https://doi.org/10.17221/377/2025-PSE

Geographical variations in soil properties and bacterial community diversity across major lavender (*Lavandula angustifolia* Mill.) cultivation regions in the Ili River Valley

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Citation: Jian J.N., Tang S.M., Zhang S.J., Zhu L., Ran B., Zhang X.C., Luo W.K., Dong S.L. (2025): Geographical variations in soil properties and bacterial community diversity across major lavender (*Lavandula angustifolia* Mill.) cultivation regions in the Ili River Valley. Plant Soil Environ., 71: 805–819.

Abstract: The Ili region hosts China's largest lavender cultivation base, yet soil bacterial diversity in its primary cultivation areas remains understudied. To address this, we compared soil bacterial communities across four major cultivation counties (Chabuchar, Agricultural Research Institute, Yining, and Huocheng). Essential oil profiles, soil properties, and bacterial community characteristics were analysed to elucidate microbial variations and environmental interactions. The results showed that: (1) The essential oil yield (1.14%) and linalool content (41.04%) in the Huocheng County cultivation area were significantly higher than those in other areas, and the essential oil quality was relatively the best; (2) the soil bacterial communities in different main cultivation areas shared certain commonalities. At the phylum level, Proteobacteria, Acidobacteriota, Gemmatimonadota, and Actinobacteriota were the dominant phyla, and their relative abundances varied by region and soil layer, and (3) the redundancy analysis results showed that soil bacterial communities were comprehensively affected by environmental factors such as pH, total nitrogen, total phosphorus, soil organic carbon, longitude, and altitude. The significant positive correlations between the abundance of Vicinamibacteraceae (Acidobacteriota) in Huocheng County soils and both soil total phosphorus and linalool content suggest a putative mechanism whereby this bacterial taxon enhances lavender terpenoid synthesis by facilitating phosphorus cycling. Overall, these results suggest that geographically driven climatic variations dynamically alter the soil bacterial community, thereby influencing lavender growth and the final essential oil quality.

Keywords: perennial herb; microbiology; soil microorganism; biosynthesis; rhizobacteria-environment interaction

Lavender (*Lavandula angustifolia* Mill.), a perennial herb of the Lamiaceae family native to the Mediterranean region, possesses significant economic and ornamental value (Zhu et al. 2018). The species was first introduced to the Ili River Valley, Xinjiang, China, from France in 1964, where systematic introduction and cultivation trials were successfully conducted (Du and Rennenberg 2018). After more than half a century of development, the lavender cultivation area in the Ili River Valley has reached 4 900 ha, accounting for 98% of China's total lavender planting area and over 90% of the national essential oil production. Consequently, it stands as the largest lavender cultivation base in China (Li et al. 2024). Major cultivation bases are concentrated in locations such as the Lucaogou Hanjia Princess Lavender Garden (Huocheng County), the Tian Shan Flower Sea Scenic Area (Yining County), and the

Supported by the Key Research and Development Project of the Xinjiang Uygur Autonomous Region, Project No. 2022B02036-2.

https://doi.org/10.17221/377/2025-PSE

River Valley Lavender Garden (Chabuchar County), demonstrating a remarkable scale effect (Tang et al. 2023). However, lavender yield across these cultivation areas exhibits instability, influenced by various factors including climate, field management practices, and varietal differences (Kara and Baydar 2012, Jiang et al. 2017). Previous studies have primarily focused on individual regions, and at the regional scale, the key soil microbial factors driving variations in lavender essential oil composition remain unclear. Similarly, systematic research is lacking on whether soil microorganisms influence lavender essential oil synthesis by altering soil physicochemical properties or through rhizosphere interactions.

In recent years, the development of high-throughput sequencing has spurred a growing body of research on soil microbial diversity and its roles within natural ecosystems (Lou et al. 2018, Baldrian et al. 2022). Soil microbial communities, particularly phyla such as Proteobacteria and Actinobacteria, exhibit a close association with the chemical constituents of lavender essential oil, including linalyl acetate and camphor (Dong et al. 2017). Rapparini demonstrated that arbuscular mycorrhizal (AM) fungi significantly upregulate the expression of key enzyme genes involved in the essential oil biosynthesis pathway, thereby promoting the production of terpenoid compounds (Rapparini et al. 2008). Bacteria play a dominant role among soil microorganisms in the utilisation of plant secondary metabolites, especially essential oils, serving as a critical carbon and energy source (Hassiotis and Dina 2010). Pang proposed that interactions occur between microorganisms and plant secondary metabolites. Under abiotic stress conditions, certain microorganisms activate plant defence signalling pathways, thereby systemically inducing the biosynthesis of these compounds (such as terpenoids and phenolics) to enhance the plant's ability to adapt to its environment (Pang et al. 2021). Bacterial communities demonstrate higher sensitivity than fungal communities, and geographical location exerts a more significant influence on bacterial community composition (Ren et al. 2018). Although standardised lavender production has been established in the Ili region, research primarily focuses on cultivation techniques, essential oil extraction, and pathology (Zheljazkov et al. 2012, Seidler-Łożykowska et al. 2014). However, studies on the diversity of soil bacteria associated with lavender across different regions remain limited and require further investigation. Therefore, guided by the theory of plant-microbe interactions, elucidating how soil bacterial communities, shaped by distinct environmental conditions, influence the quality of lavender essential oil represents an urgent research priority.

Alterations in soil microbial community structure result from the combined effects of crop cultivation practices and soil nutrient dynamics (Zhang et al. 2024b). Soil microbial diversity plays a crucial role in material transformation and cycling within rhizosphere ecosystems (Li et al. 2017), significantly contributing to the maintenance of soil health. Soil-plant-microbe interactions constitute a key research focus in agroecology (Cheng et al. 2025), particularly in lavender agriculture, where bacterially induced yellowing decline severely compromises productivity and essential oil quality (Binet et al. 2020). Nevertheless, systematic studies on bacterial diversity variations across major lavender cultivation regions remain limited and warrant further investigation. This study selected four primary lavender-growing areas in Yili Prefecture: Chabuchar County (CX), Yining City (NK), Yining County (YN), and Huocheng County (HC). The dominant lavender cultivar (French Blue) was uniformly sampled across all sites, with plant materials and rhizosphere soil collected to explore variations in soil bacterial community succession among major lavender cultivation regions through quantification of essential oil quality, soil physicochemical properties, and microbial community structure, while concurrently revealing rhizobacteria-environment interactions *via* integrated analysis of soil nutrient dynamics, thereby elucidating coordinated adaptation mechanisms in ecological evolution to establish a scientific foundation for enhancing lavender industry productivity and quality.

MATERIAL AND METHODS

Site description. (1) Chabuchar County (CX): a continental north temperate climate features mild winters and hot summers, with low precipitation and high evaporation. Annual rainfall ranges 140–400 mm, primarily in late spring and early summer. The mean annual temperature is 7.9 °C; the water table is high, and the soil is alkaline.

(2) Yining city (NK): a continental north temperate climate features abundant light and heat, prolonged sunshine duration, high cumulative temperatures, and substantial diurnal temperature variation. The mean annual temperature ranges 7.7–8.7 °C; ≥ 10 °C effective cumulative temperature is 2 900–3 025 °C,

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and the frost-free period spans 150–160 days. Soil type is grey calcium soil.

(3) Yining County (YN): A temperate continental climate is characterised by abundant heat and light. The long-term mean temperature is 8.1 °C; the mean annual frost-free period spans 159 days, and annual precipitation averages 240.2 mm, predominantly occurring between April and July.

(4) Huocheng County (HC): A temperate continental climate exhibits a long-term mean temperature of 8.2–9.4 °C, a mean annual frost-free period of 165 days, annual precipitation averaging 214 mm, and a maximum seasonal freeze depth of 1.2 m. Soils are predominantly sandy loam and meadow types, demonstrating moderate fertility and favourable workability.

Collection of experimental samples. Plant sampling: French blue lavender specimens were collected during peak flowering (mid-June) from experimental fields at four locations: Chabuchar County (Ili River Valley Lavender Garden), Yining City (Yili State Institute of Agricultural Science), Huocheng County (Tianshan Flower Sea, Luchaogou Township), and Yining County (Kashi Township, Sigong Village). Terminal inflorescences were harvested 10 cm below the flower base, with 3 kg collected per cultivar (Verma et al. 2010).

Soil sampling. The test site was subject to consistent planting, fertilisation and other management measures. Three 10 × 10 m quadrats were randomly established per plot. At each quadrat, five sampling points were selected randomly. Soil cores were extracted using a 5-cm diameter auger from two depths (0–20 cm and 20–40 cm). After removing plant debris and stones, samples were sieved (2 mm), homogenised, and stored in sealed bags at −20 °C. Each composite sample was divided: one portion was air-dried for physicochemical analysis, and the other was cryopreserved.

Determination of soil indicators. Soil pH was determined using a DELTA 320 pH meter (Mettler-Toledo, Greifensee, Switzerland) in a deionised water suspension (soil : water = 1 : 2.5). Soil organic carbon (SOC) was determined using the heat capacity method with potassium dichromate and concentrated sulfuric acid. Total soil nitrogen and phosphorus were determined on sieved, naturally air-dried samples. Total nitrogen was quantified using the Kjeldahl method after digestion in concentrated sulfuric acid. Total phosphorus was measured by the molybdenum antimony colourimetric method following digestion in a mixture of concentrated sulfuric acid and perchloric acid (Bao 2000).

Determination of the composition of lavender essential oil. Essential oil from *Lavandula angustifolia* was extracted *via* steam distillation. A flower-to-water ratio of 1:12 (g/mL) was maintained during extraction. Flowers and water were combined in a 2 000 mL round-bottom flask. The mixture was heated to a constant boiling temperature, after which distillation commenced and continued for 90 min.

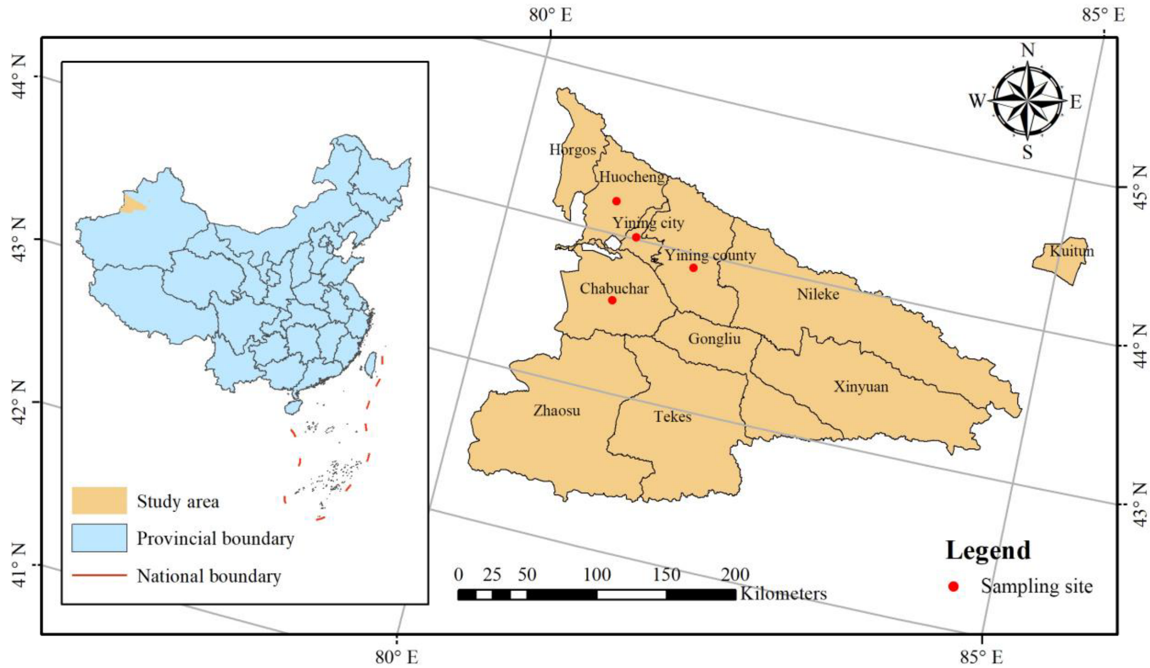

Figure 1. Sampling location information

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The upper layer in the collector was separated as crude essential oil and dried over anhydrous sodium sulphate to obtain anhydrous essential oil. The essential oil was collected and stored at 4 °C in the dark. Five replicates were performed per sample. The yield of *Lavandula angustifolia* essential oil was calculated as follows:

$$\text{Oil yield rate (mL/kg)} = \frac{\text{oil extraction volume (mL)}}{\text{flower weight (kg)}}$$

The essential oil was detected by GC-MS, and the content of the characteristic components was determined using the area normalisation method, as per the *Lavandula angustifolia* database search (Danh et al. 2013).

Determination of soil bacterial communities. Nucleic acids were extracted using an OMEGA Soil DNA Kit (D5635-02) from Omega Bio-Tek (Omega Bio-Tek, Norcross, USA). Universal primers were used to amplify the bacterial 16S rRNA gene. Primers 338F and 806R were used for soil samples, which were then sequenced and analysed using the Illumina MiSeq sequencing platform from Shanghai Parsonage Biological Co. Once sequencing was complete, the data were spliced, filtered, de-hybridised and clustered. Sequences with a homology rate of > 97% were grouped into the same OTU. All OTUs were analysed by clustering and compared with the database to obtain species distribution results at different taxonomic levels (kingdom, phylum, class, order, family, genus and species).

Statistical analysis. Statistical analysis was performed using Excel 2016 (Redmond, USA) for data organisation and descriptive statistics. A one-way ANOVA followed by Duncan's multiple range test ($\alpha = 0.05$) was conducted using SPSS 25 (Armonk, USA) to determine significant differences among treatments; results are presented as means ± standard errors. Data visualisation was carried out using Origin 2024 (Northampton, USA). Redundancy analysis (RDA) was performed with the vegan package in R, and subsequent plots were generated using the ggplot2 package.

RESULTS AND DISCUSSION

Essential oil composition and its relative content of lavender in different main planting areas. The chemical composition of lavender essential oil varies across regions, except for linalool. However, the concentrations of other components do not differ significantly. As shown in Table 1, the essential oil yield from HC is considerably higher than that from other regions, while the yields from the other three regions are not significantly different. The linalool content follows the order: HC (41.04%) > NK (35.44%) > YN (33.23%) > CX (27.65%). The linalyl acetate content was YN (30.04%) > CX (28.73%) > HC (25.30%) > NK (22.31%). There was no significant difference in the content of linalyl acetate and camphor among different regions. Overall, the lavender essential oil from HC had the highest yield and superior oil quality, with an oil content of 1.14%, a linalool content of 41.04%, and linalyl acetate and lavandulyl acetate contents of 25.30% and 5.36%, respectively. This might be related to the specific climatic conditions and soil characteristics of this region.

The physicochemical properties of soil in the different main planting areas of *Lavandula*. Significant differences were observed in the soil physicochemical properties across both regions and soil layers (Table 3). In the 0–20 cm layer, soil pH ranged from 7.76 to 8.04 across all regions, with no significant differences detected. The organic carbon content in NK, YN, and HC was significantly higher than that in CX. The total nitrogen content was highest in HC (1.48 g/kg) and lowest in CX. The total phosphorus content was relatively high in CX, NK, and HC, but significantly lower in YN.

In the 20–40 cm layer, the soil pH ranged from 7.70 to 8.10, with no significant differences observed. Organic carbon and total nitrogen contents were generally high, particularly at the YN site, where organic carbon reached 11.61 mg/kg – significantly higher than in other regions. No significant differences in

Table 1. Overview of the study area

Sampling point	Sample	Longitude (°)	Latitude (°)	Altitude (m a.s.l.)	Precipitation (mm)
Chabuchar County	CX	81.03	43.77	685	28.5
Yining city	NK	81.39	43.93	670	30.7
Yining county	YN	81.99	43.71	841	28.9
Huocheng county	HC	80.76	44.17	691	26.2

CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

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Table 2. Components and relative contents of lavender essential oil in different main planting areas

Sampling point	Oil yield	Relative content (%)			
		linalool	linalyl acetate	lavandulyl acetate	camphor
CX	0.59 ± 0.04[a]	27.65 ± 5.55[b]	28.73 ± 6.71[a]	5.75 ± 0.95[a]	0.25 ± 0.10[a]
NK	0.56 ± 0.04[a]	35.44 ± 1.05[ab]	22.31 ± 2.50[a]	3.51 ± 0.80[a]	0.26 ± 0.09[a]
YN	0.39 ± 0.09[a]	33.23 ± 2.45[ab]	30.04 ± 2.00[a]	5.15 ± 2.11[a]	0.37 ± 0.08[a]
HC	1.14 ± 0.23[b]	41.04 ± 2.65[a]	25.30 ± 3.36[a]	5.36 ± 1.77[a]	0.31 ± 0.13[a]

Different lowercase letters indicate significant differences among different treatments ($P < 0.05$), as shown below. CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

total nitrogen were observed among NK, YN, and HC, though all three were significantly higher than CX. Total phosphorus content varied considerably across soil layers, with the highest value recorded in YN (1.43 g/kg) and the lowest in NK (0.68 g/kg).

The bacterial α-diversity index of soil in different lavender main cultivation areas. The α-diversity index is a comprehensive indicator of the richness and evenness of microbial communities. As demonstrated in Figure 2, the soil bacterial coverage index in the 0–20 cm soil layer ranges from 0.9984 to 0.9998, indicating that the sequencing results can fully reflect the diversity of soil bacteria. The Chao1 index demonstrated the highest NK value and the lowest HC value, and the NK bacterial richness was found to be significantly higher than that of HC. The Shannon and Simpson indices both demonstrate the highest NK value, which is greater than that observed in other regions. It is evident that YN exhibits the lowest value, while NK demonstrates a substantial discrepancy compared to YN, signifying that NK harbours a greater diversity of soil bacteria compared to other regions. It is evident that the bacterial richness and diversity of NK soil are maximised within the 0–20 cm soil layer.

The soil bacterial coverage index in the 20–40 cm soil layer ranges from 0.9981 to 0.9996 (B2). In contrast to the results observed in the 0–20 cm soil layer, the Chao1 index attains its maximum value in HC, thereby signifying that the bacterial richness in HC is the most abundant and significantly exceeds that of NK (B1). The Simpson index of NK is elevated, and there is a significant difference in comparison to YN, which is consistent with the results observed in the 0–20 cm soil layer (B4). The Shannon and Simpson indices both demonstrate that YN exhibits the lowest YN value, thus indicating that YN is characterised by the lowest diversity of soil bacteria in comparison to other regions.

Soil bacterial community composition of lavender in different main planting areas. The composition and relative abundance of soil bacterial communities in the rhizosphere of lavender across major cultivation areas are presented in Figure 3. At the phylum level, Proteobacteria, Acidobacteriota, Gemmatimonadota, and Actinobacteriota were the

Table 3. Changes in the physical and chemical properties of soil in the different main lavender cultivation areas

Soil layer (cm)	Sampling point	pH	Organic carbon (mg/kg)	Total nitrogen (g/kg)	Total phosphorus (g/kg)
0–20	CX	8.04 ± 0.02[a]	4.96 ± 0.23[b]	0.87 ± 0.03[c]	1.39 ± 0.09[a]
	NK	7.98 ± 0.05[a]	8.80 ± 0.57[a]	1.33 ± 0.04[b]	1.55 ± 0.07[a]
	YN	7.76 ± 0.27[a]	7.75 ± 0.45[a]	1.33 ± 0.04[b]	0.93 ± 0.06[b]
	HC	8.00 ± 0.23[a]	7.86 ± 0.35[a]	1.48 ± 0.05[a]	1.54 ± 0.08[a]
20–40	CX	7.96 ± 0.08[a]	9.88 ± 0.74[b]	0.84 ± 0.05[b]	1.22 ± 0.04[b]
	NK	8.10 ± 0.05[a]	8.97 ± 0.20[b]	1.25 ± 0.03[a]	0.68 ± 0.03[c]
	YN	7.70 ± 0.20[a]	11.61 ± 0.07[a]	1.29 ± 0.05[a]	1.43 ± 0.05[a]
	HC	7.90 ± 0.15[a]	8.53 ± 0.37[b]	1.19 ± 0.03[a]	1.09 ± 0.04[b]

CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

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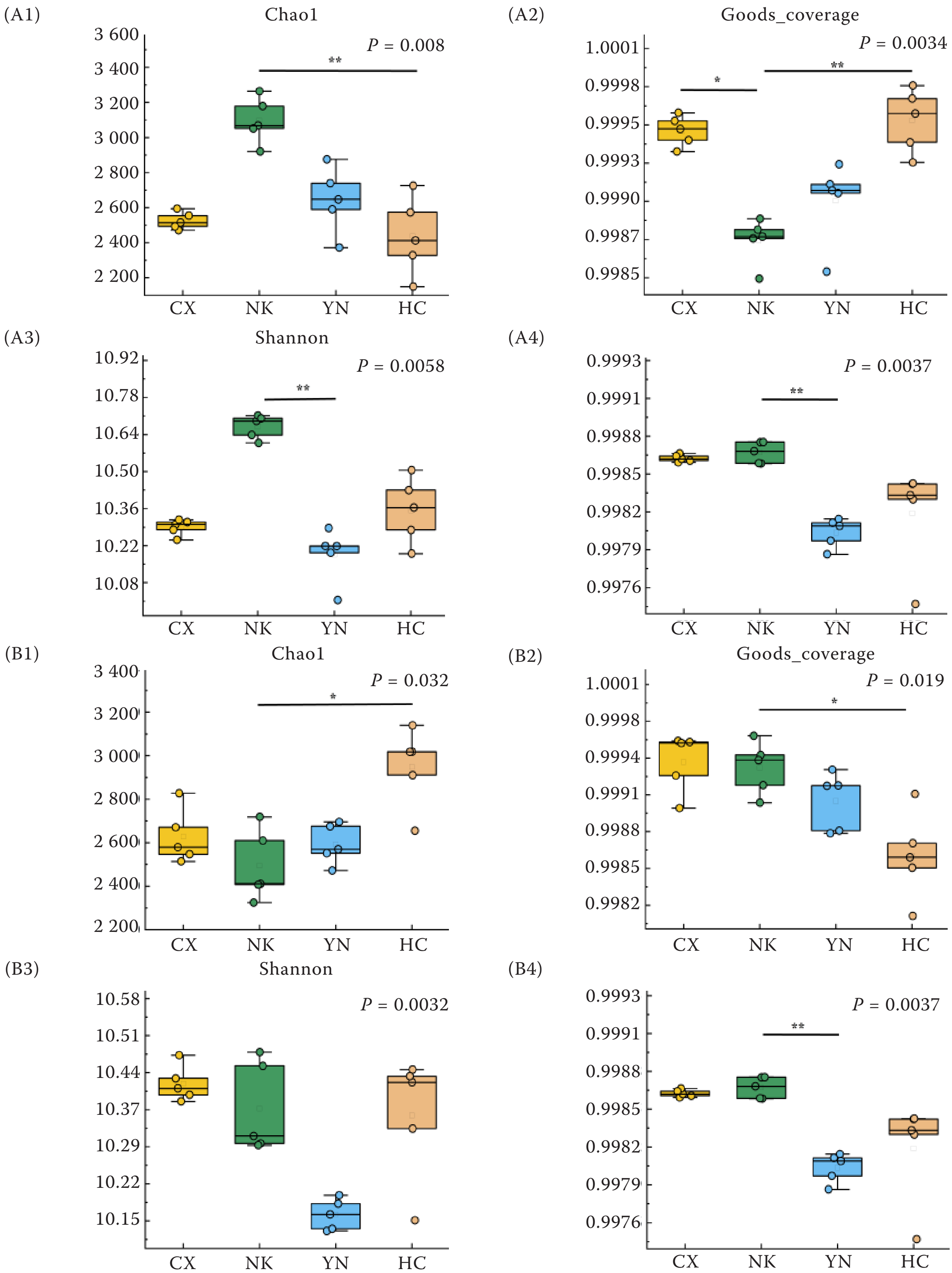

Figure 2. α-diversity index of rhizosphere soil bacteria in different main planting areas of lavender. Different letters above bars indicate significant differences among groups according to Duncan's multiple range test ($P < 0.05$). Soil samples from the (A) 0–20 cm and (B) 20–40 cm layers are shown, as shown below. CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

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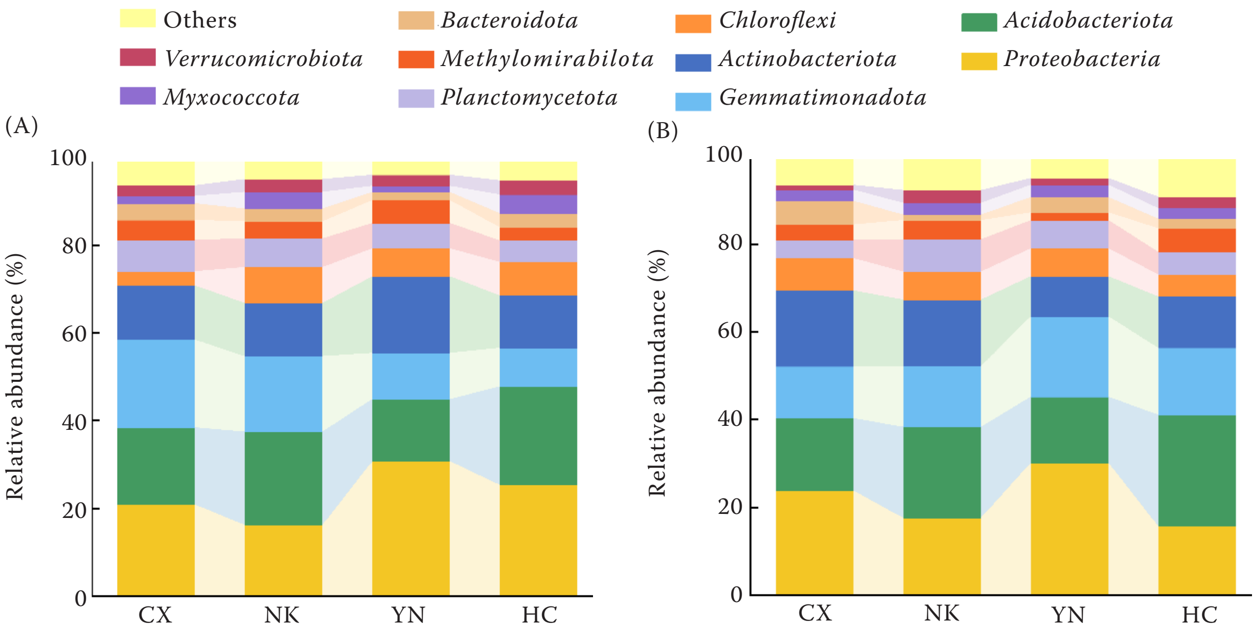

Figure 3. Relative abundance of soil bacteria in different main planting areas of lavender at the phylum level. CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

four dominant phyla, collectively accounting for 66.89% to 72.92% of the sequences, with the remaining taxa comprising 27.08% to 33.11%. In the 0–20 cm soil layer, Proteobacteria was most abundant in YN at 30.76%, whereas HC showed the lowest abundance of this phylum at 16.28%. Acidobacteriota was most prevalent in HC (22.48%) and least prevalent in YN (14.19%). Actinobacteriota represented the third most abundant phylum, reaching 20.03% in CX but only 8.78% in HC. Gemmatimonadota was most abundant in YN at 17.41%.

In the 20–40 cm layer, Proteobacteria remained most abundant in YN (30.19%) and least abundant in HC (15.77%). Similarly, Acidobacteriota was least abundant in YN (15.03%) and most abundant in HC (23.37%). Gemmatimonadota was most abundant in YN

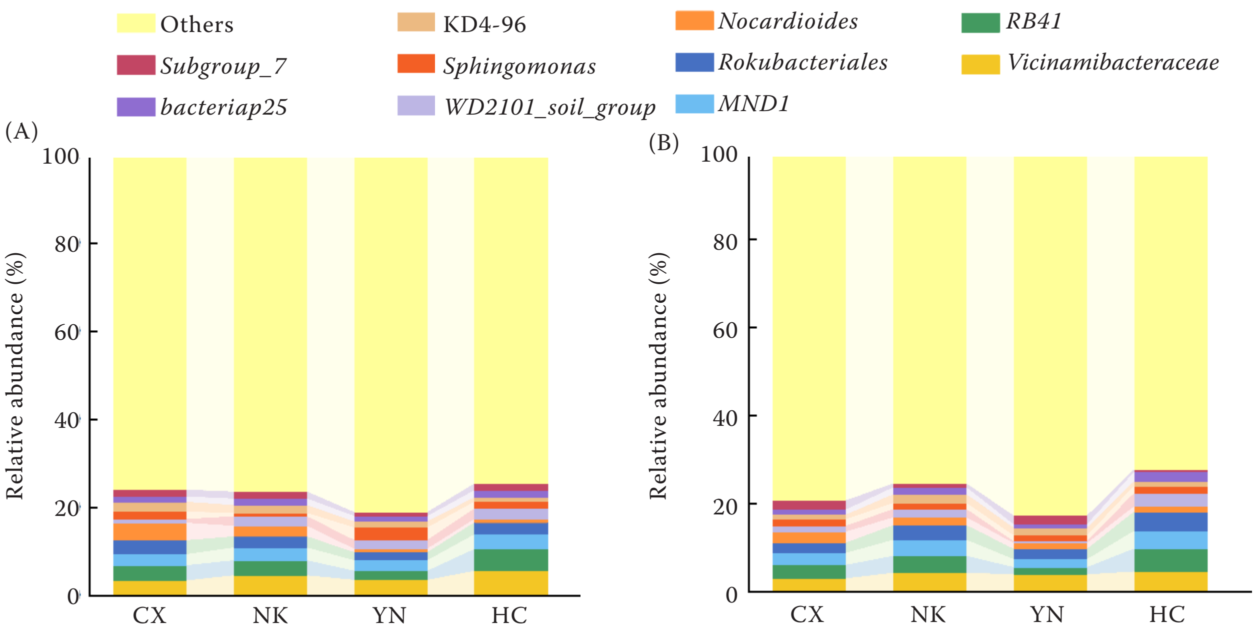

Figure 4. Relative abundance of rhizosphere soil bacteria in different main planting areas of lavender at the genus level. CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

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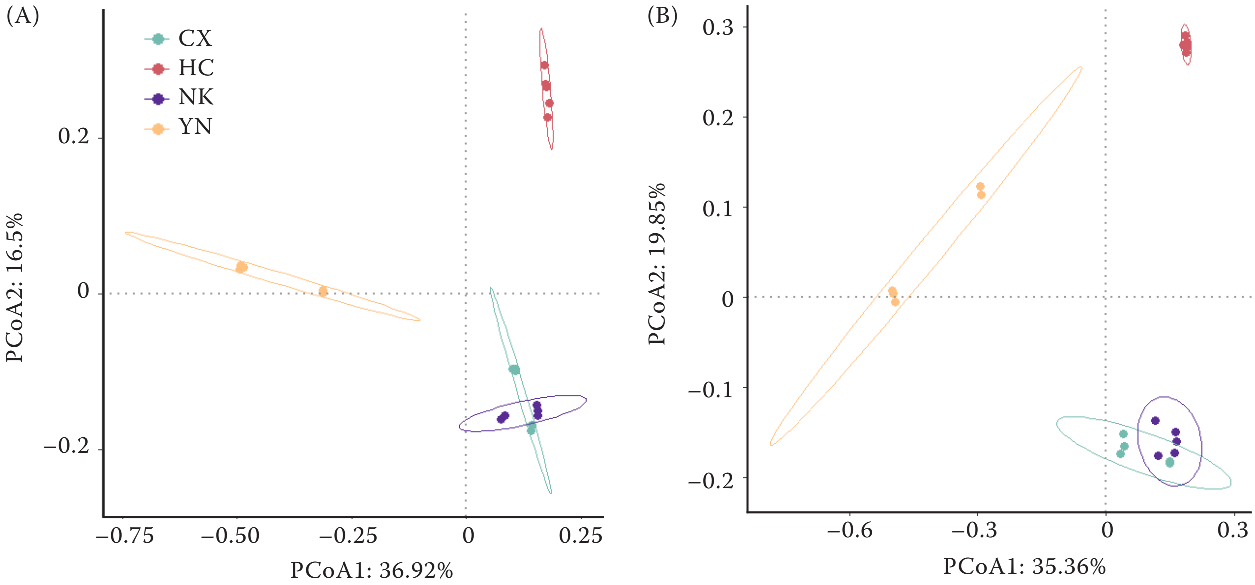

Figure 5. Principal coordinate analysis (PCoA) of bacterial communities in lavender soil from different growing regions. CX – Chabuchar County; NK – Yining City; YN – Yining County, HC – Huocheng County

(18.39%) and least abundant in CX (11.83%). Conversely, Actinobacteriota showed the lowest relative abundance in YN (9.13%) and the highest in CX (17.28%).

The relative abundance of soil bacterial communities in the rhizosphere of lavender at the genus level is shown in Figure 4. The four most abundant genera were Vicinamibacteraceae, RB41, MND1, and Rokubacteriales. Notably, Vicinamibacteraceae and RB41 belong to the acidobacterial phylum. In the 0–20 cm soil layer, Vicinamibacteraceae and RB41 were the most prevalent taxa, with relative abundances of 5.59% and 4.94%, respectively. A similar pattern was observed in the 20–40 cm layer, with both genera also most abundant in HC, at 4.56% and 5.16%, respectively.

PCoA analysis of lavender in different main cultivation areas. Figure 5 presents the results of the PCoA analysis of the bacterial community structure. In the 0–20 cm soil layer, PC1 and PC2 explained 36.92% and 16.5% of the total variance, respectively, together accounting for 53.4% of the observed variation. In the 20–40 cm layer, PC1 and PC2 explained 35.36% and 19.85% of the variance, respectively, with a cumulative contribution of 55.21%. In both layers, samples from NK and CX were distinctly clustered, indicating notable similarity in bacterial communities between these two sites and distinguishing them from other regions. Furthermore, NK and HC samples formed tight clusters with minimal intragroup variation, whereas YN and CX showed greater dispersion and higher within-group variability, suggesting more stable bacterial communities in NK and HC.

The influence of environmental factors on soil bacterial communities. Redundancy analysis (RDA) of the bacterial community revealed distinct environmental associations across soil depths (Figure 6). In the 0–20 cm layer, RDA1 and RDA2 explained 47.34% and 30.18% of the total variance, respectively, cumulatively accounting for 77.52%. The bacterial community composition was primarily influenced by pH, TP, longitude, and altitude. Specifically, Proteobacteria showed a positive correlation with altitude. Acidobacteriota and Methylomirabilota were positively associated with pH but negatively correlated with longitude and altitude. Gemmatimonadota exhibited positive correlations with longitude and altitude, but a significant negative correlation with pH and TP. Myxococcota and Verrucomicrobiota were positively correlated with soil organic carbon and latitude.

In the 20–40 cm layer, RDA1 and RDA2 accounted for 49.02% and 26.25% of the variance, respectively, with a cumulative explanation of 75.27%. Proteobacteria and Planctomycetota were positively correlated with TP and SOC, and negatively correlated with latitude. Acidobacteriota was positively associated with latitude but negatively correlated with TP and SOC. Actinobacteriota correlated positively with pH and negatively with altitude, while Gemmatimonadota was positively linked to altitude and total nitrogen. Chloroflexi showed a negative correlation with TN.

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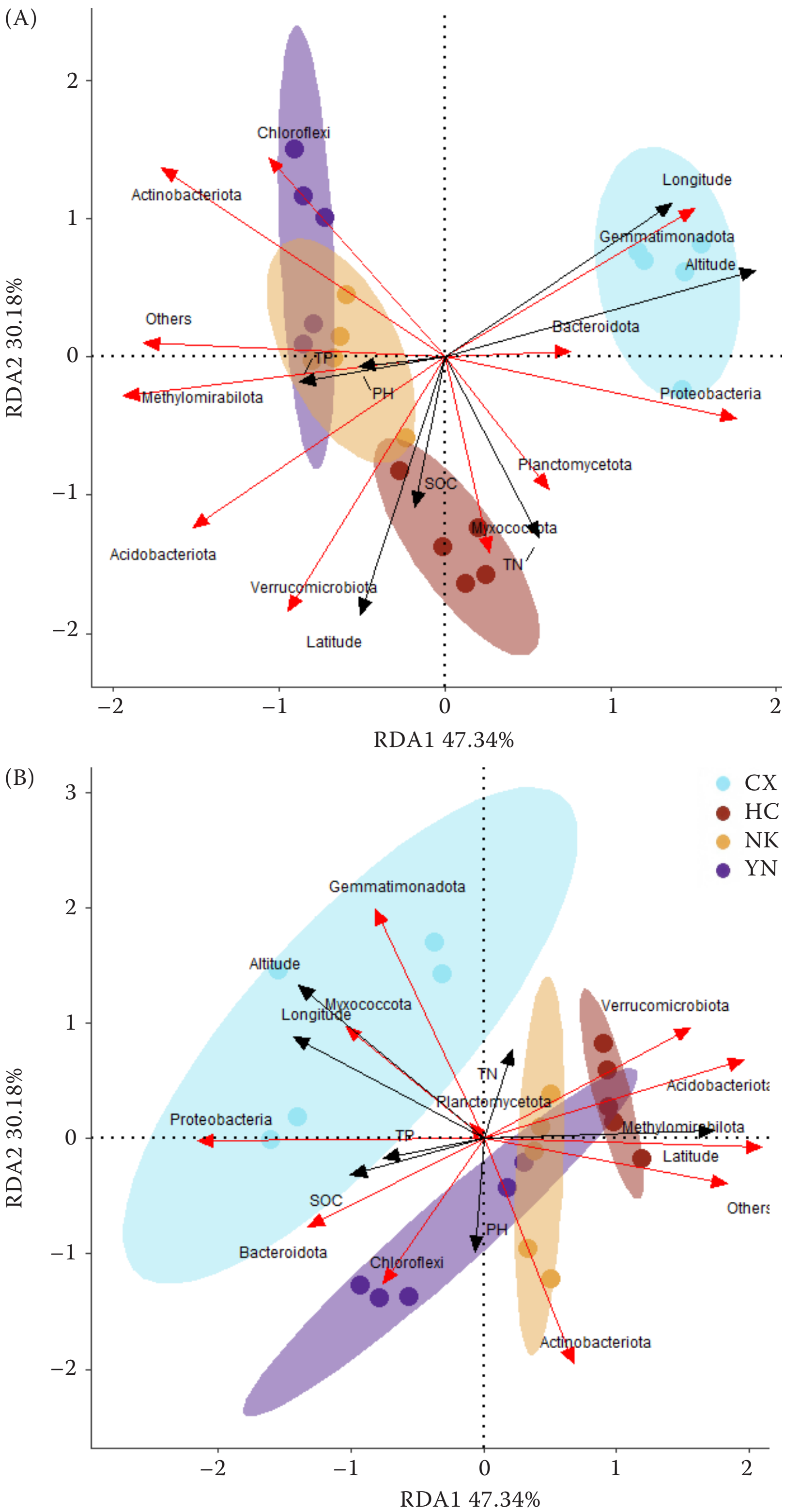

Figure 6. Redundancy analysis of soil physical and chemical properties and bacterial communities. CX – Chabuchar County; NK – Yining City; YN – Yining County (YN), HC – Huocheng County

DISCUSSION

Differences in soil physicochemical properties and essential oil quality of lavender in different main planting areas. Soil pH is a significant chemical indicator, with fluctuations in pH capable of substantially modifying the availability of soil nutrients and crop absorption efficiency (Mitsuta et al. 2025). In lavender cultivation areas of the Ili River Valley, soil pH ranges from 7.70 to 8.10. Although

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regional pH variations are minimal, significant spatial heterogeneity occurs in soil physicochemical properties. Comparative environmental analyses reveal that regional climatic variations drive pronounced differences in soil nutrient content (Liang et al. 2022). The Huocheng production area has been found to have higher levels of key nutrients, such as carbon, nitrogen, and phosphorus, in the soil compared to other major cultivation areas. This area is characterised by elevated levels of beneficial elements, which correlate directly with essential oil yield. Consequently, Huocheng is identified as the region's highest-yielding premium production area, demonstrating optimal suitability for lavender cultivation. These findings align with prior conclusions (Gulina 2024). Furthermore, linalool, which is a key quality indicator of lavender essential oil, exhibits significant regional variation across cultivation areas in Huocheng County. Studies demonstrate that linalool content in Huocheng-derived lavender essential oil is markedly higher than in other production zones, a distinction attributed to the region's unique soil properties. A reduced organic matter content has been shown to diminish the populations of beneficial soil microorganisms, directly impairing crop nutrient uptake and secondary metabolite synthesis (Wang et al. 2009). Soil nutrient analysis of the primary lavender production area in the Ili River Valley revealed that the Huocheng cultivation zone exhibited significantly higher levels of organic carbon and total nitrogen compared to other regions. These favourable soil fertility conditions not only promote robust lavender growth but also significantly enhance essential oil biosynthesis and accumulation. These findings underscore that optimised soil management practices can directly improve essential oil quality.

Variations in soil microbial diversity and community structure in different main cultivation areas. Significant climatic variations exist among different regions, exerting varying degrees of influence on crop growth and development. These environmental differences, combined with long-term microorganism-crop co-evolution processes, have led to distinct patterns of soil bacterial diversity across geographical areas (Deng et al. 2024). Regarding bacterial diversity, the conclusions derived from the analysis of both soil layers were consistent, with bacterial diversity present in the Yining city plot being significantly higher than in Yining County. This phenomenon may be associated with the precipitation levels experienced during the sampling process. The data demonstrated that the monthly precipitation levels at Yining city exceeded those observed in Yining County, characterised by higher rainfall volumes, thereby fostering favourable conditions for bacterial proliferation. Conversely, insufficient rainfall has been demonstrated to restrict bacterial activity and reduce bacterial diversity (Guo et al. 2023). Furthermore, the Yining city's plot is situated in proximity to farmland, which is characterised by a more intricate and varied surrounding ecosystem. This environment has the potential to introduce a broader spectrum of microorganisms into the soil, thereby enhancing bacterial diversity (Zuo et al. 2023). In contrast, the experimental site in Yining County is characterised by lavender fields, with a single crop and a simpler ecological environment, resulting in a more homogeneous bacterial community in the soil. The results of the PCoA analysis demonstrate that the bacterial communities at Yining City and Chabuchar County exhibit a certain degree of similarity, which may be attributable to their close geographical proximity. At the phylum level, although there is some variation in soil bacterial communities depending on soil type and climatic characteristics, the dominant groups in the soil are essentially the same, which is consistent with the results of previous studies (Ding 2018). The results show that at the phylum level, Proteobacteria, Acidobacteriota, Gemmatimonadota, and Actinobacteriota are the dominant phyla, exhibiting strong adaptability, with their combined relative abundances exceeding 60%. Specifically, Acidobacteria and Gemmatimonadota prevail in acidic soils, while Proteobacteria and Actinobacteria predominate in alkaline soils (Ligi et al. 2014).

The Chao1 index, an important indicator of bacterial community richness, revealed a distinct pattern: it was significantly higher in the Agricultural Research Institute (NK) site than in the Huocheng (HC) site in the 0–20 cm soil layer, whereas the opposite trend was observed in the 20–40 cm layer, where HC exhibited significantly higher richness than NK. This difference may be attributed to the different cultivation years and management methods employed in the two locations (Patra et al. 2008). As a traditional lavender cultivation area, Huocheng County has a longer history of cultivation and more mature soil development. This not only promotes the formation of stable aggregates but also facilitates the vertical transport and accumulation of plant-derived carbon into deeper soil layers (Yang et al. 2012).

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This input of relatively recalcitrant organic carbon into the subsurface provides energy substrates and ecological niches for oligotrophic microorganisms (such as Acidobacteriota and Chloroflexi) adapted to nutrient-poor environments (Hansel et al. 2008), resulting in higher microbial richness in its deep soil. In contrast, the Agricultural Research Institute (NK) site, likely due to its shorter cultivation history and higher clay content, which leads to poor aeration, may inhibit the growth of some aerobic bacteria (Schmidt et al. 2018). To explore the potential functional relationships between the soil bacterial community and lavender essential oil quality in greater detail, we conducted a Spearman correlation analysis between the relative abundance of the dominant bacterial genera and the content of key essential oil components (S1). In the 20–40 cm layer, we observed even more significant correlations. Vicinamibacteraceae was significantly positively correlated with Linalool ($P < 0.05$). Furthermore, a consortium of genera including RB41, Rokubacteriales, Latescibacterota, and Subgroup_17 were significantly positively correlated with each other ($P < 0.05$), suggesting potential co-occurrence or synergistic relationships that may influence the soil microenvironment and indirectly affect plant physiology (Figure 7). Further research in this area is needed.

The impact of environmental factors on soil microbial communities. As a core component of the soil ecosystem, the rhizosphere soil microbial community is structurally and functionally regulated by a combination of environmental factors (Richter et al. 2018). Soil bacterial communities are primarily influenced by factors such as pH, total nitrogen, total phosphorus, soil organic carbon, along with longitude and altitude (Figure 6). Previous studies have suggested that pH is the primary factor influencing the composition of soil microbial communities, with acidophilic bacteria thriving in acidic environments (Ding and Ruyan 2017, Wang et al. 2018). However, our results revealed a significant positive correlation between Acidobacteriota abundance and soil pH. This contrasts with the findings of Shen, who reported a strong negative correlation between pH and Acidobacteria relative abundance (Shen et al. 2013). Collectively, these findings suggest Acidobacteriota exhibits broad pH adaptability. This demonstrates that Acidobacteria exhibit strong pH tolerance. The phylum Actinobacteriota also shows a positive correlation with pH, preferring neutral to slightly alkaline conditions. The composition and diversity of soil microbial communities are often shaped by nutrient availability (Zheng et al. 2019). Studies have shown that nitrogen input can indirectly influence soil bacterial communities by modifying plant diversity and carbon availability (Ling et al. 2017). Zhang et al. (2024b) reported that nitrogen addition increased the relative abundance of Proteobacteria and Bacteroidetes. Our study revealed a significant positive correlation among Proteobacteria, Gemmatimonadota, and Chloroflexi with total nitrogen content, underscoring the essential role of nitrogen in building microbial biomass and stimulating community development (Hu et al. 2020). Notably, the relative abundance of Acidobacteriota was the highest in the soils of Huocheng County across both soil layers, and Vicinamibacteraceae, a genus belonging to Acidobacteriota, showed a significant positive correlation with linalool. Previous research has indicated that certain groups within Acidobacteriota are involved in soil phosphorus activation (Ling et al. 2017). Our results further demonstrate a positive correlation between Acidobacteriota and soil total phosphorus content (Figure 5). Therefore, we speculate that the enrichment of Vicinamibacteraceae in Huocheng County soils may enhance the soil phosphorus cycling function. Phosphorus is a key element for plant biosynthesis, such as the synthesis of terpenoid precursors (Cheng et al. 2020). This could be a potential mechanism underlying its positive correlation with linalool content. Furthermore, the PCoA results indicated lower within-group variation in the Huocheng samples, suggesting a more stable equilibrium in the soil microbial ecosystem. This stable community is likely to maintain balanced nutrient cycling, thereby consistently meeting the high metabolic demands of terpenoid biosynthesis in lavender. This serves as an important contributing factor to the high yield and superior quality of essential oil observed in Huocheng County.

Large-scale geographical gradients shape the distribution patterns of dominant bacterial communities by modifying thermal conditions and habitat heterogeneity (Bryant et al. 2008). This study revealed that the composition of bacterial communities varied substantially across different altitudes, with the richness of dominant Acidobacteriota exhibiting a significant negative correlation with elevation. Acidobacteriota abundance was negatively correlated with longitude in the 0–20 cm soil layer and positively correlated with latitude in the 20–40 cm layer. In contrast, Gemmatimonadota showed similar

https://doi.org/10.17221/377/2025-PSE

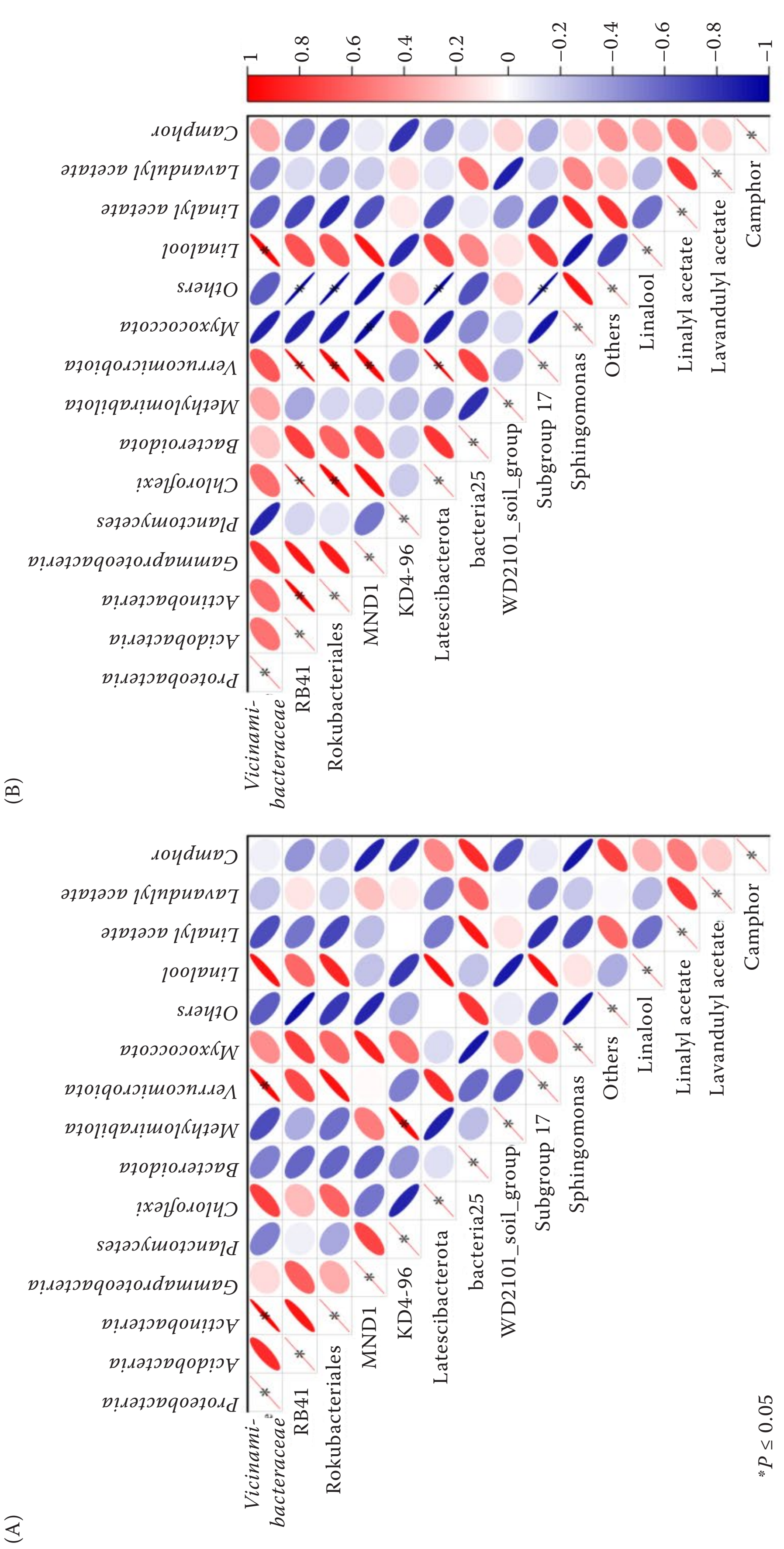

Figure 7. Correlation between relative abundance of genus-level bacteria and essential oil components. (A) 0–20 cm soil layer and (B) 20–40 cm soil layer. Only the top 10 most abundant genera are shown. The color and size of the circles represent the correlation coefficient (r), as indicated by the scale bar. *denote significance at the 0.05 levels

https://doi.org/10.17221/377/2025-PSE

distribution patterns in both soil layers, displaying a positive correlation with longitude (Figure 6). These results align with previous reports indicating a significant positive relationship between soil bacterial abundance and longitude, and a significant negative association with latitude (Fu et al. 2023). Indeed, geographical factors and soil chemical properties act together to shape microbial community structure through a "geography-environment-biology" interactive mechanism. Studies suggest that climate variations driven by latitude and longitude affect the composition of plant litter inputs. Through humification, this litter is transformed into distinct soil organic matter components, thereby promoting the dominance of microbial communities that are more efficient at decomposition (Zeng et al. 2017, Zhang et al. 2024a). Other studies have suggested that soil microenvironments – such as root exudates and litter quality – exert a stronger influence on bacterial communities than elevational differences (Fierer et al. 2011). This interaction suggests that rhizosphere microbial communities act as "ecological sensors" of environmental change, whereby even subtle fluctuations can induce cascading effects on microbial structure, ultimately impacting soil nutrient cycling, plant health, and other ecosystem services. Nonetheless, current research remains limited in scope. Future studies should incorporate multi-omics approaches, including metagenomics and metabolomics, to decipher the mechanistic basis of environmentally driven functional differentiation in microbial communities. When combined with long-term *in situ* monitoring, such strategies will enhance our understanding of the successional dynamics and ecological adaptation of rhizosphere microbial communities under climate change.

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Received on: August 27, 2025
Accepted: November 4, 2025
Published online: November 26, 2025