medium (all from Jinan Bobo Biotechnology Co., Ltd.).

2.3 Experimental Design and Soil Sampling

A total of 10 sampling sites were set up, including 8 sites along different altitude gradients and 2 sites affected by human activities (a wheat field and a residential area). The locations of all sampling sites are shown in Figure 1. Soil sampling was conducted following the *GB/T 36197-2018 Guidelines for Soil Sampling Technology*. At each site, the five-point sampling method was used: surface soil (5-15 cm depth) was collected from the four corners and center of the sampling plot using a sterile sampler, placed in sterile bags, and immediately stored in an insulated box with ice packs at 4 °C for transportation to the laboratory.

Soil samples were divided into two parts: One part was passed through a 2 mm sieve and stored at 4 °C for microbial analysis; the other part was air-dried in a cool, dry place (with regular turning to remove debris). A 10 g subsample of the air-dried soil was sealed in a bag, labeled with sampling date, location (latitude and longitude), soil depth, land use type, and sampler, and stored in a dry, cool place for determination of soil nutrients [20].

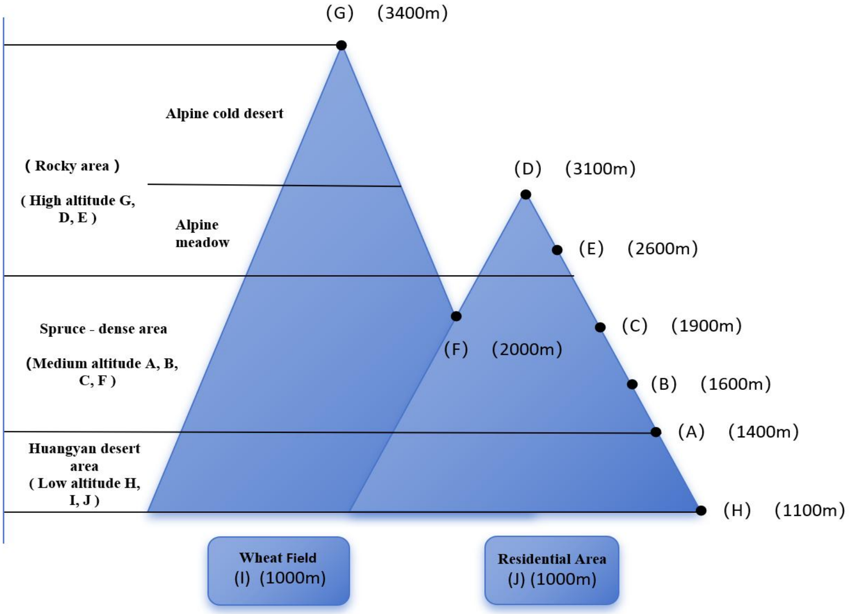

Figure 1. Schematic diagram of sampling points on the north slope of the eastern foot of the Bogda Mountain Range.

Note: The sample point numbers are assigned according to the sampling sequence and the order of English letters, and have no other practical significance.

2.4 Determination of Soil Physicochemical Properties

pH value: 10 g of air-dried soil was mixed with 25 mL distilled water at a soil-to-water ratio of 1:2.5. After stirring for 1 min and standing for 30 min, the filtrate was measured using a pH meter in a constant temperature environment (25±1) °C.

Moisture content (oven-drying method): 10 g of soil (weighed to 0.01 g) was placed in a pre-weighed crucible, dried at 105 °C for 24 h to constant weight (weight difference <0.01 g). The calculation formula was:

$$\text{Moisture content (\%)} = (W_1 - W_1)/(W_2 - W_0) \times 100\% \quad (1)$$

(W_0: weight of the crucible; W_1: weight of wet soil + crucible; W_2: weight of dry soil + crucible after constant weight).

Organic matter: Determined by the potassium dichromate oxidation-external heating method. 0.4 g of soil (passed through a 0.25 mm sieve) was mixed with 0.1 g silver sulfate, 5 mL of 0.8 mol/L potassium dichromate solution, and 5 mL concentrated sulfuric acid, then digested in an oil bath at 170-180 °C for 5 min. After cooling, the sample was titrated with 0.2 mol/L ammonium ferrous sulfate using o-phenanthroline as an indicator, with a blank test performed simultaneously.

Available phosphorus: 1.25 g of soil (passed through a 2 mm sieve) was extracted with 25 mL of 0.5 mol/L $NaHCO_3$ solution (pH 8.5) by shaking at 25 °C for 40 min. After filtration, 2 mL of the filtrate was mixed with molybdenum-antimony color reagent, reacted in the dark for 30 min, and absorbance was measured at 700 nm (quantified using a standard curve).

Available potassium: 2.5 g of soil (passed through a 2 mm sieve) was extracted with 25 mL of 1 mol/L neutral ammonium acetate solution (pH 7.0) by shaking at 25 °C for 30 min. After filtration, the concentration was determined using a flame photometer (quantified using a standard curve).

Total nitrogen: Determined by the sulfuric acid-hydrogen peroxide digestion method. 0.5 g of soil (passed through a 100-mesh sieve) was mixed with 1.5 g of K_2SO_4-$CuSO_4$ catalyst (10:1) and 4 mL concentrated sulfuric acid, pre-digested at 150 °C, then heated to 350 °C for 1.5 h. After distillation using a Kjeldahl nitrogen analyzer, the boric acid absorption solution was titrated with 0.01 mol/L HCl. The calculation formula was:

$$\text{Total Nitrogen (g/kg)} = [(V - V_0) \times C \times 14.01 \times 1000]/m \tag{2}$$

(V: volume of HCl consumed by the sample; V_0: volume of HCl consumed by the blank; C: concentration of HCl; m: mass of soil sample. Note: 14.01 represents the molar mass of nitrogen, with the unit g/mol.)

2.5 Soil Microbial Enumeration

Microbial counts were performed using the plate count method according to *HJ 717-2014*. For sample pretreatment: 10 g of fresh soil (passed through a 2 mm sieve) was added to 90 mL of sterile physiological saline (0.85% NaCl, pH 7.0±0.2), shaken at 180 r/min for 30 min, and serially diluted to 10^{-6} (for bacteria), 10^{-4} (for fungi), and 10^{-5} (for actinomycetes).

Cultivation conditions were as follows:

Bacteria: nutrient agar medium, incubated at 28 °C for (48±2) h;

Fungi: rose bengal martin medium, incubated at 25 °C for (72±3) h;

Actinomycetes: modified Gao's No. 1 medium, incubated at 28 °C for (120±5) h.

Each dilution gradient was replicated 4 times, and plates with 30-300 colonies were selected for counting [21]. Microbial species identification was based on morphological and physiological biochemical characteristics: (1) Morphological observation: the shape, color, edge, elevation, and transparency of the colonies were recorded; (2) Physiological and biochemical tests: carbon source utilization, enzyme activity (such as catalase), and salt tolerance; (3) Classification criteria: Species classification referenced Bergey's Manual® of Systematic Bacteriology [21] for bacteria and Fungi Classification And Identification [22] for fungi, combined with colony and cell morphological characteristics. The calculation formula was:

$$\text{Microbial Count (CFU/g dry soil)} = (N \times D \times V \times Wf)/(Wd \times A) \tag{3}$$

(N: average number of colonies; D: dilution factor; V: inoculation volume; Wf: weight of fresh soil; Wd: weight of dry soil; A: inoculation volume coefficient (0.1 mL)).

2.6 Data Analysis

Data were collated and analyzed using Excel 2024 and Origin 2024. One-way analysis of variance (ANOVA) was employed to compare differences in soil physicochemical properties and microbial counts among different altitudes/regions, with statistical significance set at $P < 0.05$.

RDA was performed using Canoco 5.0:

Detrended correspondence analysis (DCA) was first used to determine the distribution type of community data (RDA was applied if the longest gradient length <3);

Microbial counts and species richness (response variables) were analyzed with soil physicochemical factors (explanatory variables) using 499 Monte Carlo permutation tests to identify significant influencing factors ($P < 0.05$);

Ordination plots were used to visualize the correlation strength between factors and communities, and the explanation rate of each factor and total explanation rate were calculated.

3. Results

3.1 Soil Physicochemical Properties and Microbial Characteristics at Different Sampling Sites

As indicated by the data in Table 1, Table 2, and Table 3:

3.1.1 Low-altitude Huangyan Desert Area (H, I, J)

The low-altitude Huangyan desert area, affected by the combined effects of arid climate and human activities, exhibited significant heterogeneity in soil physicochemical properties. Site H (1100 m) had an extremely low moisture content (3.67%) and a high electrical conductivity (2020 μS/cm), reflecting salt accumulation in the desert environment. Sites I (wheat field, 1000 m) and J (residential area, 1000 m) had slightly higher moisture contents (I: 17.91%; J: 1.3%), but their organic matter contents (I: 24.33 g/kg; J: 7.15 g/kg) were significantly lower than those in the mid-altitude spruce area, indicating the modification of soil carbon pools by agricultural cultivation and domestic activities.

Microbial communities showed differential responses to environmental stress: Site H had an abnormally high bacterial count (118.33×10^4 CFU/g), presumably due to the selection of stress-tolerant flora by the high-salt environment; fungal count (8.33×10^4 CFU/g) was significantly inhibited by drought stress, with a total of 23 microbial species and a Shannon-Wiener index (H') of 2.37. Site I (wheat field) had moderate microbial counts (bacteria: 90×10^4 CFU/g; fungi: 11.5×10^4 CFU/g), while exogenous nutrients from fertilization and fragmented habitats caused by tillage disturbance jointly restricted microbial diversity (total 13 microbial species, 7 bacterial species; 4 fungal species)and the Shannon-Wiener index (H') was only 1.52. Site J (residential area) had 11 bacterial species, with a total of 19 microbial species and a Shannon-Wiener index (H') of 2.11; input of domestic waste increased flora richness, but deficient available phosphorus (1.51 mg/kg) limited microbial biomass accumulation, and actinomycete count (43.31×10^4 CFU/g) was significantly lower than that in the spruce area due to insufficient organic matter supply.

3.1.2 Mid-altitude Dense Spruce Area (A, B, C, F)

The mid-altitude dense spruce area, supported by forest ecosystems, formed a soil environment with high moisture content (A: 43.16%) and high organic matter (A: 77.53 g/kg). Continuous input of spruce litter and microbial decomposition jointly drove nutrient accumulation; soil pH remained in the weakly acidic to weakly alkaline range (6.72-7.53), creating a microhabitat suitable for the reproduction of forest microorganisms.

Microbial communities showed significant enrichment: Bacterial counts were generally high (A: 81×10^4 CFU/g; C: 81.33×10^4 CFU/g), with abundant organic matter providing sufficient carbon sources for bacterial metabolism; fungal counts increased simultaneously (A: 23×10^4 CFU/g), as lignin components in spruce litter drove the proliferation of saprophytic fungi. Microbial species diversity was prominent (A: 6 bacterial species, 7 fungal species, total 20 microbial species, and the Shannon-Wiener index (H') reached 2.63 (the highest among all sampling sites); C: 10 bacterial species, total 20 microbial species, and the Shannon-Wiener index (H') was 2.51), and complex nutrient structures (total nitrogen in A: 3.57 mg/kg) supported niche differentiation of flora, verifying the "forest ecology-microbial co-evolution" mechanism.

3.1.3 High-altitude Meadow/Cold Desert Area (D, E, G)

High-altitude meadows (D: 3100 m; E: 2600 m) and cold desert (G: 3400 m) were subject to extreme low temperatures and drought stress, with low vegetation coverage, scarce input of soil organic matter (G: 4.81 g/kg), and extremely low moisture content (G: 1.21%); soil pH was weakly alkaline (7.26-7.47), mainly controlled by the weathering of parent materials.

Microbial communities showed significant impoverishment: Microbial counts decreased continuously with increasing altitude (G: bacteria 14.33×10^4 CFU/g, fungi 5.33×10^4 CFU/g). Extreme environments limited community biomass accumulation by inhibiting microbial metabolic activity and reducing enzymatic reaction efficiency; microbial species were simple (G: 5 bacterial species, 4 fungal species, total 13 microbial species, and the Shannon-Wiener index (H') was 1.89), with simplified niches. Although sites D and E (meadows) were at lower altitudes than G, site D had 19 microbial species and a Shannon-Wiener index (H') of 2.43 (bacteria 51×10^4 CFU/g), and site E had 14 microbial species and a Shannon-Wiener index (H') of 2.07; their microbial counts were still significantly lower than those in the mid-altitude area. Nutrient supply limitation caused by insufficient meadow vegetation productivity verified the “altitude-vegetation-microbe” gradient attenuation law.

Table 1. Soil physical and chemical properties at different sampling points.

Sampling point	Moisture content (%)	Electrical conductivity (μS/cm)	Electrical conductivity (μS/cm)	Organic matter (g/kg)	Total nitrogen (mg/kg)	Available phosphorus (mg/kg)	Available potassium (mg/kg)
A	43.16 ± 0.7	6.72 ± 0.13	1680 ± 10.83	77.53 ± 0.64	3.57 ± 0.31	5.73 ± 0.13	173.61 ± 1.37
B	28.6 ± 0.3	7.49 ± 0.1	758 ± 21.32	58.34 ± 0.32	2.83 ± 0.5	4.97 ± 0.21	162.51 ± 10.43
C	27.17 ± 0.5	7.53 ± 0.24	674 ± 9.54	53.92 ± 0.13	2.35 ± 0.12	5.35 ± 0.1	156.55 ± 21.3
D	22.45 ± 0.78	7.47 ± 0.33	615 ± 23.33	25.11 ± 0.13	1.99 ± 0.2	4.75 ± 0.1	100.66 ± 4.5
E	9.7 ± 0.1	7.42 ± 0.51	738 ± 17.6	31.33 ± 0.64	1.67 ± 0.44	3.13 ± 0.14	88.35 ± 7.62
F	11.74 ± 0.2	7.37 ± 0.12	593 ± 22.5	48.02 ± 0.71	1.87 ± 0.08	3.89 ± 0.16	85.36 ± 3.54
G	1.21 ± 0.05	7.28 ± 0.2	685 ± 21.11	4.81 ± 0.21	0.52 ± 0.24	1.91 ± 0.23	33.22 ± 1.77
H	3.67 ± 0.2	7.26 ± 0.13	2020 ± 87.32	4.98 ± 0.11	0.43 ± 0.25	1.88 ± 0.08	39.33 ± 5.55
I	17.91 ± 0.4	7.55 ± 0.09	383 ± 13.21	24.33 ± 0.31	2.01 ± 0.05	11.37 ± 0.2	90.03 ± 1.33
J	1.3 ± 0.1	7.45 ± 0.2	654 ± 17.89	7.15 ± 0.5	0.31 ± 0.1	1.51 ± 0.07	34.77 ± 1.79

Table 2. Microbial quantity and species number at different sampling points.

Sampling point	Bacterial count ($\times 10^4$ CFU/g)	Actinomycete count ($\times 10^4$ CFU/g)	Fungal count ($\times 10^4$ CFU/g)	Number of bacterial species	Number of actinomycete species	Number of fungal species
A	81	64	23	6	7	7
B	58	28	25	6	3	6
C	81.33	31	22.5	10	4	6
D	51	36	21.5	10	4	5
E	71.33	19	8.5	5	4	5
F	50.66	46	6	7	6	3
G	14.33	12	5.33	5	4	4
H	118.33	28.66	8.33	14	4	5
I	90	19.33	11.5	7	2	4
J	74	43.31	11.4	11	3	5

Table 3. Shannon-Wiener Index of soil microbial communities at each sampling site.

Sampling Site	Altitude (m)	Total Individual Count ($\times 10^4$ CFU/g)	Total Number of Species	Shannon-Wiener Index (H')
A	1400	168	20	2.63
B	1600	111	15	2.28
C	1900	134.83	20	2.51
D	3100	108.5	19	2.43
E	2600	98.83	14	2.07
F	2000	102.66	16	2.15
G	3400	31.66	13	1.89
H	1100	155.32	23	2.37
I	1000	120.83	13	1.52
J	1000	128.72	19	2.11

Note: The calculation is based on the following assumptions and logic: ① Total individual count = bacterial count + actinobacterial count + fungal count; ② Total number of species = number of bacterial species + number of actinobacterial species + number of fungal species; ③ Due to the lack of species-level individual count breakdown data, it is assumed that the individual counts of species within each microbial group (bacteria / actinobacteria / fungi) are evenly distributed; ④ The natural logarithm (ln) is used for the logarithmic calculation, and two decimal places are retained.

3.2 Distribution Patterns of Microbial Abundance and Species Richness along Key Gradients

3.2.1 Altitudinal Gradient Differentiation

Microbial abundance and species richness showed a clear decreasing trend along the altitudinal gradient (Figure 2 and Figure 3). In the low-altitude Huangyan desert area, affected by human disturbance and drought stress, microbial abundance exhibited abnormally high values (e.g.,for example, at point H with an altitude of 1100 meters, the water content is extremely low (3.67%), and the electrical conductivity is high (2020 microseconds/cm)). Correlation analysis shows that soil electrical conductivity is significantly positively correlated with the bacterial abundance in the low-altitude area ($r = 0.83$, $P < 0.05$), indicating that the high-salt environment promotes the proliferation of salt-tolerant bacterial communities, resulting in an abnormally high bacterial count (118.33×10^4 CFU/g).), but species diversity was significantly restricted by habitat fragmentation. The mid-altitude dense spruce area, supported by high nutrient supply and stable microhabitats in forest ecosystems, sustained microbial abundance enrichment and species differentiation. In the high-altitude meadow/cold desert area, constrained by extreme environments, microbial communities showed dual impoverishment characteristics of "sharp reduction in abundance and simplification of species".

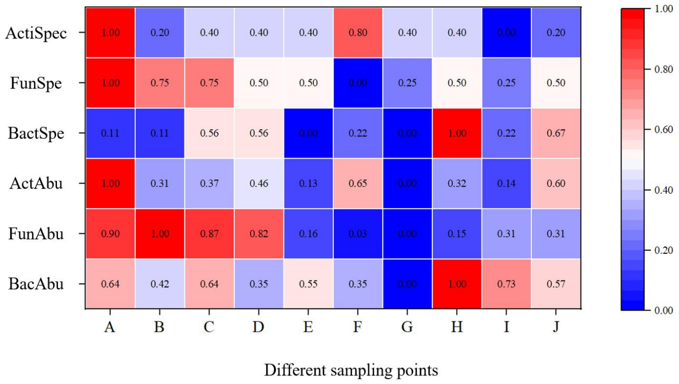

Figure 2. Correlation heatmap of soil microbial quantity and species number at different sampling points.

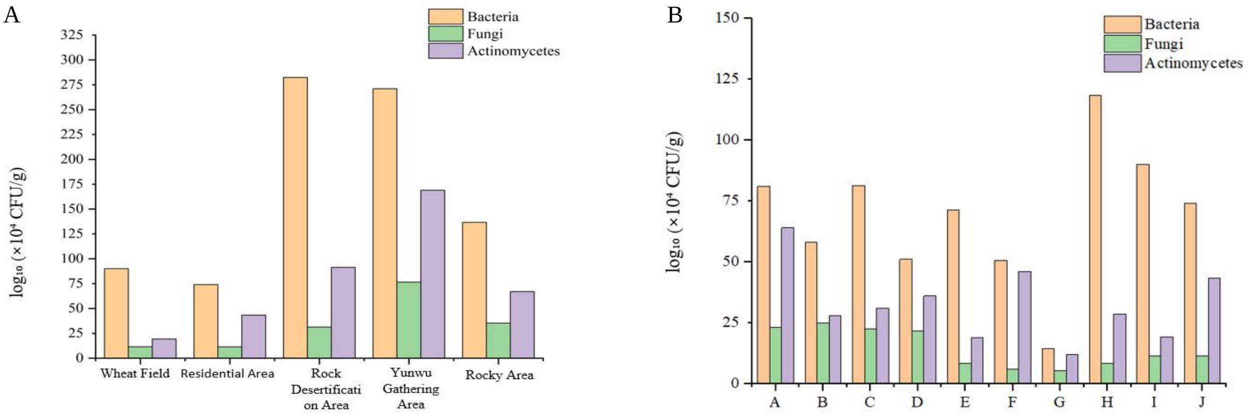

Figure 3. The relationship between soil microbial biomass and species abundance in different land types (as shown in the Figure 3A) and sampling points (as shown in the Figure 3B).

3.2.2 Ecotype Differentiation

Different ecotypes exerted significant regulatory effects on microbial community assembly (Figure 2 and Figure 3). Forest ecosystems (dense spruce areas) shaped microbial communities with high biomass and high diversity through litter input and nutrient cycling. Agricultural ecosystems (wheat fields), regulated by tillage disturbance and fertilization, maintained moderate microbial abundance but reduced diversity. Desert ecosystems (Huangyan desert area), filtered by high-salt environments, formed stress-tolerant characteristic flora. Alpine cold deserts and meadow ecosystems, due to low vegetation coverage and insufficient nutrient input, exhibited typical impoverished patterns in microbial communities.

3.3 Correlation between Soil Physicochemical Properties and Microbial Communities (RDA)

RDA (Figure 4) was used to quantify the driving effects of soil physicochemical properties on microbial communities and reveal the regulatory mechanisms of key environmental factors:

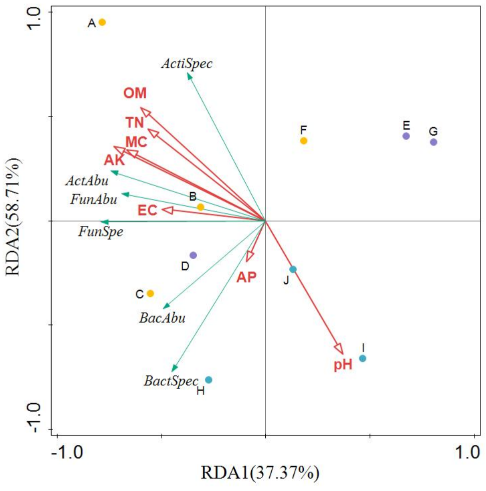

Figure 4. Redundancy analysis of soil physical and chemical properties, microbial quantity and species number at different sampling points.

Note: The red lines represent explanatory variables; the green lines represent response variables; the length of the arrows indicates the degree of influence; the angle between the arrows indicates the degree of correlation; the purple dots represent high-altitude areas, the yellow dots represent mid-altitude areas, and the blue dots represent low-altitude areas.

3.3.1 Core Driving Role of Organic Matter and Total Nitrogen

Organic matter and total nitrogen were the core driving factors in microbial community assembly. In the mid-altitude dense spruce area, high contents of organic matter and total nitrogen directly promoted the accumulation of bacterial and fungal biomass and flora differentiation by providing carbon and nitrogen metabolic substrates. In the RDA ordination, they showed a strong positive correlation with microbial communities (explanatory power >40%), verifying the "soil carbon-nitrogen pool-microbial community" co-evolution mechanism.

3.3.2 Microhabitat Regulatory Role of Moisture Content and pH

Moisture content significantly affected community distribution by regulating water availability for microbial survival: low moisture content in the low-altitude desert area inhibited fungal proliferation, while high moisture content in the mid-altitude spruce area promoted microbial metabolism. Soil pH (in the weakly acidic to weakly alkaline range), as a basic environmental factor for microbial metabolism, regulated community structure by affecting enzyme activity and substrate decomposition efficiency. In the RDA analysis, it showed a moderate correlation with microbial distribution (explanatory power 15%-25%).

3.3.3 Auxiliary Regulatory Role of Electrical Conductivity and Available Nutrients

Soil salinity, reflected by electrical conductivity, shaped specific microbial communities in the low-altitude desert area by selecting salt-tolerant flora. Available nutrients such as available phosphorus and available potassium exerted short-term regulatory effects on microbial abundance in human-influenced areas (e.g., wheat fields) by supplementing the immediate nutritional needs of microorganisms. However, these factors had weak explanatory power (<10%) and mainly acted as auxiliary factors in community assembly.

4. Discussion

Redundancy analysis revealed that altitude induces an ecological filtering effect by regulating soil moisture content and pH (neutral pH in high-altitude cold regions vs. acidic pH in low-altitude areas), resulting in bacterial/actinomycete dominance at low altitudes and fungal enrichment at mid-to-high altitudes. This pattern aligns with the slow decomposition of organic matter in high-altitude regions, where accumulated total nitrogen provides carbon sources for fungi [7,12]. Such findings support the general consensus that altitude-driven environmental gradients (e.g., temperature, vegetation) shape microbial community structure by altering resource availability [6,9].

Human activities, particularly agricultural cultivation, significantly influenced microbial communities. RDA results indicated that agricultural practices promoted bacterial proliferation through increased moisture content (via irrigation) and available potassium (via fertilization), with an explanatory power of 29.4%. However, this intervention reduced the niche breadth of fungi and actinomycetes, which showed a negative correlation with total nitrogen. This could be attributed to soil C:N ratio imbalance caused by chemical fertilizers-fungi, being more sensitive to C:N fluctuations [10], exhibited greater vulnerability. These observations suggest that while anthropogenic disturbances can modify local nutrient conditions, they may disrupt the natural equilibrium of microbial communities, consistent with previous studies on agricultural impacts on soil biota [8,13].

Among soil physicochemical factors, moisture content emerged as the primary driver (31.2% explanatory power), directly regulating microbial metabolic activity: high moisture in wheat fields created humid microhabitats favorable for bacteria, whereas extremely low moisture (1.23% at site G) in high-altitude areas constrained microbial activity. Total nitrogen, by enhancing fungal saprophytic capacity (positive correlation), explained fungal dominance in mid-to-high altitudes. These results underscore that the *adaptation* between environmental factors and microbial functional groups is central to community assembly [4,11].

Our findings are consistent with similar studies in global arid and semi-arid mountainous areas. For instance, Zhu et al. (2023) 's research on the Qilian Mountains demonstrated that the soil microbial diversity and biomass in the mid-altitude Qilian Yuanbailin area were the highest [23], mainly driven by the synergistic effects of soil organic matter, total nitrogen, and moisture content - this is in complete agreement with the results of microbial enrichment in the mid-altitude spruce forest belt (A and C sites) of the Bogeda Mountains in this study. However, Savanah et al. [24] (2020) 's study on urban farms in Los Angeles revealed that the overall abundance of soil microorganisms in low-altitude areas was relatively low, which significantly differed from the abnormally elevated bacterial abundance (118.33 10" CFU/g) at the H site (1100 m) in the low-altitude Huangyan area of Bogda Mountain in this study. The core reason for this difference lies in the high-salt environment 1 (conductivity 2020 uS/cm) where the H site of Bogda Mountain is located. The high-salt stress has screened out bacterial groups with strong salt tolerance, while the low-altitude area of Los Angeles City Farm does not have such extreme salinization characteristics, reflecting the adaptability differences of microbial distribution to the specific habitats of the region.

This study also has several limitations: the sampling was conducted only in a single growing season, which may miss the seasonal dynamics of the microbial community; the study focused on microbial abundance and diversity, due to experimental limitations, it did not use high-throughput sequencing, which limited the detailed characterization of the microbial community composition and the quantitative determination of microorganisms relying on plate counting methods, which may underestimate the abundance of uncultivated dominant groups, etc. Future studies will incorporate multi-season sampling and metagenomic analysis to more comprehensively capture long-term change trends and functional mechanisms. However, this study focused on the comprehensive assessment of biodiversity-environmental ecology-local economic policies. In arid and semi-arid mountainous areas like Xinjiang, exploring the balance and sustainable development of economy and environment is acceptable with these errors.

Overall, our findings highlight that altitude and human activities synergistically affect soil microbial communities via soil physicochemical properties. Maintaining the natural C:N balance and moisture regime may be critical for preserving microbial diversity in arid-semiarid mountain ecosystems, with implications for ecological conservation and sustainable agricultural practices.

5. Conclusion

Soil physicochemical properties and microbial communities on the northern slope of the eastern foot of the Bogda Mountains exhibit significant vertical and spatial differentiation under the combined effects of elevational gradients and anthropogenic disturbances (e.g., agricultural cultivation and tourism). The low-elevation desert zone is dominated by enriched bacteria and actinomycetes, the mid-elevation spruce forest zone harbors the highest fungal abundance and overall microbial diversity, and the high-elevation meadow/cold desert zone is characterized by sharply reduced microbial abundance and simplified species composition. These patterns represent the hierarchical responses of the mountain ecosystem to natural environmental filtering and anthropogenic interference, with redundancy analysis confirming that soil moisture, total nitrogen and pH are the key driving factors regulating soil microbial community structure and diversity in this region.

Anthropogenic activities exert divergent and disruptive impacts on soil-microbe synergy: agricultural cultivation alters the natural balance of soil moisture and available potassium, and chemical fertilizer input causes soil C:N ratio imbalance, further reducing microbial diversity; other disturbances such as tourism and resource exploitation degrade soil structure via habitat fragmentation, damaging the inherent synergy between soil physicochemical properties and microbial communities. Targeted management strategies are proposed: establishing a coordinated framework for agricultural production and tourism development to avoid excessive disturbance in key ecological zones, implementing regulated irrigation and precision fertilization to maintain soil moisture and C:N balance, promoting low-impact development for tourism and resource exploitation, and constructing a regional ecological management system with soil organic matter, total nitrogen and moisture as core monitoring indicators.

This study clarifies the regulatory mechanisms of natural and anthropogenic factors on soil microbial communities in the Bogda Mountains, and provides a scientific reference for ecological conservation and sustainable land use in global arid-semiarid mountainous regions, which is vital for enhancing the ecological resilience of mountain ecosystems under global environmental change.

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Conflict of Interest

The authors declare they have no conflicts of interest.

Generative AI Statement

The authors declare that no Generative AI was used in the creation of this manuscript.

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