Distribution Characteristics and Influencing Factors of Soil Microbial Community Structure and Enzyme Activity Along an Altitudinal Gradient in Changbai Mountain (Postprint)

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Abstract

Changbai Mountain is a mountain ecosystem formed by volcanic eruption and serves as a natural laboratory for studying ecosystem reconstruction and succession processes. This study investigated soils from the subalpine coniferous forest belt, subalpine Betula ermanii forest belt, alpine meadow belt, and alpine tundra belt in the vertical zones of the western slope of Changbai Mountain. The phospholipid fatty acid (PLFA) method and microplate method were used to determine soil microbial community structure and enzyme activity, respectively, to explore (1) the distribution characteristics of microbial community structure and enzyme activity along elevation on the western slope of Changbai Mountain, and (2) the effects of vertical belt vegetation factors and soil factors on microbial community structure and enzyme activity. The results showed that soil organic carbon, total nitrogen, and total phosphorus contents all first increased and then decreased with increasing elevation, with the maximum values of organic carbon and total nitrogen appearing in the Betula ermanii forest belt. With increasing elevation, total soil microbial PLFA and PLFA of various microbial groups exhibited a pattern of first increasing and then decreasing, showing the trend of subalpine Betula ermanii forest belt > subalpine coniferous forest belt > alpine meadow belt > alpine tundra belt. In terms of contribution rate to total soil microbial PLFA, the pattern was bacteria > fungi > actinomycetes, and G- > G+. Regarding PLFA correlations, bacteria, actinomycetes, G+, and G- showed strong associations among themselves, while fungi showed weaker associations with these four groups. Soil total nitrogen content exhibited significant positive correlations with all microbial groups, whereas C/N ratio showed negative correlations with all microbial groups; these two factors were the main factors regulating soil microbial variation along elevation. Activities of soil hydrolases βG and AP gradually increased with elevation, with AP activity showing a good response to the alpine tundra ecosystem. Soil moisture content, C/N ratio, and soil temperature were the main factors controlling the vertical variation of soil enzyme activity. The meadowization process in the alpine tundra belt had significant impacts on soil moisture content, total phosphorus content, and hydrolase AP activity, but had little effect on soil microbial PLFA content and other enzyme activities. The soil microbial community structure and enzyme activity in the vertical belts of Changbai Mountain are closely related not only to soil environmental factors and hydrothermal conditions, but also to vegetation community composition and litter properties.

Full Text

Preamble

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Soil Microbial Community Structure, Enzyme Activities, and Their Influencing Factors Along Different Altitudes of Changbai Mountain

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Abstract

Changbai Mountain is a mountainous ecosystem strongly affected by volcanic eruptions with distinct vegetation zonations along different altitudes, offering a natural laboratory for studying post-volcanic ecosystem reconstruction and forest succession. Owing to the existence of elevation change in the vertical direction, ecological factors in mountainous ecosystems occur in a series of changes over a relatively small space. Therefore, mountainous ecosystems have become an important area to study correlation mechanisms among soil microbes, enzyme activities, and ecological factors. The objectives of the present study were to: (1) examine the distribution of microbial phospholipid fatty acids (PLFA) and enzyme activities of soils along different altitudes of Changbai Mountain and investigate factors affecting the PLFA and enzymes, and (2) explore the effects of influencing factors, vegetation, and soil on the microbial community structure and enzyme activities in four vertical zones.

We sampled soils in the coniferous forest zone, Erman' s birch forest zone, alpine meadow zone, and alpine tundra zone along the altitudinal gradient. We determined soil microbial community structure with the PLFA method and enzyme activities with the microplate method. The results demonstrated that three environmental factors—the concentration of soil organic carbon, total nitrogen (TN), and total phosphorus—increased and then decreased as elevation increased. Soil organic carbon and TN varied with altitude, with the highest value detected in the Erman' s birch forest zone. Both the total microbial PLFA and various types of microbes PLFA initially increased and then decreased as elevation increased. The rank of the PLFA amount was Erman' s birch forest zone > coniferous forest zone > alpine meadow zone > alpine tundra zone. The rank of the contribution rate of total microbial PLFA was bacteria > fungi > actinomycetes, and Gram-negative bacteria (G^-) > Gram-positive bacteria (G^+). In terms of microbial PLFA correlation, bacteria, actinomycetes, Gram-positive bacteria (G^+), and Gram-negative bacteria (G^-) were significantly correlated, while fungi was poorly correlated with these microbes. TN showed a significant positive correlation with various types of microbes while the C/N ratio was negatively correlated with various types of microbes. Thus, it can be seen that TN and C/N ratio were the two main factors differentiating soil microbial community structure along the altitudinal gradient.

Both soil β-glucosidase and acid phosphatase (AP) activities increased with increased elevation. The AP activity showed high response to the alpine tundra ecosystem. Soil water content, soil organic carbon, and C/N ratio were the main factors affecting the vertical distribution of soil enzyme activities. The meadow processes of alpine tundra strongly affected the soil water content, soil total phosphorus, and AP activity; however, had little effect on soil microbial PLFA and other enzyme activities. In conclusion, the soil microbial community structure and enzyme activities along different altitudes of Changbai Mountain were not only affected by soil environmental factors and hydrothermal conditions, but were also closely related to the vegetation community composition and litter chemical quality.

Keywords: Changbai Mountain; altitudinal zonations; soil microbes; PLFA; enzyme activities; soil factors

Introduction

Soil microbes and enzymes are the primary participants and regulators of material cycling and biochemical processes in ecosystems, playing crucial roles in driving nutrient transformation and regulating ecosystem functions [1-2]. Soil microbes and enzymes also exhibit sensitive responses to environmental changes, with variations in vegetation community types, soil physicochemical properties, and hydrothermal conditions significantly influencing microbial community structure and enzyme activities, thereby creating distinct geographical distribution patterns [3-4]. Mountainous ecosystems, characterized by vertical elevation changes, cause ecological factors to shift systematically within relatively small spatial scales, triggering microclimatic, soil physicochemical, and vegetation type gradient effects that make them hotspots for studying the correlation mechanisms between soil microbes, enzyme activities, and ecological factors [5-6].

Numerous studies indicate that the altitudinal distribution of soil microbes and enzymes may be influenced by multiple biotic and abiotic factors. Männistö et al. [7] studied soils at different altitudes and vegetation types in the Arctic region of Finnish Lapland and found corresponding changes in dominant microbial populations. Cao Rui et al. [3] investigated alpine canyons along the Zagunao River in Sichuan and reported that soil microbial biomass and enzyme activities were extremely significantly positively correlated with soil water content, organic carbon, and total nitrogen. Lucas-Borja et al. [8] found that humidity played a key role in the vertical differentiation of enzyme activity in Mediterranean regions, while Si Guicai et al. [9] and others [10] discovered that enzyme activities were not significantly correlated with temperature changes along altitudinal gradients but were significantly correlated with soil physicochemical indicators such as organic carbon and total nitrogen. Djukic et al. [11] suggested that habitat decomposition conditions and vegetation composition were the main factors affecting vertical changes in microbes and enzymes. Due to differences in zonal or azonal hydrothermal conditions and ecosystem types at their base locations, the dominant factors influencing soil microbes and enzymes along altitudes also vary across different mountainous ecosystems, particularly in the alpine tundra zone of Changbai Mountain.

Located on the border between China and North Korea, Changbai Mountain possesses a complete vertical vegetation distribution belt in the temperate zone of the Northern Hemisphere and represents the only typical alpine tundra vegetation ecosystem within China’ s territory. As a world-famous active volcano with a history of multiple eruptions, Changbai Mountain’ s vertical belt serves as an ideal natural laboratory for studying ecosystem reconstruction and succession processes [12]. Especially under the background of global warming, Changbai Mountain' s high-latitude, high-altitude ecosystems exhibit particularly sensitive responses to climate change. Due to differences in hydrothermal conditions among various slopes and differential impacts of volcanic eruptions on vegetation across slopes, distinct vegetation distribution patterns and succession processes have formed on different slopes of Changbai Mountain, with particularly significant differences in the alpine and subalpine regions [13]. On the western slope of Changbai Mountain, expansion phenomena of subalpine forest vertical belt herbaceous plants, represented by *Deyeuxia angustifolia*, encroaching into the alpine tundra zone have emerged [14], leading to the development of large areas of herbaceous plants and the formation of a preliminary, relatively continuous alpine meadow zone vegetation community type between the Erman' s birch forest belt and tundra belt (2000-2200 m). This also indicates that the ecosystem on Changbai Mountain' s western slope is currently in a successional process.

To explore the ecosystem processes and future development trends of Changbai Mountain' s western slope, this study investigated soils from different vertical vegetation belts in the alpine and subalpine regions. Using phospholipid fatty acid (PLFA) and microplate methods to determine soil microbial community structure and enzyme activities, we examined the distribution characteristics of microbial community structure and enzyme activities along altitudes and the effects of vertical belt vegetation and soil factors on them, aiming to elucidate the vertical differentiation mechanisms of soil microbial communities and enzymes on Changbai Mountain' s western slope. This research provides a theoretical basis for understanding the impacts of succession processes on Changbai Mountain' s ecosystem and revealing soil microbial variation patterns in temperate mountain ecosystems.

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1. Study Area Overview

The study area is located on the western slope of Changbai Mountain Nature Reserve (41°54 -42°00 N, 127°54 -128°03 E), characterized by a typical continental monsoon climate with cold, windy winters and cool, brief summers. Along the altitudinal gradient from 530 m to 2500 m, the mean annual temperature decreases from 2.9°C to -4.8°C, while mean annual precipitation increases from 750 mm to 1340 mm, with precipitation concentrated above 1500 m. These climatic and topographic variations have created a relatively complete vegetation vertical belt.

This study selected four typical alpine and subalpine vertical belts on Changbai Mountain' s western slope between 1500-2500 m: subalpine coniferous forest zone (CF), subalpine Erman' s birch forest zone (EB), alpine meadow zone (AM), and alpine tundra zone (AT). The main environmental characteristics of the study area are shown in and [Figure 1: see original paper].

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2. Methods

2.1 Soil Sample Collection and Processing

Typical experimental plots were established in areas with similar slope and aspect. Five 20 m × 20 m sample plots were selected in each vertical belt, and five soil samples were collected along an S-shaped transect using a soil auger. Since the average soil thickness in the tundra zone is 10 cm, a uniform sampling depth of 0–10 cm was adopted for all vertical belts, excluding the litter layer. After removing stones and plant roots, the samples were placed in portable iceboxes, transported to the laboratory at low temperature, and used for PLFA, enzyme activity, and soil physicochemical property analyses, totaling 20 soil samples.

2.2 Soil Physicochemical Property Determination

Soil water content (SWC) was measured using a portable soil three-parameter meter (Field operated meter for moisture/temperature/salinity) and the oven-drying method. Soil organic carbon (SOC) was determined by the potassium dichromate oxidation method, with a ratio to organic matter of 1:1.724. Total nitrogen (TN) was measured using potassium persulfate digestion [15] with an automatic chemical analyzer (AMS/Westco SmartChem 140, Italy). Total phosphorus (TP) was determined by sulfuric acid-perchloric acid digestion. Soil pH was measured potentiometrically. Each soil sample was measured in triplicate.

2.3 Soil Microbial PLFA Analysis

Phospholipid fatty acid (PLFA) analysis was used to identify microbial groups and determine soil microbial biomass [16]. The extraction method followed Bossio et al. [17-18] and is detailed in . This method enables rapid and accurate extraction and determination of PLFAs from living microbial cell membranes in soil.

2.4 Soil Enzyme Assay Methods

Three hydrolytic enzymes—β-1,4-glucosidase (βG), β-1,4-N-acetylglucosaminidase (NAG), and acid phosphatase (AP)—were analyzed using microplate fluorometric methods [19] with a multifunctional microplate reader (Synergy H4, BioTek). For the assay, 1.0 g of fresh soil was weighed and prepared as a soil suspension in 125 mL of 50 mmol/L sodium acetate buffer (pH = 5). Substrates included 4-methylumbelliferyl-β-D-glucopyranoside, 4-methylumbelliferyl-β-D-glucosaminide, and 4-methylumbelliferyl phosphate. All samples were incubated in microplates under dark conditions for 1 hour, with 10 L of 1 mol/L NaOH automatically added to each well before measurement at 365 nm excitation and 450 nm emission wavelengths. Each sample was measured in triplicate.

For soil peroxidase (PER) and polyphenol oxidase (PPO) activities, soil suspension preparation was identical to that for hydrolases. For activity determination, 600 L of soil suspension and 150 L of substrate were placed in deep-well plates and incubated under dark conditions for 5 minutes. After incubation, 10 L of 0.3% H_2O_2 was added. Following centrifugation at 3000 r/min, 250 L of supernatant was transferred to shallow transparent plates and measured at 460 nm using the same multifunctional microplate reader.

2.5 Data Analysis

All data were analyzed using SPSS 20.0 statistical software. One-Way ANOVA was used for significance testing, with Tukey' s HSD test for multiple comparisons. Origin Pro 8.5 and Canoco 4.5 software were used for ordination analysis. Using established data matrices of soil microbial PLFA, enzyme activities, and soil environmental factors across vertical belts, detrended correspondence analysis (DCA) was first employed to determine gradient lengths of ordination axes. Redundancy analysis (RDA) was then used to analyze relationships between soil microbes, enzyme activities, and environmental factors. Prior to analysis, species data were transformed and centered, with ordination scaling focusing on inter-species correlations. Variable significance was tested using Monte-Carlo permutation tests.

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3. Results

3.1 Distribution Characteristics of Soil Environmental Factors Across Vertical Belts

Inter-group variance analysis of soil environmental factors across vertical belts showed highly significant differences ($p < 0.01$). Soil temperature and water content exhibited typical mountain patterns: water content generally increased with altitude, while temperature decreased gradually. Soil water content was highest and similar in the EB and AM zones, slightly lower in the AT zone, with no significant difference between CF and AT zones. All vertical belts had acidic soils.

Soil organic carbon controls the cycling of energy and nutrients in soil, providing a stable source of energy and nutrients for microbial communities [20]. Soil total nitrogen, primarily organic nitrogen (accounting for over 90% of TN [21]), becomes available to plants after microbial absorption, utilization, and degradation. This study showed that soil organic carbon, TN, and TP contents all initially increased then decreased with altitude. The highest values of organic carbon and TN appeared in the EB zone, while TP peaked in the AM zone and was significantly higher than in other vertical belts, indicating that meadow processes significantly affected soil TP content. The C/N ratio showed an overall increasing trend with altitude, with significant differences between the AM and AT zones and the other two zones ($p < 0.05$) ().

3.2 Characteristics and Comparison of Soil Microbial Community Structure Across Vertical Belts

Microbial community structure refers to the biomass of each microbial group and their proportional composition in soil [22]. One-way ANOVA revealed highly significant inter-group differences in total PLFA and major microbial groups across vertical belts ($p < 0.01$), showing a trend of initial increase followed by decrease with altitude. No significant differences were observed between CF and AM zones for most groups, while EB zone showed significantly higher contents than other zones. Minimum values appeared in the AT zone.

Bacteria, fungi, and actinomycetes are the three major microbial groups in soil. Bacteria and fungi are the two main functional microbial components [23]. The F/B ratio can indicate the relative abundance and growth status of these two populations. In this study, the F/B ratio showed a trend of first decreasing then increasing with altitude, with EB and AM zones being similar but significantly higher than the other two zones. The G^+/G^- ratio, which can indicate bacterial community structure changes and soil nutrient status, showed a trend of first increasing then decreasing with altitude, peaking in the EB zone and significantly higher than in CF and AT zones. The contribution rate of each microbial group to total PLFA showed the pattern: bacteria > fungi > actinomycetes, with $G^- > G^+$ ([Figure 2: see original paper]).

3.3 Characteristics and Comparison of Soil Enzyme Activities Across Vertical Belts

Significant inter-zone differences were observed for βG, NAG, and AP activities ($p < 0.01$), which showed a gradual increasing trend with altitude, demonstrating good continuity. AP activity was particularly responsive to the tundra ecosystem, being significantly higher in the AT zone than in other zones. NAG activity was lowest in the CF zone, with no significant differences among the other three zones.

For soil oxidases, PER activity showed a trend of first increasing, then decreasing, then increasing again with altitude, peaking in the EB zone and being lowest in the AT zone. PPO activity showed a trend of first increasing then decreasing, but differences among vertical belts were not significant. The activities of these two oxidases showed differential responses to the AT zone ([Figure 3: see original paper]).

3.4 RDA Analysis of Microbial Community Structure and Enzyme Activities with Soil Environmental Factors

3.4.1 Microbial Community Structure and Soil Environmental Factors RDA analysis of soil microbes and environmental factors across four vertical belts on Changbai Mountain’ s western slope showed that the first two ordination axes explained 95.2% of the soil microbial information and 99.5% of the soil microbial-environment relationship. Monte-Carlo tests showed that all environmental variables contributed significantly to explaining the response variables (F_{microbe} = 8.46, p = 0.022). Soil water content and C/N ratio showed large correlation coefficients with ordination axes.

Correlation analysis revealed that bacteria, actinomycetes, G^+, and G^- were strongly correlated, while fungi showed weaker correlation with these four groups. In terms of contribution to total PLFA, the pattern was bacteria > fungi > actinomycetes. From the perspective of soil environment and microbial community composition, the EB zone was most similar to the AM zone. Maximum values of various microbial groups appeared in the EB zone, which was similar to the AM zone, corroborating previous results. Among soil environmental factors, total nitrogen showed significant positive correlations with bacteria, actinomycetes, G^+, and G^-, while C/N ratio showed negative correlations with all microbial groups. Total phosphorus was significantly negatively correlated with total PLFA, bacteria, actinomycetes, G^+, and G^-, and significantly positively correlated with fungi ([Figure 4: see original paper]).

3.4.2 Enzyme Activities and Soil Environmental Factors For soil enzyme activities, Monte-Carlo tests also reached significance levels (F_{enzyme} = 7.5, p = 0.018). The first two ordination axes explained 87.5% of soil enzyme information and 95.6% of the soil enzyme-environment relationship. Soil organic carbon, TN, and C/N ratio showed large correlations with ordination axes.

Based on angles between enzyme activity arrows, βG, NAG, and AP showed strong correlations. Angles between enzyme activities and environmental factors revealed that βG and AP were significantly positively correlated with soil water content ($p < 0.05$; $p < 0.01$), significantly and highly significantly positively correlated with C/N ratio, and highly significantly negatively correlated with soil temperature and TN. NAG was significantly or highly significantly positively correlated with soil water content and C/N ratio, and significantly negatively correlated with soil temperature. PER and PPO showed no significant correlations with any soil environmental factors, though PPO was significantly positively correlated with total phosphorus ([Figure 4: see original paper]).

4. Discussion

4.1 Relationship Between Soil Microbial Community Structure and Vertical Belt Vegetation Types

Total PLFA and various microbial groups in the EB zone were significantly higher than in other zones. The dominant species, Erman’ s birch (*Betula ermanii*), is a broadleaf tree whose abundant litter provides a relatively stable environment and large amounts of available substrates for microbes, promoting microbial reproduction and metabolism. The CF zone is dominated by coniferous trees such as Korean pine (*Pinus koraiensis*) and spruce-fir, which are evergreen with limited litterfall that decomposes slowly. The AT zone is dominated by low-growing, cushion-shaped tundra woody plants such as *Rhododendron aureum* and *Dryas octopetala*, whose litter is also difficult to decompose. The cold climate and low mean annual temperature in the AT zone result in limited available organic substrates and slow microbial metabolic activity.

Fungi and bacteria are the two main functional microbial components in soil [23]. The F/B ratio can indicate the relative abundance and growth status of these populations. Studies show that fungi and bacteria utilize different substrates, and different vegetation communities affect microbial community structure by altering litter types and substrate quality [22,24]. The EB zone’ s broadleaf litter provides large quantities of high-nutrient, easily decomposable substrates suitable for bacterial proliferation [25]. As vegetation shifts from forest to herbaceous, fungi decrease while bacteria increase. In alpine meadows, herbaceous plants have well-developed root systems with dense fine roots in surface layers, providing abundant high-quality, easily decomposable organic matter through root exudates and decaying roots that promotes bacterial growth and high bacterial biomass [27]. In contrast, the AT zone’ s low-nutrient environment with acid-loving shrubs results in higher F/B ratios [28]. The G^+/G^- ratio, which indicates soil nutrient status, peaked in the EB zone, showing a significant negative correlation with C/N ratio ($p < 0.05$), suggesting more intense nutrient stress at higher ratios [30–31].

4.2 Relationship Between Soil Enzyme Activities and Vertical Belt Vegetation Types

Previous studies suggest soil enzyme activities in high-altitude regions are lower than in low-altitude regions [32], but our results show no clear negative correlation with altitude. Instead, hydrolase activities (βG, NAG, AP) showed increasing trends with altitude, with AP activity significantly higher in the AT zone than others. This is primarily because the AT zone, located at high latitude with year-round low temperatures and strong winds, creates a harsh environment where most plants struggle to grow, resulting in nitrogen- and phosphorus-poor conditions [33]. When phosphorus availability is low, AP activity increases to promote soil phosphorus cycling and meet plant and microbial growth needs [34].

βG degrades cellulose and releases glucose, playing an important role in degrading complex organic compounds. Its hydrolysis products are major energy sources for soil microbes [35] and are closely related to soil organic carbon and nitrogen transformations. NAG converts chitin to amino sugars and is a primary source of mineral nitrogen in soil [36]. The high organic carbon content in the EB and AM zones may produce negative feedback effects on organic matter-decomposing enzymes, limiting nutrient release [37] and thus inhibiting βG and NAG activities. PER and PPO are major lignin-decomposing enzymes that oxidize phenolic rings and break down lignin macromolecules into simple phenols, directly affecting soil organic matter accumulation and mineralization [38]. Oxidases are primarily synthesized and secreted by fungi and are closely related to soil organic matter input components [39]. The high fungal content and organic matter content in the EB zone may be responsible for high oxidase activities.

4.3 Relationship Between Soil Microbial Community Structure and Vertical Belt Soil Environmental Factors

Microbes mineralize organic matter to release mineral nutrients that meet plant and microbial needs, while microbial immobilization of inorganic nitrogen reduces soil nitrogen loss. Soil microbes are not only executors of nitrogen mineralization and retention but also active pools of plant nutrients. All microbial groups showed significant positive correlations with soil TN. In mountainous ecosystems, alpine and subalpine regions are typically nitrogen-poor, and nitrogen availability affects plant productivity and substrate quality for microbial aerobic metabolism, thereby influencing microbial communities [40]. For Changbai Mountain at high latitude, soil TN content can be considered a primary factor regulating microbial changes along altitudinal gradients. In nitrogen-poor environments, the EB, AM, and AT zones at high altitudes are typical nitrogen-deficient habitats.

Nitrogen in terrestrial ecosystems is stored in soil organic matter pools, so soil nitrogen changes are closely linked to soil organic carbon changes. The C/N ratio is not only a sensitive indicator of soil quality but also affects soil organic carbon and nitrogen cycling. A lower C/N ratio provides more energy for microbes, enhancing their activity. However, although mineralized nitrogen promotes plant uptake, it rarely accumulates in soil and is eventually lost through leaching or denitrification. The study showed that soil TP was significantly negatively correlated with total PLFA, bacteria, actinomycetes, G^+, and G^-. Tan et al. [41] found that long-term phosphorus fertilization increased bacterial community diversity, while Lauber et al. [42] showed that TP content could cause shifts in fungal dominant groups. Soil organic matter is coupled with nutrients like phosphorus, and changes in phosphorus may alter carbon substrates used by microbes. Different microbial groups select different carbon substrates, changing the bacterial-fungal structure in the overall microbial community.

4.4 Relationship Between Soil Enzyme Activities and Vertical Belt Soil Environmental Factors

All three hydrolases showed significant positive correlations with soil water content, primarily because increased water provides reaction conditions and venues for enzymatic reactions, enhancing enzyme activities [43]. While enzyme activities are typically positively correlated with temperature within certain thresholds [44], this study showed βG, NAG, and AP were significantly negatively correlated with soil temperature but significantly positively correlated with water content and C/N ratio. This indicates that the hydrothermal combination process in mountain ecosystems differs fundamentally from the synergistic water-heat effects in horizontal zones. As altitude increases, environmental heat decreases while precipitation increases, and the promoting effect of increased soil water content on enzyme activities may offset the limiting effect of decreased temperature. Combined with vegetation type differences affecting microbial substrate utilization, this makes altitudinal patterns of soil enzyme activities more complex.

In addition to water content and temperature, carbon is an important factor affecting soil enzyme activities. Organic matter can alter soil porosity and aggregate structure, has significant buffering and water-holding capacity, serves as an important carrier for enzymes, and provides venues and suitable conditions for enzyme function [45]. Therefore, higher soil organic carbon and organic matter content can promote enzyme synthesis and become a primary factor influencing enzyme activities.

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5. Conclusion

Significant differences existed in soil physicochemical properties, microbial community structure, and enzyme activities among vertical belts on Changbai Mountain’ s western slope. With increasing altitude, soil microbial total PLFA and various microbial groups showed an initial increase followed by decrease, following the pattern: Erman’ s birch forest zone > coniferous forest zone > alpine meadow zone > alpine tundra zone. In terms of contribution to total PLFA, the pattern was bacteria > fungi > actinomycetes. Soil TN content showed significant positive correlations with all microbial groups, while C/N ratio showed negative correlations with all groups—both being primary factors regulating microbial changes along altitudes.

Soil hydrolase activities (βG, NAG, AP) showed strong correlations with each other and exhibited gradually increasing trends with altitude, with AP activity showing particularly good response to the alpine tundra ecosystem. Soil water content, C/N ratio, and soil temperature were the main factors regulating vertical changes in enzyme activities. The meadow processes in the alpine tundra zone strongly affected soil water content, total phosphorus, and AP activity but had little effect on soil microbial PLFA and other enzyme activities.

In conclusion, soil microbial community structure and enzyme activities along different altitudes of Changbai Mountain were not only affected by soil environmental factors and hydrothermal conditions but were also closely related to vegetation community composition and litter chemical quality.

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