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Coordinated regulation of nutritional quality in Dendrocalamus latiflorus shoots by multi-environmental factors and rhizosphere microorganisms

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Research Article

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Posted Date: November 24th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-11591853/v1

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Additional Declarations: No competing interests reported.

Coordinated regulation of nutritional quality in *Dendrocalamus latiflorus* shoots by multi-environmental factors and rhizosphere microorganisms

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Abstract: Nutritional quality of *Dendrocalamus latiflorus* shoots varies across geographical locations, but the environmental determinants remain unclear. We examined climate, soil, and rhizosphere microbiomes across 53 sites in nine provinces of southern China. Pronounced site-specific nutritional differentiation was observed. Guizhou had high soluble protein and starch contents, whereas Yunnan had high starch content, and Fujian showed total amino acid contents >2.5-fold higher than those of other sites, consistent with the growth-differentiation balance hypothesis. Soil available potassium and non-capillary porosity were positively correlated with total amino acid content, but neither had a significant direct SEM path to total amino acid. In the SEM, unclassified bacteria directly promoted total amino acid accumulation, whereas mean annual temperature directly and negatively affected total amino acid content. Precipitation seasonality indirectly affected starch content through available potassium and Bradyrhizobium; available potassium also directly suppressed starch content, and Bradyrhizobium directly suppressed starch content. PCoA and PERMANOVA revealed significant site-driven differentiation in bacterial (16S: $F = 1.460$, $R^2 = 0.210$, $P = 0.0203$) and fungal (ITS: $F = 1.222$, $R^2 = 0.182$, $P = 0.0181$) community structures, with bacterial intra-group dispersion significantly heterogeneous (betadisper: $F = 6.449$, $P = 0.0001$) but fungal dispersion not ($F = 1.046$, $P = 0.4137$). Fujian sites were specifically enriched in Lactobacillus, suggesting a potential but not yet causal link to amino acid accumulation. SEM further indicated that MAT affected non-capillary porosity and directly suppressed total amino acid, whereas precipitation seasonality affected available potassium, which was linked to Bradyrhizobium and starch; unclassified bacteria directly promoted total amino acid. These findings provide a theoretical foundation for site selection, soil amelioration, and rhizosphere microecology engineering for high-quality bamboo shoot production.

Keywords: *Dendrocalamus latiflorus*; geographical location; rhizosphere microbiome; structural equation modeling; amino acid and starch accumulation; growth-differentiation balance hypothesis

1 Introduction

Bamboo forests play critical roles in soil and water conservation, vegetation restoration, and soil fertility enhancement, while also serving as a key forest type for developing three-dimensional hill plantation systems. As a major multipurpose clumping bamboo species cultivated for both shoot and timber production in southern China, *Dendrocalamus latiflorus* is one of the rare bamboo varieties that can be fully processed and utilized, thus boasting high utilization value. This species exhibits strong environmental adaptability and performs prominent functions in water retention, soil stabilization, and slope protection. Its tender shoots have a deliciously sweet taste and are rich in nutrients; cultivation of this bamboo requires low investment, yields rapid returns, and generates considerable income (Wang et al., 2025). Although *D. latiflorus* cultivation is characterized by low input and quick economic returns, its profitability is highly dependent on shoot quality. Amino acid and starch contents directly determine the sweet flavor, texture, nutritional value, and commercial grading of bamboo shoots (Wang et al., 2026; Jia et al., 2024). Currently, the amino acid accumulation, starch concentration, and flavor compound profiles of *D. latiflorus* shoots vary drastically across geographical production regions, leading to inconsistent product quality and severely undermining the market reputation of high-quality bamboo shoots. Conventional cultivation practices, including water, fertilizer, and irrigation management, can hardly eliminate quality differentiation induced by environmental heterogeneity (Xu et al., 2021). Therefore, it is urgent to elucidate the internal regulatory mechanisms by which climatic conditions, soil physicochemical properties, and the rhizosphere microenvironment jointly shape bamboo shoot quality (Zhang et al., 2025). The findings will provide theoretical support for the scientific zoning of high-quality production areas and the establishment of targeted cultivation technology systems, thereby overcoming the bottleneck restricting the standardized development of the industry.

Previous studies have demonstrated that climatic factors-such as mean annual temperature and precipitation patterns, exert significant effects on nutrient accumulation in bamboo shoots (Li et al., 2024). Likewise, soil physicochemical properties, including porosity, available potassium, and hydrolyzable nitrogen, have been shown to directly govern bamboo shoot nutritional quality

(Li et al., 2018). Nevertheless, most existing investigations focus solely on either soil or climatic factors in isolation, lacking a systematic, integrated analysis of both. Importantly, even within regions characterized by relatively homogeneous soil nutrient status, marked quality discrepancies persist among shoots harvested from different plots, implying that additional critical regulatory variables beyond climate and edaphic properties remain underexplored. Large-scale spatial patterns driven by environmental conditions are further mediated by plant roots in the rhizosphere. The rhizosphere serves as a hotspot for organic matter decomposition and nutrient cycling, and constitutes a core interface for tripartite interactions among plants, soil, and microorganisms, playing a pivotal role in plant nutrient turnover (Henneron et al., 2020; Guyonnet et al., 2018). Soil physicochemical attributes, including aeration, porosity, and potassium availability, can directly or indirectly alter the abundance, composition, and functional profiles of rhizosphere microbial communities by modulating oxygen concentration, water–nutrient transport, and root exudate composition (Xia et al., 2022; Alizadeh et al., 2025; Ebrahimi et al., 2015). Regarded as the plant's second genome, rhizosphere microorganisms are capable of nitrogen fixation, nitrogen mineralization, and regulation of plant carbon and nitrogen metabolism (Luo et al., 2025). Enhanced microbial activity facilitates efficient nutrient utilization, thereby improving the nutritional quality of bamboo shoots (Li et al., 2022). Inoculation with Bacillus subtilis increased bamboo shoot protein content by 21.81% and elevated amino acid and soluble sugar concentrations (Cheng, 2021), underscoring the considerable potential of rhizosphere microorganisms in modulating shoot quality.

However, current relevant studies are predominantly confined to single or a limited number of varieties, and systematic research addressing the spatial distribution patterns of rhizosphere microbial communities across distinct geographical locations of *D. latiflorus*-and their subsequent effects on shoot quality-remains conspicuously absent.The limitations of existing studies are summarized as follows. The spatial differentiation patterns of rhizosphere bacterial and fungal alpha diversity as well as genus-level community composition of *D. latiflorus* from different geographical locations remain unclear, and systematic quantitative analysis on how climatic and edaphic conditions across various habitats shape rhizosphere microbial community characteristics is still insufficient (Li et al., 2023a). Most previous studies only explored the correlations between a single category of factors (soil, microorganisms or climate) and bamboo shoot quality, without

integrated multi-factor correlation analysis, making it difficult to quantify the relative contribution of each factor (Guo et al., 2025; Wang et al., 2026). To date, no systematic pathway analysis has clarified whether climate and soil physicochemical properties regulate the accumulation of total amino acids and starch in bamboo shoots via rhizosphere microorganisms as mediators through multi-level cascading pathways (Fan et al., 2026), which greatly restricts the development of targeted microbial regulation technologies.

To bridge these knowledge gaps, we collected samples from 53 sites of *D. latiflorus* in southern China. We determined physicochemical indices (e.g., soil porosity and potassium content) and key bamboo shoot quality traits (e.g., total amino acids and starch) to examine site-specific variations in soil properties and shoot quality. Using 16S rRNA and ITS high-throughput sequencing, we characterized variations in alpha diversity and genus-level community composition of rhizosphere bacteria and fungi across sites. Pearson correlation analysis was used to clarify pairwise correlations among climatic factors, soil properties, keystone microbial taxa, and bamboo shoot quality. Structural equation modeling (SEM) was further performed to disentangle the direct and indirect pathways through which climatic and edaphic factors regulate amino acid and starch accumulation, with rhizosphere microorganisms considered as potential mediators. Key regulatory factors were identified, and critical environmental and microbial indicators beneficial for enhancing shoot quality were screened. Overall, this study aims to provide a theoretical foundation and data reference for site selection of high-quality *D. latiflorus* production areas, refined cultivation management, and high-quality shoot production.

2 Overview of the Study Area

The study area spans 53 sites across nine provinces and municipalities in southern China, geographically located between 97°56′34″ E and 120°16′12″ E, and between 18°58′ N and 30°08′ N. It encompasses Fujian, Hunan, Chongqing, Yunnan, Guangxi Zhuang Autonomous Region, Guangdong, Hainan, Guizhou, and Jiangxi, covering core, suitable, transitional, and marginal cultivation regions of *D. latiflorus*. Southern China is dominated by tropical and subtropical monsoon climates, characterized by hot, rainy summers and mild, dry winters. The tropical monsoon climate features high temperatures year-round, with distinct dry and rainy seasons. Annual precipitation ranges from approximately 800 to 2000 mm; windward mountain slopes receive abundant rainfall, whereas the eastern coastal regions are markedly affected by typhoons

in summer and autumn.

3 Materials and Methods

3.1 Site Establishment

Soil and root samples were collected in July-August 2024, and bamboo shoots were collected in early to mid-August 2024. A total of 53 representative sampling sites were selected across the natural distribution range of *D. latiflorus* using a grid sampling strategy, with a minimum distance of 50 km between adjacent sampling sites. The plant species (*D. latiflorus*) was identified based on morphological characteristics. No voucher specimens were deposited in a public herbarium. The geographical locations of the sampling sites are shown in Figure 1 and Table 1.. Within each site, three plots were randomly arranged, and three bamboo clumps were selected per plot from pure stands (either artificial or natural) of *D. latiflorus* with similar stand conditions. All selected culms were 2-3 years old. One shoot was collected from one representative culm in each plot, and the three shoots per site were measured individually and averaged. At each site, rhizosphere soil from the nine selected culms (three plots × three culms) was thoroughly mixed into one composite sample.

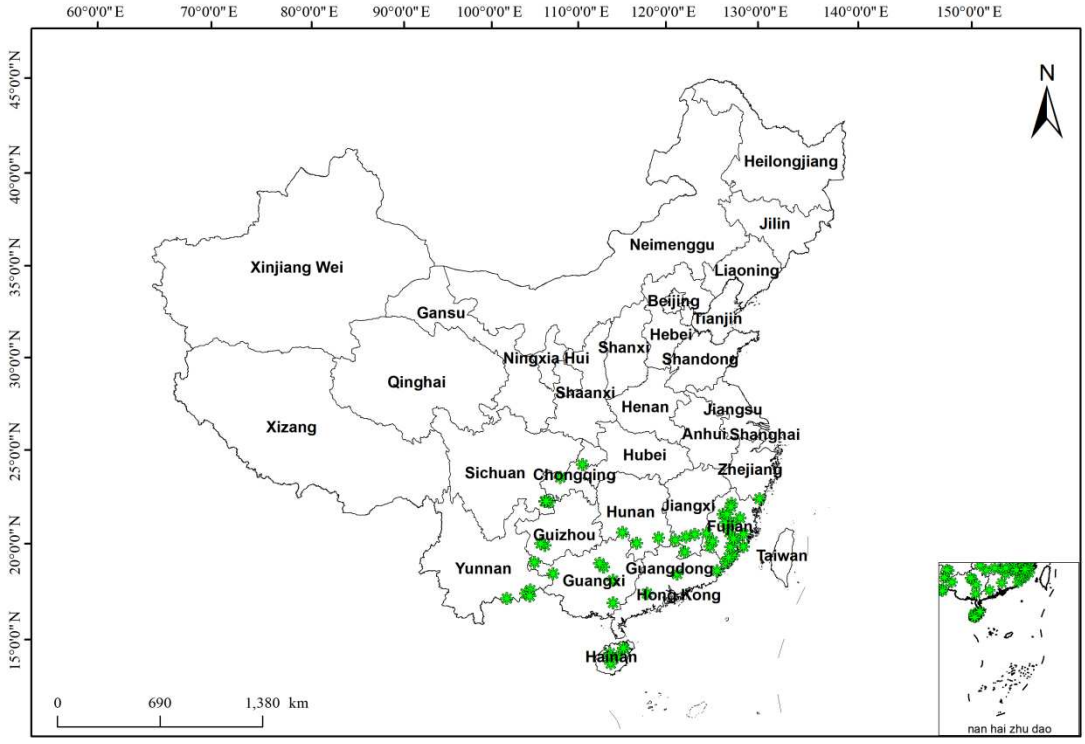


Fig. 1 Distribution map of 53 sampling sites of *Dendrocalamus latiflorus*

Note: The base map data is obtained from the National Geomatics Center of China (Map Review No. GS(2020)4619), and no modifications have been made to the base map.

Table 1 Geographical locations and numbers of the 53 sampling sites of *D. latiflorus*

Number	site	Number	site
A	Yubei	BB	Jianyang
AA	Shuangpai	BC	Shunchang
AB	Xinning	BD	Jianou
AC	Nanfeng	C	Datong
AD	Tunchang	D	Hushi
AE	Baisha	E	Tiantai
AF	Jiazizhen	F	Duanqiao
AG	Dingan	G	Shaying
AI	Wuzhishan	H	Maguan
AJ	Fuding	I	Xichou
AK	Gutian	J	Malipo
AL	Changting	K	Jinping
AM	Shanghang	M	Xinping
AN	Liancheng	N	Zouma
AO	Datian	O	Shierling
AP	Jiangle	P	Guiping
AQ	Youxi	Q	Tianlin
AR	Sanming	R	Bobai
AS	Pinghe	T	Jiangdong
AT	Yunxiao	U	Longmen
AU	Dongshan	V	Yunfu
AV	Zhangpu	W	Longnan
AW	Changtai	X	Chongyi
AX	Xianyou	Y	Yudu

AY	Jinjiang	Z	Chenzhou
AZ	Nanan		
B	Wanzhou		
BA	Anxi		

3.2 Data Collection

3.2.1 Climate Data Collection

We obtained 19 bioclimatic variables (BIO1-BIO19) from the WorldClim version 2.1 database (http://www.worldclim.org; accessed 9 September 2025) at a spatial resolution of 30 arc-seconds. Mean annual temperature (MAT) was represented by BIO1, and precipitation seasonality was represented by BIO15.

3.2.2 Sample Collection

Based on individual tree survey results, three representative *D. latiflorus* clumps were selected per standard plot. After removing surface litter, we collected undisturbed soil cores adjacent to bamboo roots at a depth of 0–15 cm using a soil corer to determine physical properties. Fine roots (diameter ≤ 2 mm) with adhering soil were gently excavated with a small hoe, and rhizosphere soil was defined as the approximately 1-mm-thick soil layer adhering to root surfaces. Samples from each clump were placed into sterile ziplock bags, kept in an ice box at low temperature, and immediately transported to the laboratory.

Non-rhizosphere soil was removed on an ultra-clean workbench. The root samples with adhering soil were transferred into 50-mL centrifuge tubes containing 20 mL of sterile 10 mM PBS buffer and then shaken at 120 rpm for 20 min at room temperature. After root fragments were removed, the suspension was centrifuged at 6,000 × g for 20 min to harvest rhizosphere soil. The obtained rhizosphere soil was divided into two subsamples: one was air-dried and sieved for chemical property analysis, and the other was stored at −80°C for microbial diversity analysis.

We conducted bamboo shoot sampling in early to mid-August 2024, between 8:00 and 10:00 AM. For each sampling site, three fresh shoots of *D. latiflorus* were collected at the commercial maturity stage, defined as shoots with tight sheaths, no leaf expansion, and no lignification. All shoots were free of mechanical damage and pests. Because shoot length varied considerably among sites and individuals (9.5-82.2 cm), no fixed aboveground height was used as a harvest

criterion. After pretreatment, external quality indicators were measured. Edible portions were retained and stored at −80 °C for subsequent analysis of nutritional components and flavor compounds, and the storage time before analysis did not exceed 30 days. DNA was extracted from the composite soil sample, yielding one sequencing sample per site (n = 53).

3.3 Sample Analyses

3.3.1 Determination of Soil Physicochemical Properties and Microbial Diversity

Soil physical properties-including bulk density, water content, capillary porosity, and non-capillary porosity-were determined by the core method (Chinese forestry standard LY/T 1215-1999). Soil organic matter was quantified using the potassium dichromate external heating method (LY/T 1237-1999), while total nitrogen was determined by the semi-micro Kjeldahl method (LY/T 1228-1999). Total phosphorus was measured via the molybdenum-antimony colorimetric method (LY/T 1232-1999), and total potassium by ammonium acetate extraction combined with flame photometry (LY/T 1234-1999). Alkali-hydrolyzable nitrogen was analyzed using the alkaline diffusion method (LY/T 1229-1999). Available phosphorus and potassium were extracted with hydrochloric acid-sulfuric acid solution (LY/T 1233-1999) and ammonium acetate solution (LY/T 1236-1999), respectively. Soil pH was recorded by the potentiometric method (LY/T 1239-1999).

Total soil microbial DNA was extracted using the PowerSoil DNA Isolation Kit. DNA concentration and purity were checked with a NanoDrop 2000 spectrophotometer. The bacterial 16S rRNA gene was amplified with primers 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3'), while fungal ITS sequences were amplified using primers ITS1F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and ITS2R (5'-GCTGCGTTCTTCATCGATGC-3'). After PCR amplicon purification, high-throughput sequencing was performed on the Illumina MiSeq platform (Caporaso et al., 2010).

3.3.2 Determination of Bamboo Shoot Traits

Fresh weight and husked weight of bamboo shoots were recorded using an electronic balance (accuracy: 0.5 g), and basal diameter was measured with a vernier caliper. Edible rate was calculated as the percentage of husked shoot flesh weight relative to total fresh weight. Moisture content was determined based on the percentage of weight loss (fresh weight minus dry weight) relative to fresh weight.

Vitamin C was quantified by the 2,6-dichloroindophenol redox titration method (National Health Commission, 2016a). Total phenolics were measured using the polyphenol extraction protocol of Li et al. (2008) with minor modifications. Soluble protein was quantified via the Coomassie Brilliant Blue G-250 colorimetric method (National Health Commission, 2016b). Crude fat was determined using a crude fat analyzer (Ren et al., 2003). Soluble sugars, starch, and cellulose were assayed by the anthrone colorimetric method (Zhang et al., 2020). Total amino acids were quantified by pre-column derivatization with phenyl isothiocyanate coupled with reversed-phase HPLC (Yang et al., 2002). Total flavonoids were determined by the sodium nitrite-aluminum nitrate colorimetric spectrophotometric method (Yan et al., 2020). Tannins were analyzed using the Folin-Denis spectrophotometric method (Geng et al., 2013). Free amino acids were determined following the same protocol as used for total amino acids. All nutrient contents (soluble protein, starch, total amino acids, etc.) were expressed on a dry weight basis (mg/g DW). Dry weight was determined after freeze-drying or oven-drying at 75 °C to constant weight.

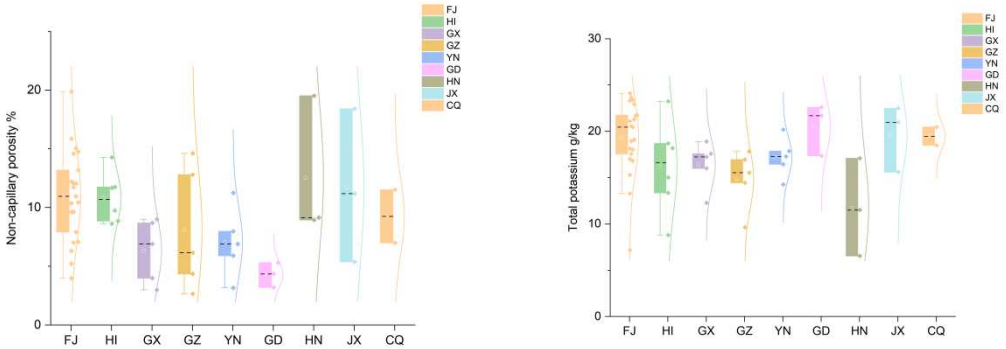
3.4 Data Processing and Statistical Analysis

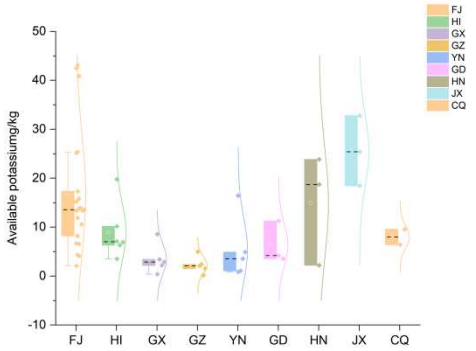
One-way ANOVA followed by Tukey's HSD test was used to compare soil physicochemical properties and shoot nutritional and flavor compounds among geographical locations after normality (Shapiro–Wilk) and homoscedasticity (Levene) tests. For rhizosphere microbial data, alpha diversity (Shannon and Chao1) was compared using Kruskal–Wallis tests with Dunn's post hoc tests, and P values were FDR-corrected. Beta diversity was assessed by PCoA based on Bray–Curtis distances. PERMANOVA (999 permutations) and betadisper were performed using the vegan package in R 4.3.3 to test community composition and dispersion homogeneity. LEfSe identified discriminatory taxa (LDA > 4.0). Pearson correlation analysis explored relationships among environmental factors, core microbial taxa, and shoot quality indicators; microbial relative abundances were CLR-transformed when normality was violated, and all correlation P values were FDR-corrected. SEM was constructed using the lavaan package. Based on Pearson correlation and a priori ecological hypotheses, variables with significant effects and VIF < 5 were retained. Model fit was evaluated using χ^2, df, P, CFI, TLI, RMSEA, and SRMR, and modification indices were used to refine the model when theoretically justified. The reported χ^2 and P values were recalculated to ensure consistency. All analyses were conducted in SPSS 26.0, R 4.3.3, and QIIME2.

4 Results and Analysis

4.1 Differences in Soil Potassium Characteristics, Porosity Traits and Nutritional Components of Bamboo Shoots among Different Geographical Locations

Among the three soil indices in Figure 2, only available potassium showed significant pairwise differences among sites. Non-capillary porosity and total potassium showed numerical variation but no significant pairwise differences ($P > 0.05$). For non-capillary porosity, samples from Hunan (HN) and Jiangxi (JX) contained numerous high values, whereas those from Guangdong (GD) were consistently low. However, all pairwise comparisons were non-significant ($P > 0.05$). Samples from the other sites fell mostly within the medium range, displaying varying degrees of dispersion. Total potassium concentrations remained relatively high in most sites, with Hunan being the notable exception (consistently lower values). No pairwise comparison was statistically significant ($P > 0.05$). Available potassium showed marked spatial differentiation: Jiangxi yielded the highest number of samples with elevated concentrations, followed by Fujian, whereas most samples from Guizhou and Guangxi exhibited low available potassium levels. Available potassium in Jiangxi was significantly higher than that in Guizhou, Guangxi and Yunnan; available potassium in Fujian was significantly higher than that in Guizhou and Guangxi. However, Jiangxi and Fujian did not differ significantly, and Guizhou and Guangxi did not differ significantly.





246 Fig. 2 Distribution characteristics of soil porosity and potassium content for different geographical locations. Each
247 point represents one sampling site (n = 53)
248

249 As illustrated in Figure 3, significant differences ($P < 0.05$) in soluble protein, starch, and
250 total amino acid contents were detected among bamboo shoot samples of *D. latiflorus* from nine
251 geographical locations (based on the 53 samples). In terms of soluble protein, most samples from
252 Guizhou (GZ) showed relatively high values, significantly exceeding those from other sites.
253 Samples from Yunnan (YN), Guangdong (GD), and Jiangxi (JX) clustered predominantly in the
254 medium range, whereas those from Hainan (HI) were generally low. Samples from Fujian (FJ),
255 Guangxi (GX), Hunan (HN), and Chongqing (CQ) were scattered across the remaining ranges,
256 with varying degrees of dispersion among groups.
257 The spatial pattern of starch content largely mirrored that of soluble protein. Starch was
258 highest in GZ and YN, which did not differ significantly. GZ was significantly higher than FJ, GD,
259 GX, HI and JX, while YN was significantly higher than FJ, GD, GX and HI. FJ and HI were
260 relatively low, but did not differ significantly from each other; both were significantly lower than
261 CQ, GZ, HN and YN in several pairwise comparisons. For total amino acids, many samples from
262 Fujian displayed markedly higher contents than those from the other eight sites, with some
263 exceeding 70 mg/g. Most samples from Hainan (HI), Guangxi (GX), Guizhou (GZ), Yunnan (YN),
264 Guangdong (GD), Hunan (HN), Jiangxi (JX), and Chongqing (CQ) fell within the 20 – 30 mg/g
265 range, with overall levels comparable among these sites and substantially lower than those of
266 Fujian. These results underscore pronounced spatial differentiation in nutrient accumulation
267 patterns of *D. latiflorus* shoots across geographical locations..

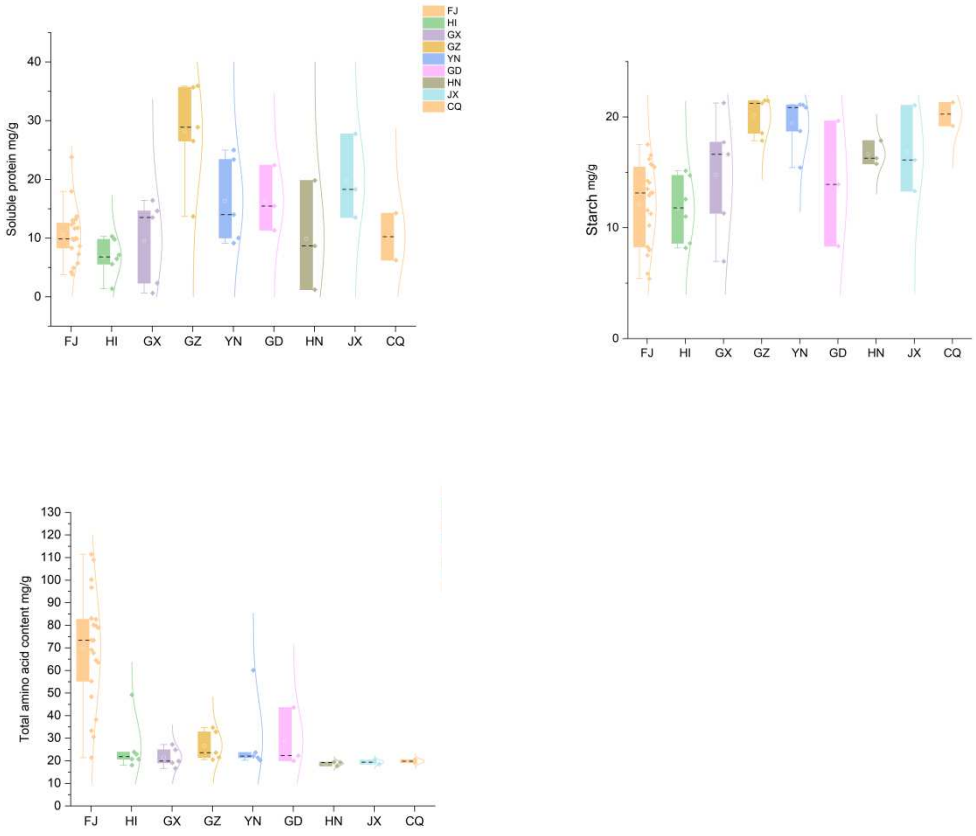


Fig. 3 Distribution characteristics of main nutrient contents of *D. latiflorus* shoots from different geographical locations. Each point represents one sampling site (n = 53)

4.2 Assembly Patterns of Rhizosphere Soil Microbial Communities

Using 16S rRNA gene high-throughput sequencing data, we assessed bacterial alpha diversity via the Shannon and Chao1 indices for 53 rhizosphere soil samples of *D. latiflorus* from nine geographical locations (Figure 4). Most samples from Chongqing (CQ), Jiangxi (JX), and Hunan (HN) displayed higher bacterial diversity, whereas those from Guangxi (GX) and Guangdong (GD) were generally lower. The Shannon index for Fujian (FJ) samples varied widely, indicating substantial within-group variation. However, Kruskal-Wallis tests followed by Dunn's post hoc tests showed no significant differences among the nine sites for either Shannon or Chao1 ($P > 0.05$).

The Chao1 index, which reflects community species richness, showed a distribution pattern largely parallel to that of the Shannon index. Samples from CQ, JX, and HN harbored high bacterial species richness, whereas those from GX and GD exhibited generally low richness. The Chao1 index for the FJ site also covered a broad range, with marked within-group variation.

Together, these results indicate numerical variation in bacterial alpha diversity and species richness among sites, but Kruskal-Wallis tests followed by Dunn's post hoc tests were not statistically significant ($P > 0.05$).

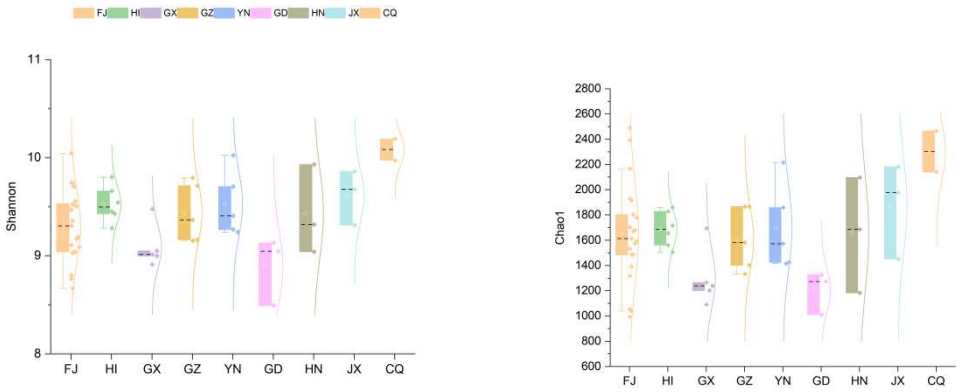
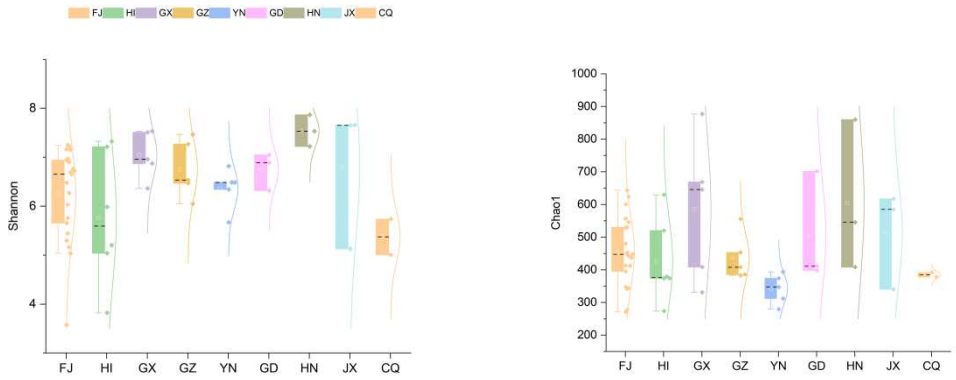


Fig. 4 Alpha diversity of soil bacterial communities from different geographical locations. Each point represents one sampling site (n = 53)

Using ITS high-throughput sequencing data, we assessed fungal alpha diversity via the Shannon and Chao1 indices for 53 rhizosphere soil samples of *D. latiflorus* from nine geographical locations (Figure 5). Most samples from Jiangxi (JX) and Hunan (HN) displayed higher Shannon values, whereas those from Chongqing (CQ) were generally lower. The Shannon index for Fujian (FJ) and Hainan (HI) samples varied widely, indicating substantial within-group variation. However, Kruskal-Wallis tests followed by Dunn's post hoc tests indicated no significant differences among sites for fungal Shannon or Chao1 ($P > 0.05$).

Samples from Hunan (HN) and Guangxi (GX) harbored relatively high Chao1 values, whereas fungal species richness was lower in samples from Yunnan (YN) and Chongqing (CQ). The median Chao1 values for most samples across all sites fell within the 350-700 range, with marked inter-group variation in data dispersion. These results indicate numerical spatial variation in fungal alpha diversity and species richness, but no significant pairwise differences were detected among sites ($P > 0.05$).



303 Fig. 5 Alpha diversity of soil fungal communities from different geographical locations. Each point represents one
304 sampling site (n = 53)

305 Based on 16S high-throughput sequencing data, PCoA was used to analyze the beta diversity of bacterial
306 communities in 53 rhizosphere soil samples of Dendrocalamus latiflorus under 9 geographic site groups (Figure
307 6A). The explained variance of PCo1 and PCo2 was 35.03% and 7.35%, respectively. The Fujian (FJ) group had
308 the largest number of samples and the widest distribution, showing strong intra-group dispersion; the Guangdong
309 (GD), Hunan (HN), Guizhou (GZ), and Hainan (HI) groups had relatively wide ellipse coverage, with obvious
310 sample interleaving; some samples from the Jiangxi (JX), Yunnan (YN), and Guangxi (GX) groups were located
311 near the ordination center, while the Chongqing (CQ) group had fewer samples. PERMANOVA showed significant
312 differences among groups ($F = 1.460$, $R^2 = 0.210$, $P = 0.0203$), and betadisper showed significant heterogeneity in
313 intra-group dispersion ($F = 6.449$, $P = 0.0001$). The results indicated that there was spatial differentiation in
314 bacterial community structure among *D. latiflorus* rhizosphere soil samples corresponding to different geographic
315 site groups.

316 Based on ITS high-throughput sequencing data, PCoA was used to analyze the beta diversity of fungal
317 communities in 53 rhizosphere soil samples of *D.latiflorus* under 9 geographic site groups (Figure 6B). The
318 explained variance of PCo1 and PCo2 was 13.56% and 9.29%, respectively. The Fujian (FJ) group had the largest
319 number of samples and a relatively wide distribution, showing strong intra-group dispersion; the Guangdong (GD),
320 Hunan (HN), Guizhou (GZ), and Hainan (HI) groups had relatively wide ellipse coverage, with obvious sample
321 overlap and interleaving; some samples from the Guangxi (GX), Yunnan (YN), and Jiangxi (JX) groups were
322 relatively concentrated, while the Chongqing (CQ) group had fewer samples. PERMANOVA showed significant
323 differences among groups ($F = 1.222$, $R^2 = 0.182$, $P = 0.0181$), while betadisper showed no significant difference
324 in intra-group dispersion ($F = 1.046$, $P = 0.4137$). The results indicated that there was spatial differentiation in

fungal community structure among *D. latiflorus* rhizosphere soil samples corresponding to different geographic site groups.

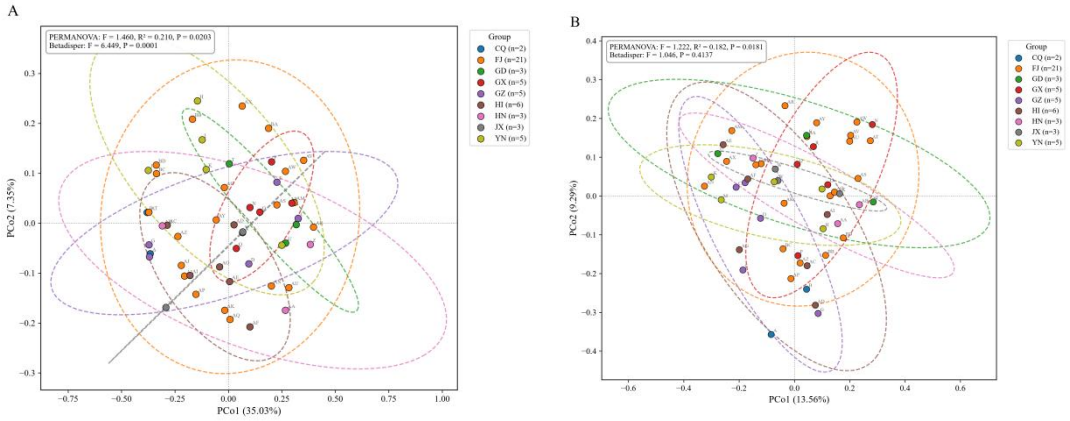


Fig. 6 PCoA of bacterial and fungal community structures in rhizosphere soil of *D.latiflorus* from different geographic sites

Note: A: Bacterial communities (16S, Bray-Curtis distance); B: Fungal communities (ITS, Bray-Curtis distance).

To investigate the rhizosphere microbial community structure of *D. latiflorus* across different geographical locations, we statistically analyzed the relative abundances of fungal and bacterial genera. In the figures, only the top 10 most abundant genera are presented, with all remaining low-abundance genera pooled into “Others”.

The genus-level composition of soil bacterial communities differed markedly across geographical locations (Figure 7). Bradyrhizobium was the most abundant genus across all samples and constituted the core dominant taxon, albeit with marked inter-site fluctuations in its relative abundance. The remaining community was composed of other dominant genera, including *Acidiferromicrobium*, *Sphingomonas*, *Bryobacter*, MND1, *Acidothermus*, *Acidibacter*, *Candidatus Solibacter*, unclassified_Bacteria, and Incertae_Sedis, the proportions of which also varied considerably among sites.

In terms of dominant bacterial genera, *Bradyrhizobium* dominated the rhizosphere bacterial community of *D. latiflorus*, with relative abundances exceeding 40% in most samples and approaching 60% at some sites. Acidobacterial taxa-including *Candidatus* Solibacter and *Acidibacter*-were consistently present across all sites and constituted important persistent dominant groups. In addition, marked spatial divergence was observed in the proportions of low-

abundance genera, unclassified bacteria, and other rare groups. At several sites, the relative abundances of unclassified bacteria and *Acidothermus* were significantly higher than at others. These findings collectively indicate that geographical location alters the relative proportions of bacterial genera in the rhizosphere, consequently shaping the overall community structure.

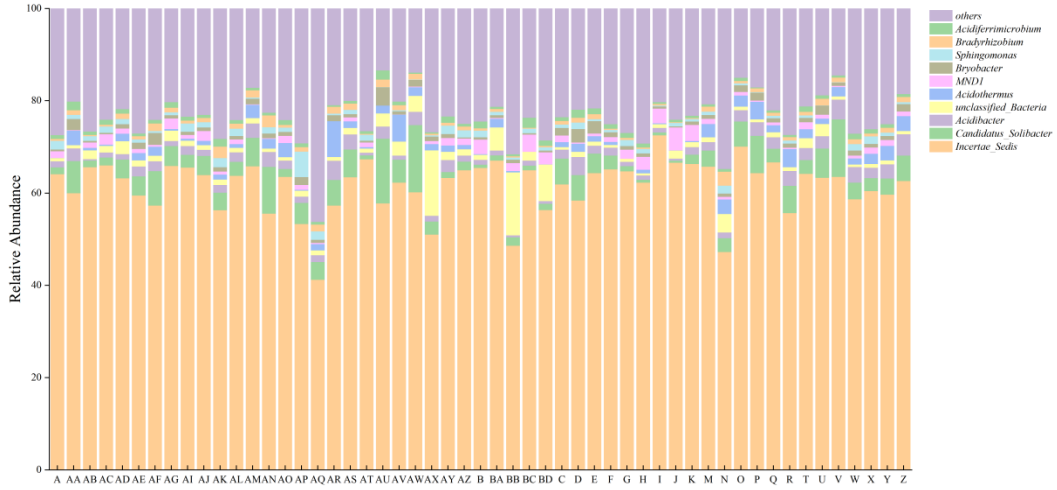


Fig. 7 Abundance of soil bacterial communities from different geographical locations. Each bar represents one sampling site (n = 53)

Aside from the "Others" group, most of the top dominant fungal taxa were assigned to Incertae sedis and unclassified fungal lineages, with their distribution showing pronounced spatial heterogeneity across geographical locations(Figure 8). Unclassified Fungi and Fungi gen. Incertae sedis dominated the core community in the majority of samples, and their combined relative abundance substantially exceeded that of all other fungal genera. Other taxa-including *Mortierella*, *Archaeorhizomyces*, *Fusarium*, *Streilitiana*, *Hygrocybe*, as well as unidentified members of Agaricomycetes and Pleosporales-displayed differential enrichment patterns among samples from different producing regions.

Fungal community structure differed significantly among sampling groups, with Unclassified Fungi and Incertae sedis dominating the community at most sites. Certain taxa were specifically enriched in particular sites: for example, unidentified Agaricomycetes and *Archaeorhizomyces* showed marked increases in some samples, whereas *Fusarium*, *Streilitiana*, and *Hygrocybe* reached substantial proportions only at a limited number of sites. Overall, geographical origin substantially reshaped the relative abundance distribution of rhizosphere fungal taxa, ultimately

driving pronounced divergence in community composition among sites.

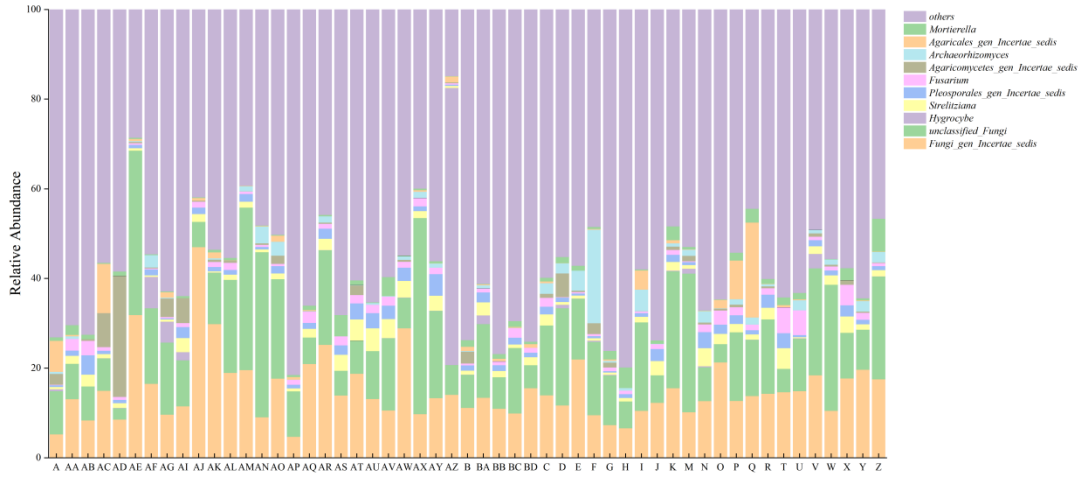


Fig. 8 Abundance of soil fungal communities from different geographical locations. Each bar represents one sampling site (n = 53)

To further resolve the differential composition of soil bacterial communities among geographical locations, we performed LEfSe analysis to identify statistically significant biomarker taxa for each group. The cladogram (Figure 9) illustrates the phylogenetic relationships of these differential taxa from phylum to genus level, while the LDA score histogram (Figure 10, threshold set at LDA > 4.0) presents the enriched taxa and their effect sizes specific to each site.

Most sites displayed unique enriched bacterial taxa, with the exception of Guizhou (GZ). Chongqing (CQ) harboured the largest number of significantly enriched taxa, including Sphingomonas, unidentified genera within Vicinamibacteraceae, *Haliangium*, RB41, and Subgroup_7. Fujian (FJ) was characterized by specific enrichment of a complete lineage from Lactobacillales and Lactobacillaceae down to Lactobacillus. Jiangxi (JX) was enriched in clades from Firmicutes to Bacillus, as well as taxa belonging to Burkholderiaceae and genus Ellin6067. Hainan (HI) showed significant enrichment of clades affiliated with Myxococcota. Hunan (HN) exhibited a complete enriched clade from the candidate phylum WPS-2 down to genus level, along with a subgroup of Acidobacteriaceae (f__Acidobacteriaceae_Subgroup_1). Yunnan (YN) was dominated by enriched Nitrosomonadaceae and genus MND1. By contrast, Guangdong (GD) and Guangxi (GX) contained fewer biomarker taxa: GD was specifically enriched in Verrucomicrobiota, whereas GX harboured enriched clades of the family and genus JG30_KF_AS9.

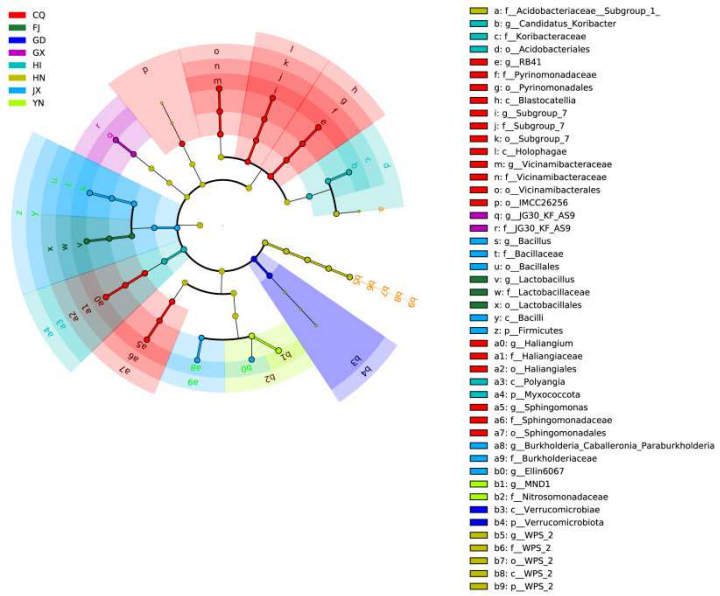


Fig. 9 Circular cladogram of LEfSe analysis for soil bacteria from different geographical locations

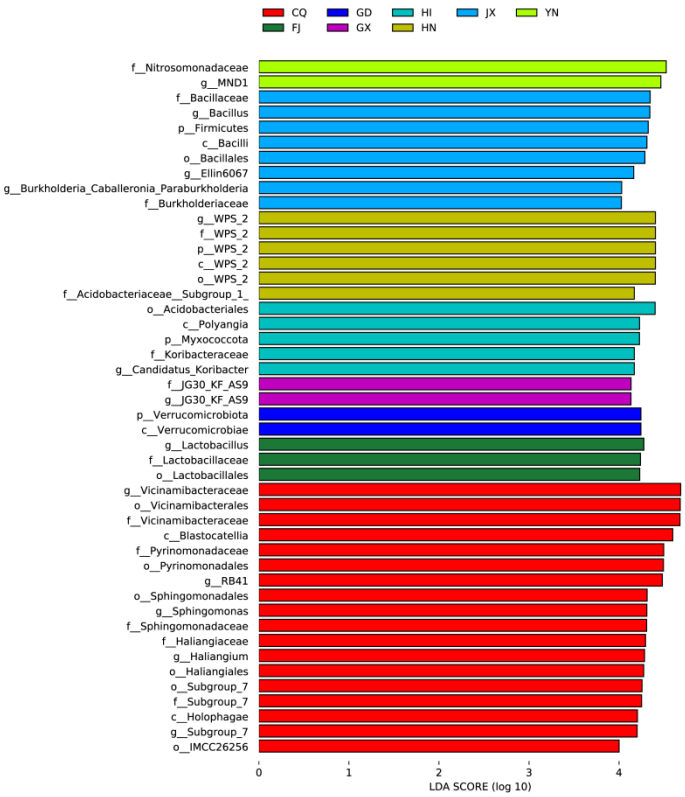


Fig. 10 LDA bar chart of LEfSe analysis for soil bacteria from different geographical locations

To further identify characteristic fungal taxa across geographical locations, we used LEfSe analysis to screen biomarkers for each group. The fungal cladogram (Figure 11) and LDA score

histogram (Figure 12, threshold set at LDA > 4.0) revealed that the distribution patterns of fungal biomarkers across geographical locations contrasted sharply with those of bacterial communities.

At the defined significance threshold, no specific fungal indicator taxa were significantly enriched in the Fujian (FJ) site. Significant biomarkers were identified in the other eight sites. Chongqing (CQ) was dominated by Polyporales, along with clades affiliated with *Rhizochaete* and *Ramariopsis*. Guizhou (GZ) exhibited enrichment of a complete lineage from Archaeorhizomycetes down to genus level (g__Archaeorhizomycetes_gen_Incertae_sedis), together with Omphalotaceae. Guangdong (GD) was particularly enriched in *Fusarium*, Nectriaceae, and Trechisporales. Guangxi (GX) showed significant enrichment of Dothideomycetes, Pleosporales, and Venturiales. Biomarkers enriched in Hunan (HN) included Eurotiales, Aspergillaceae, Tremellomycetes, Entolomataceae, *Clitopilus*, and Chaetomiaceae. Hainan (HI) was characterized by specific enrichment of an unassigned order within Agaricomycetes (Agaricomycetes_ord_Incertae_sedis). By contrast, only a limited number of biomarkers were detected in Jiangxi (JX) and Yunnan (YN), which were enriched in Cantharellales and Clavaria, respectively.

Geographical space was associated with numerical variation in rhizosphere bacterial and fungal alpha diversity, but pairwise comparisons were not significant ($P > 0.05$). In contrast, community composition differed markedly among sites, as revealed by LEfSe: Fujian showed exclusive strong enrichment of Lactobacillus, whereas for fungal communities, specific biomarkers-including Polyporales and Fusarium-were identified in the other eight sites, with no significantly enriched taxa detected in Fujian.

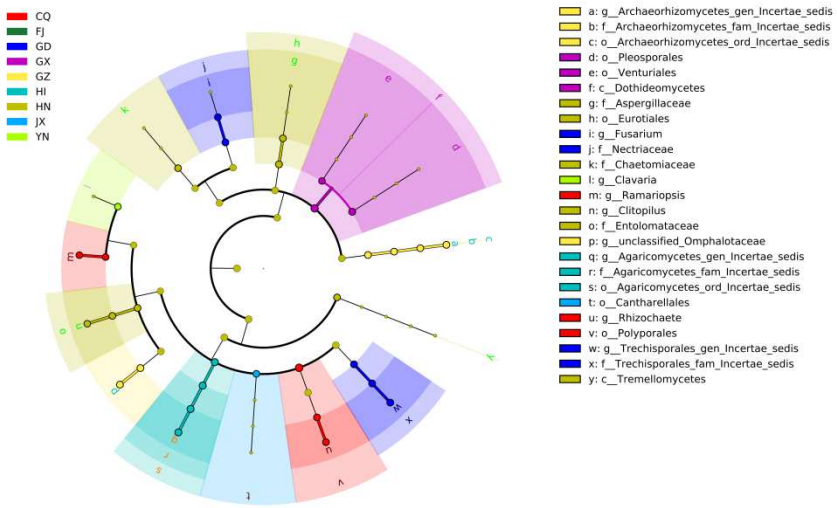


Fig. 11 Circular cladogram of LEfSe analysis for soil fungi from different geographical locations

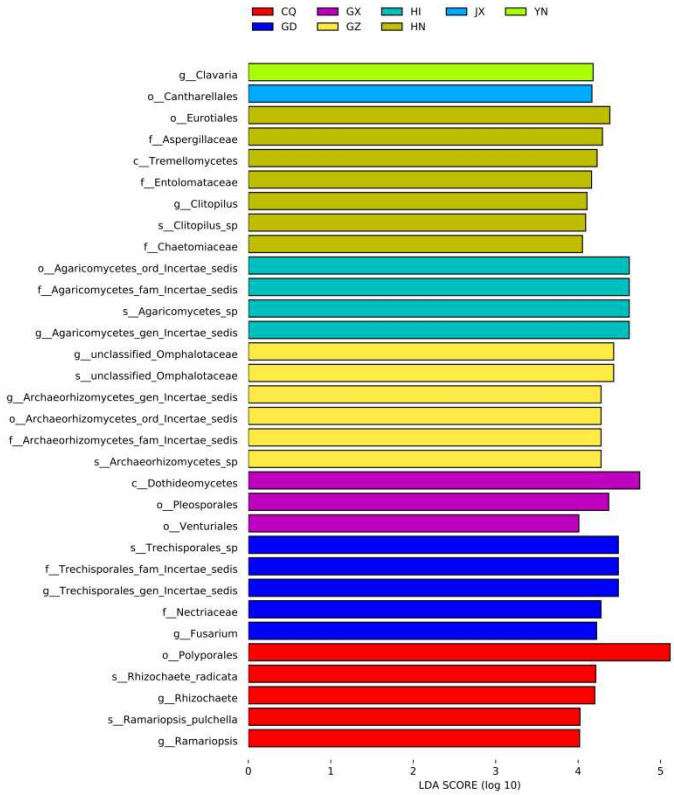


Fig. 12 Circular cladogram of LEfSe analysis for soil fungi from different geographical locations

4.3 Correlations and Regulatory Pathways among Environmental Factors, Rhizosphere Microorganisms and Shoot Quality of *Dendrocalamus latiflorus*

As shown in Figure 13, total amino acid and starch contents of bamboo shoots were strongly correlated, albeit with varying strength. Multiple soil physicochemical indices-including

non-capillary porosity, available potassium, alkali-hydrolyzable nitrogen, soil pH, and total potassium-were significantly interlinked. Soil pH was highly positively correlated with several soil nutrient indicators ($P < 0.001$). Available potassium displayed significant correlations with total amino acid and starch concentrations ($P < 0.05$), as well as with other soil properties (positive or negative, $P < 0.05$). Mean annual temperature (MAT) and mean annual precipitation (MAP) were significantly associated (positively or negatively) with numerous soil physicochemical properties and core microbial taxa ($P < 0.05$). Notably, MAT showed a highly significant positive correlation with starch content ($P < 0.001$), and MAP was strongly positively correlated with soil pH and *Candidatus* Solibacter ($P < 0.001$).

Candidatus Solibacter, *Sphingomonas*, *Bradyrhizobium*, MND1, and Incertae Sedis bacterial taxa were significantly correlated with soil physicochemical properties and climatic factors. *Bradyrhizobium* showed a strong positive correlation with soil pH and MND1 ($P < 0.001$) and a strong negative correlation with mean annual temperature ($P < 0.001$). Both *Sphingomonas* and *Candidatus* Solibacter exhibited highly significant positive correlations with soil pH ($P < 0.001$). MND1 and Incertae Sedis bacteria were also strongly correlated with *Bradyrhizobium* and soil pH ($P < 0.001$). By contrast, *Archaeorhizomyces*, *Fusarium*, *Mortierella*, unidentified Agaricomycetes, and *Hygrocybe* displayed generally weak associations with edaphic and climatic variables, with only a few taxa-such as *Mortierella* and unidentified Agaricomycetes—showing significant correlations ($P < 0.05$).

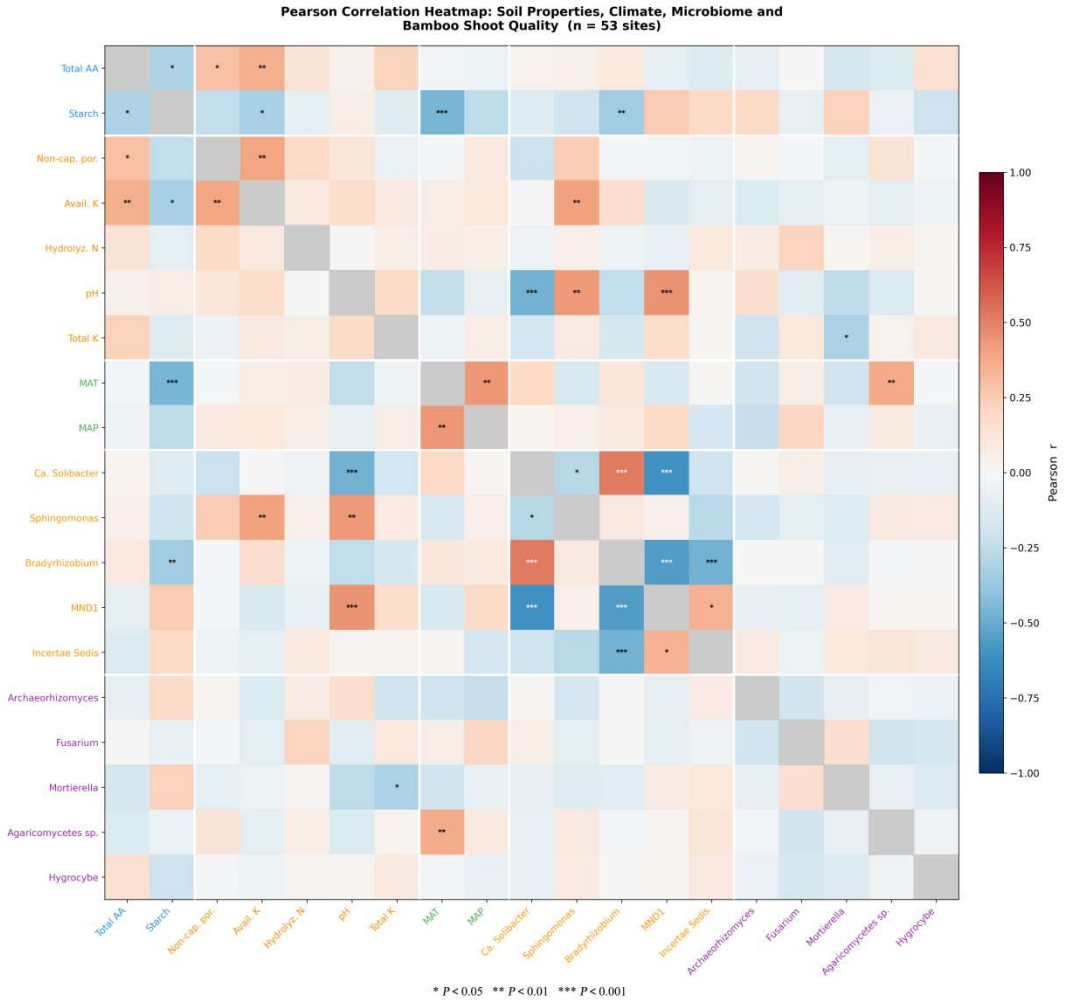


Fig. 13 Pearson correlation heatmap of soil properties, climate, core microbial taxa and bamboo shoot quality indices for different geographical locations

Based on Pearson correlation results, we identified environmental and microbial variables with significant effects on bamboo shoot quality. After removing variables with severe multicollinearity, we constructed a structural equation model (SEM; Figure 14). The overall model fit was acceptable ($\chi^2 = 28.05$, df = 18, $P = 0.061$; CFI = 0.828; RMSEA = 0.104), indicating that the model adequately captures the relationships among pathways. Precipitation seasonality showed a significant negative effect on soil non-capillary porosity ($\beta = -0.292$, $P < 0.05$) and a highly significant negative effect on available potassium ($\beta = -0.436$, $P < 0.001$). Soil available potassium positively governed total amino acid content ($\beta = 0.301$, $P < 0.05$) while exerting a direct negative effect on starch content ($\beta = -0.235$, $P < 0.05$). Unclassified bacteria showed a strong positive effect on total amino acid content ($\beta = 0.330$, $P < 0.01$). Bradyrhizobium exerted a direct negative influence on starch content ($\beta = -0.247$, $P < 0.05$). Mean annual temperature

directly and negatively affected starch content (β = −0.368, $P < 0.001$). Precipitation seasonality indirectly affected total amino acid content through available potassium, with an indirect effect of −0.131. Unclassified bacteria directly promoted total amino acid accumulation, while Bradyrhizobium and available potassium directly suppressed starch content. Non-capillary porosity had a non-significant positive effect on total amino acid content (β = 0.163, $P = 0.188$). The direct paths from soil properties to microbial taxa were not significant and are therefore not shown in Figure 14. Collectively, these results reveal that precipitation seasonality shapes soil available potassium and porosity, which in turn influence rhizobacterial taxa and ultimately regulate amino acid and starch accumulation in bamboo shoots, though the microbial mediation pathway was only partially supported.

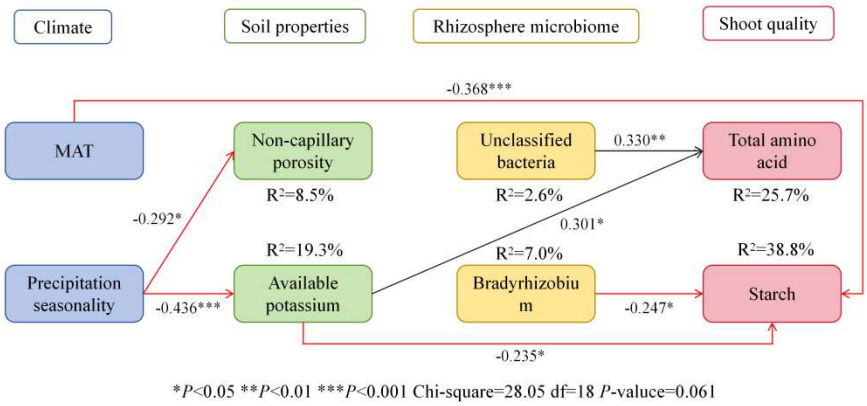


Fig. 14 Structural equation model illustrating the effects of climate, soil properties and rhizosphere microbiome on bamboo shoot quality\

5 Discussion

Numerous studies have established that plant phenotypic traits and nutrient contents are shaped by long-term interactions between genotypes and habitats (Gao et al., 2026). The accumulation of carbon and nitrogen metabolites not only governs growth rates but also modulates resource allocation between primary and secondary metabolism through sophisticated signaling networks, ultimately driving marked divergence in plant phenotypes and chemical profiles across heterogeneous environments. In this study, systematic analyses of morphological traits and nutritional quality of *D. latiflorus* shoots from nine provinces and municipalities revealed highly significant inter-regional differences. Guizhou had higher soluble protein and starch, while

Yunnan had higher starch. However, Guizhou soluble protein did not significantly differ from Guangdong. In contrast, shoots from Fujian displayed total amino acid levels more than 2.5-fold higher than those of other sites-a clear case of metabolic differentiation. This pattern aligns closely with the classic growth-differentiation balance hypothesis (GDBH) in ecology (Glynn et al., 2007).

The GDBH states that under conditions of sufficient water, thermal energy, and soil nutrients, plants preferentially allocate photosynthetic carbon and nitrogen to primary metabolism, promoting the synthesis of starch and structural proteins for rapid biomass accumulation (Hale et al., 2005). This may account for the vigorous growth and elevated starch contents observed in bamboo shoots from the southwestern production regions (Yunnan and Guizhou), as well as the high soluble protein content in Guizhou. By contrast, the Fujian production area lies within a subtropical monsoon climate zone characterized by high temperature, humidity, and abundant precipitation. Fujian shoots exhibited the highest total amino acid content and relatively high available potassium. Given the significant positive correlation between available potassium and total amino acids and the significant SEM path, potassium availability may partly contribute to the high amino acid accumulation in Fujian. However, other factors such as rhizosphere microbial composition may also play a role (Hale et al., 2005). Under such resource-limited conditions, plants reduce resource allocation to growth and shift metabolic priorities from growth toward defense and environmental adaptation (Su et al., 2010). Consequently, carbon and nitrogen allocation may shift toward amino acid metabolism rather than starch synthesis. This metabolic reprogramming could contribute to the high total amino acid content in Fujian shoots, although the underlying mechanisms require further investigation (Su et al., 2005; Caretto et al., 2015), .

Quality differentiation among producing regions is closely linked to regional variation in soil physicochemical properties. Both soil available potassium and non-capillary porosity showed significant positive correlations with total amino acid content ($r = 0.359$, $P = 0.008$; $r = 0.296$, $P = 0.031$, respectively).. From a plant nutrition perspective, potassium acts as a cofactor for numerous enzymes and plays a key role in amino acid metabolism (Yang et al., 2023). Adequate potassium supply substantially enhances solute transport efficiency within phloem sieve tubes, facilitating the accumulation of quality?related compounds such as sugars and amino acids (Chen et al., 2017). Soil non?capillary porosity modulates root metabolic activity by altering rhizosphere aeration.

Improved aeration accelerates potassium mobility in soil and promotes root aerobic respiration, ensuring sufficient ATP supply and consequently driving mineral nutrient uptake and amino acid biosynthesis (Wang et al., 2023; Savijoki et al., 2006; Yan et al., 2024). As a shallow?rooted bamboo species, *D. latiflorus* is particularly sensitive to rhizosphere oxygen conditions and potassium availability governed by high non-capillary porosity. Rhizosphere alkali-hydrolyzable nitrogen showed no significant correlation with total amino acid content ($r = 0.140$, $P = 0.317$), suggesting that amino acid accumulation is not simply determined by nitrogen availability. This finding suggests that amino acid accumulation is not simply determined by nitrogen availability, but is instead synergistically regulated by the balance between carbon and nitrogen metabolism, mineral element availability, and the rhizosphere microecosystem (Nunes-Nesi et al., 2010).

Using rhizosphere soil microbial sequencing data of *D. latiflorus* across all provinces, this study revealed the potential regulatory effects of divergent microbial communities on bamboo shoot quality. PCoA based on Bray-Curtis distance revealed clear site-level separation of both bacterial and fungal communities. PERMANOVA confirmed significant differences among nine site for bacteria and fungi . Betadisper further indicated significant heterogeneity in bacterial intra-group dispersion but not in fungi. This suggests that site effects were more strongly reflected in community composition than in alpha diversity. LEfSe identified Lactobacillus as specifically enriched in the Fujian site. Although its relative abundance was not included in the correlation analysis with individual amino acids, this specific enrichment suggests a potential role in amino acid accumulation. Lactobacillus is known for strong proteolytic activity, degrading macromolecular organic nitrogen and releasing free amino acids (Savijoki et al., 2006; Murindangabo et al., 2023; Satilmış et al., 2023), and its organic acid production can reduce rhizosphere pH and modulate nitrogen transformation (Khan et al., 2023; Li et al., 2023b). However, direct evidence in bamboo rhizosphere is lacking; thus, the enrichment of Lactobacillus in Fujian may be associated with high amino acid accumulation, but a causal role remains speculative and requires further validation. Rhizosphere microorganisms are not passive responders but active participants in shaping bamboo shoot quality.

Pearson correlation analysis showed that mean annual temperature and precipitation seasonality governed soil non-capillary porosity and available potassium, corroborating earlier reports that potassium is susceptible to leaching under long-term hydrothermal conditions in

southern red-soil regions (Cong et al., 2020; Luo et al., 2004). Soil pH was strongly correlated with the abundances of Bradyrhizobium and Candidatus Solibacter, while available potassium was directly linked to total amino acid and starch contents in the SEM. Moreover, soil variables and the abundances of core microbial taxa showed significant correlations with total amino acid and starch contents in bamboo shoots, albeit with varying strengths.

Structural equation modeling revealed that precipitation seasonality indirectly affected shoot quality by regulating non-capillary porosity and available potassium, while mean annual temperature directly and negatively affected starch content. However, the direct paths from soil properties to individual microbial taxa were not significant in the SEM. This does not indicate that soil properties do not shape the rhizosphere microbiome; rather, PCoA and PERMANOVA revealed significant community-level differentiation among site, suggesting that soil and climate may influence rhizosphere communities through coordinated shifts in overall composition rather than single-taxon abundance. This contrasts with previous studies reporting close soil-microbe links (Waldrop et al., 2017; Gao et al., 2023), but is consistent with indirect or context-dependent microbial responses (Wendel et al., 2025; Zheng et al., 2025). Soil available potassium was directly linked to total amino acid and starch contents in the SEM, whereas the direct paths from soil properties to individual microbial taxa were not significant. At the microbe-quality interface, unclassified bacteria promoted total amino acid content, while Bradyrhizobium suppressed starch content (Forrest et al., 1991), revealing contrasting regulatory roles. These results clarify that significant pairwise correlations do not necessarily translate into significant direct paths in a multivariate causal framework, underscoring the complexity of climatic regulation of bamboo shoot quality (Yu et al., 2026).

6 Conclusions

This study systematically examined the synergistic regulatory mechanisms by which climate, soil physicochemical properties, and rhizosphere microbial communities govern the nutritional quality of *D. latiflorus* shoots. Nutritional quality differed significantly among geographical locations, a pattern consistent with the growth-differentiation balance hypothesis (GDBH). Soil available potassium emerged as a key edaphic factor directly affecting amino acid accumulation, primarily by modulating root metabolism and nutrient transport, whereas non-capillary porosity was correlated with amino acid content but lacked a significant direct SEM path and pairwise site

differences, suggesting an indirect or covarying role. Rhizosphere microbial communities exhibited marked spatial differentiation. PCoA and PERMANOVA further confirmed significant site-driven differentiation in both bacterial and fungal community structures, with bacterial intra-group dispersion also significantly heterogeneous. *Lactobacillus* was specifically enriched in the Fujian site and may be associated with amino acid accumulation. However, this remains correlative and requires strain isolation and inoculation validation. *Lactobacillus* was specifically enriched in the Fujian site and may be associated with amino acid accumulation. However, this remains correlative and requires strain isolation and inoculation validation. Climate factors mainly affected soil properties, while rhizosphere bacteria were directly linked to shoot quality. Soil available potassium had significant direct paths to total amino acid and starch contents, and rhizosphere bacteria were directly linked to shoot quality.

Nevertheless, the link between *Lactobacillus* enrichment and amino acid accumulation remains correlative, and causal relationships warrant further validation through strain isolation and inoculation experiments. Moreover, the single-year cross-sectional design does not fully capture the influence of interannual climatic variability on quality stability. Future studies should integrate long-term fixed-site monitoring with multi-omics approaches to systematically unravel the relevant dynamics. Finally, manipulative field experiments are needed to provide a theoretical basis for regional planning of high-quality *D. latiflorus* shoot production and the development of standardized cultivation practices.

Abbreviations

MAT: Mean annual temperature; MAP: Mean annual precipitation; SEM: Structural equation modeling; PCoA: Principal coordinates analysis; PERMANOVA: Permutational multivariate analysis of variance; ITS: Internal transcribed spacer; FDR: False discovery rate; VIF: Variance inflation factor.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data and materials

The datasets generated and/or analysed during the current study are available in the

[Sequence Read Archive (SRA)] repository, [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1559820]. BioProject accession number: PRJNA1559820.

Competing Interests

The authors declare that they have no competing interests.

Funding

This work was supported by the National Key Research and Development Program of China during the 14th Five-Year Plan Period (Grant No. 2023YFD2201201) and the Science and Technology Innovation Special Fund of Fujian Agriculture and Forestry University (Grant No. KFB24066).

Authors' contributions

JL and HT: Conceptualization, Methodology, Formal Analysis, Writing-original draft, Visualization. LQ: Software, Writing-review & editing. YL: Data curation, Validation, Investigation. TH: Funding acquisition. JR: Project administration. YZ: Resources. LC and LC: Supervision. All authors read and approved the final manuscript.

Acknowledgements

The authors sincerely thank all funding agencies for their financial support.

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Supplementary table:

Table S1. Pairwise comparisons of available potassium among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.603	0.794	0.496	0.404	0.926	0.725	0.337	0.642
FJ		1	0.357	0.030*	0.012*	0.467	0.878	0.404	0.101
GD			1	0.603	0.467	0.725	0.534	0.165	0.769
GX				1	0.777	0.337	0.213	0.022*	0.769
GZ					1	0.210	0.157	0.012*	0.603
HI						1	0.722	0.210	0.467
HN							1	0.467	0.357
JX								1	0.044*
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction. Asterisks denote significant differences: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Table S2. Pairwise comparisons of non-capillary porosity among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.821	0.455	0.693	0.918	0.821	0.821	0.895	0.772
FJ		1	0.234	0.234	0.455	1	0.945	0.966	0.259
GD			1	0.821	0.455	0.234	0.260	0.259	0.693
GX				1	0.738	0.260	0.332	0.397	0.939
GZ					1	0.570	0.570	0.693	0.821
HI						1	0.945	0.966	0.378
HN							1	0.945	0.397
JX								1	0.455
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction.

Table S3. Pairwise comparisons of total potassium among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.881	0.991	0.410	0.325	0.436	0.294	0.891	0.436
FJ		1	0.863	0.325	0.207	0.370	0.207	0.991	0.372
GD			1	0.370	0.294	0.410	0.257	0.881	0.410
GX				1	0.784	0.914	0.506	0.436	0.912

GZ					1	0.606	0.832	0.359	0.629
HI						1	0.436	0.501	0.991
HN							1	0.303	0.440
JX								1	0.502
YN									1

773 Note: Values are adjusted P values based on Dunn's test with FDR correction.

774

775 Table S4. Pairwise comparisons of starch content among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	<0.001***	0.008**	0.011*	0.757	<0.001***	0.109	0.017*	0.361
FJ		1	0.321	0.053	<0.001***	0.672	0.008**	0.059	<0.001***
GD			1	0.661	0.003**	0.263	0.246	0.641	0.025*
GX				1	0.003**	0.059	0.377	0.932	0.041*
GZ					1	<0.001***	0.100	0.008**	0.377
HI						1	0.011*	0.061	<0.001***
HN							1	0.415	0.377
JX								1	0.059
YN									1

776 Note: Values are adjusted P values based on Dunn's test with FDR correction. Asterisks denote significant
777 differences: **P* < 0.05, ***P* < 0.01, ****P* < 0.001.

778

779 Table S5. Pairwise comparisons of soluble protein content among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.973	0.189	0.973	0.006**	0.376	0.818	0.358	0.244
FJ		1	0.045*	0.992	<0.001***	0.151	0.818	0.110	0.041*
GD			1	0.096	0.138	0.006	0.0829	0.722	0.818
GX				1	<0.001***	0.257	0.818	0.189	0.110
GZ					1	<0.001***	<0.001***	0.033*	0.041*
HI						1	0.557	0.019*	0.006**
HN							1	0.151	0.096
JX								1	0.849
YN									1

780 Note: Values are adjusted P values based on Dunn's test with FDR correction. Asterisks denote significant
781 differences: **P* < 0.05, ***P* < 0.01, ****P* < 0.001.

782

783 Table S6. Pairwise comparisons of total amino acid content among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	<0.001***	0.443	0.899	0.332	0.666	0.498	0.756	0.332
FJ		1	0.006**	<0.001***	0.002**	<0.001***	<0.001***	<0.001***	0.001**
GD			1	0.416	0.872	0.661	0.076	0.195	0.886
GX				1	0.242	0.666	0.332	0.608	0.254
GZ					1	0.443	0.026*	0.076	0.956
HI						1	0.179	0.346	0.463

HN							1	0.666	0.027*
JX								1	0.076
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction. Asterisks denote significant differences: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Table S7. Pairwise comparisons of bacterial Chao1 diversity among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.217	0.074	0.074	0.241	0.285	0.269	0.635	0.269
FJ		1	0.211	0.211	0.972	0.888	0.972	0.559	0.961
GD			1	0.900	0.241	0.211	0.269	0.211	0.217
GX				1	0.269	0.211	0.316	0.211	0.241
GZ					1	0.900	0.972	0.635	0.961
HI						1	0.961	0.809	0.961
HN							1	0.706	0.972
JX								1	0.706
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction.

Table S8. Pairwise comparisons of bacterial Shannon diversity among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.141	0.054	0.054	0.292	0.304	0.292	0.511	0.294
FJ		1	0.294	0.294	0.650	0.294	0.814	0.294	0.429
GD			1	0.8367	0.234	0.141	0.294	0.141	0.154
GX				1	0.234	0.141	0.294	0.141	0.154
GZ					1	0.814	0.878	0.719	0.837
HI						1	0.791	0.837	0.878
HN							1	0.685	0.814
JX								1	0.814
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction.

Table S9. Pairwise comparisons of fungal Chao1 diversity among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.563	0.563	0.469	0.749	0.819	0.469	0.563	0.807
FJ		1	0.807	0.563	0.885	0.563	0.563	0.819	0.284
GD			1	0.819	0.807	0.563	0.807	0.916	0.441
GX				1	0.563	0.469	0.903	0.807	0.263
GZ					1	0.807	0.563	0.807	0.469
HI						1	0.469	0.563	0.563
HN							1	0.807	0.263
JX								1	0.463
YN									1

Note: Values are adjusted P values based on Dunn's test with FDR correction.

795

796 Table S10. Pairwise comparisons of fungal Shannon diversity among nine geographical groups of *D.latiflorus*

	CQ	FJ	GD	GX	GZ	HI	HN	JX	YN
CQ	1	0.403	0.369	0.172	0.316	0.521	0.119	0.267	0.502
FJ		1	0.663	0.321	0.521	0.663	0.119	0.421	0.910
GD			1	0.663	0.927	0.522	0.375	0.715	0.663
GX				1	0.663	0.300	0.521	0.939	0.369
GZ					1	0.430	0.369	0.745	0.521
HI						1	0.119	0.369	0.825
HN							1	0.521	0.172
JX								1	0.433
YN									1

797 Note: Values are adjusted P values based on Dunn’s test with FDR correction.

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799