EFFECT OF DIFFERENT FERTILIZATION COMBINATIONS ON CHINESE CABBAGE QUALITY, AMINO ACID CONTENT, AND RHIZOSPHERE MICROORGANISMS

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Abstract. This study was conducted on Chinese cabbage to examine the effects of different fertilization combinations on cabbage quality, amino acid content, and the microbial community structure in rhizosphere soil. The findings provide valuable insights for improving nutrient management and soil fertility in local cabbage cultivation. The results showed that the T4 fertilization treatment significantly increased the content of seven essential amino acids compared to the control. All fertilization treatments enhanced soil pH, hydrolytic nitrogen, and effective phosphorus levels. The content of organic matter and readily available phosphorus varied depending on the fertilizer type. Microbial diversity was a key factor influencing the availability of effective phosphorus, potassium, and organic matter in the soil. The bacterial community was primarily dominated by Actinobacteria, Chloroflexi, Proteobacteria, Acidobacteria, Firmicutes, and Bacteroidetes, with fertilization treatments increasing the abundance of Acidobacteria and Firmicutes. The fungal community was mainly composed of Ascomycota, Basidiomycota, and Entomophthoromycota, with treatments reducing Ascomycota and enhancing Basidiomycota and Zygomycota. Soil pH, organic matter, hydrolytic nitrogen, and effective phosphorus were the primary factors affecting bacterial community composition, while fungal community shifts were driven by organic matter, hydrolytic nitrogen, and pH. The fertilization strategy using high-potassium organic fertilizer (200 kg/m²), aminobutyric acid (50 g/m²), and polyglutamate (1 kg/m²) significantly improved soil health, enhanced amino acid content, and promoted microbial diversity, making it a recommended fertilization approach for improving both cabbage quality and soil fertility.

Keywords: *fertilization strategy, soil microbiota, nutrient management, crop improvement*

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Introduction

Chinese cabbage (*Brassica rapa* ssp. chinensis Makino) belongs to the cruciferous family and it has strong cold resistance. It has a high nutritional value due to its richness in vitamins A and C, abundant dietary fiber, and bioactive compounds that activate blood circulation, disperse blood stasis, and reduce swelling. The planting area in Yunnan has been very large for many years. With peoples pursuit of high quality of life, people also have higher requirements for the total amount and quality of cabbage. Therefore, it is particularly important to improve its quality. Driven by interests, farmers often simply and excessively apply chemical fertilizers at the expense of soil quality, resulting in soil acidification, nutrient imbalance, deterioration of physical and chemical properties, microbial flora imbalance (Shen et al., 2010; Huang et al., 2023), so that the sustainable development of vegetable industry is seriously hindered. In this situation, increasing the application of organic fertilizer, chemical fertilizer reduction, applying soil amendments has become an effective way to solve the above problems. The results show that the application of organic and inorganic fertilizers can significantly increase the soil microbial amount, and the moderate reduction of chemical fertilizer and the application of organic fertilizer can improve soil microbial conditions and fertility (Gu et al., 2009; Teoh et al., 2024). The application of soil amendments can improve soil pH, reduce exchangeable aluminum content, increase exchangeable calcium and magnesium levels, and effectively enhance the populations of bacteria, fungi, actinomycetes, and antagonistic bacteria in the soil. This increase in microbial quantity can further promote crop growth, quality, and yield (Gupta et al., 2017; Liu et al., 2021; Tao et al., 2024). Clarify the influence of different fertilization combinations on the quality of cabbage, physical and chemical properties of rhizosphere soil in rhizosphere and microbial community has important significance for optimizing the planting of high-quality cabbage and promoting the development of Yunnan cabbage industry (Tao et al., 2024; Irshad et al., 2024).

As one of the most complex biological systems on Earth, soil is not only the basis of plant growth, but also a key component of ecosystem function. The physical and chemical properties of soil and their microbial communities directly influence plant health, productivity and overall stability of ecosystems (Johansson et al., 2004; Eisenhauer et al., 2011; Al-Khayri et al., 2023). Different fertilization methods can have different effects on the soil, including physical factors such as soil, soil texture and precipitation variability, as well as biological components such as plant cover, richness, functional traits and microbial communities. Furthermore, chemical variables such as soil organic carbon and leaf nitrogen contribute to the different characteristics of these regions (Roesch et al., 2012; Berdugo et al., 2020). With the changes in the functional and structural properties of the ecosystem, the physic-chemical properties of soil and the functions of microbial communities transform accordingly, thus affecting plant growth and adaptability. However, a comprehensive survey of various fertilization combinations of Chinese cabbage is lacking, especially when considering soil physical and chemical properties and microbial community analysis (Berdugo et al., 2020; Kadege et al., 2024).

Amino acids are classified into essential and non-essential amino acids. Essential amino acids cannot be synthesized by the human body, or their synthesis rate is insufficient to meet physiological needs, making dietary intake necessary. In contrast, non-essential amino acids can be synthesized by the body or derived from other amino acids (Nurliyani et al., 2023). Some medicinal amino acids play a crucial role in maintaining various physiological functions of the human body (Qu et al., 2021; Ijaz et al., 2023). Amino acids can also be divided into umami amino acids, sweet amino acids and aromatic amino acids which can form rich taste levels of food. At the same time, amino acids are also one of the important indicators of vegetable nutrients, involved in many important physiological processes in the body (Abdul Wahab et al., 2015; Tang et al., 2021; Victoria et al., 2023).

Therefore, in this study, amino acids were determined by chromatography, and 16S rRNA / ITS MiSeq high-throughput sequencing was used to comprehensively analyze the microbial community structure in the rhizosphere soil and compare various fertilization combinations to analyze the soil physiochemical properties and cabbage quality. The objectives of this study are: 1) determine which fertilization method is most suitable for the growth of cabbage; 2) reveal the most suitable mechanism for the growth of cabbage from the perspective of soil physicochemical properties and microbial diversity in the rhizosphere. Ultimately, our results aim to provide valuable insights and guidance on the sustainable development of cabbage cultivation in Yunnan.

Materials and methods

Plant materials and fertilization treatments

This experiment was conducted using Chinese cabbage (Brassica rapa ssp. chinensis Makino) as the test crop. The fertilization treatments consisted of high-potassium organic fertilizer, a functional bacterial agent containing 30 billion viable bacteria per gram, aminobutyric acid (50%), and polyglutamate (3.5%). These fertilizers were applied before transplanting, with the organic fertilizer incorporated into the soil and other amendments dissolved in water and applied as foliar sprays or root drenches.

Chemical reagents and sample preparation

To analyze the amino acid composition of Chinese cabbage, various high-purity reagents were used. Methanol and acetonitrile (chromatography-grade) were employed as mobile-phase solvents in liquid chromatography. Paraformaldehyde (OPA) and 3-mercaptopropionic acid, both obtained from Shanghai Maclin Biochemical Technology Company, were used as derivatization agents to enhance amino acid detection by fluorescence detection. Buffer solutions, including boric acid, sodium hydroxide, sodium hydrogen phosphate, phosphoric acid, sodium tetraborate, and hydrochloric acid, were prepared using analytical-grade reagents sourced from Chengdu Jinshan Chemical Reagent Company to ensure precise pH control during sample preparation.

For quantification, 17 amino acid standards with a purity of over 98% (Shanghai Source Pure Biotech) were used as references to calibrate the chromatography system. These included aspartate (Asp), glutamate (Glu), serine (Ser), glutamine (Gln), histidine (His), glycine (Gly), threonine (Thr), arginine (Arg), alanine (Ala), tyrosine (Tyr), cystine (Cys), valine (Val), tryptophan (Trp), isoleucine (Ile), phenylalanine (Phe), lysine (Lys), and leucine (Leu).

Cabbage leaf samples were dried at 60°C in an oven, crushed into a fine powder, and sieved through a 40-mesh screen to achieve uniform particle size. The powdered samples were then stored in airtight, self-sealing bags in a desiccator to prevent moisture absorption and chemical degradation before analysis.

Amino acid analysis using liquid chromatography

To determine the amino acid composition of cabbage samples, high-performance liquid chromatography (HPLC) was performed using an LC-16 liquid chromatograph (DMG Instrument, Suzhou, China). The system was equipped with a DGU-20A degassing unit to remove dissolved gases from the mobile phase, an LC-16 binary high-pressure pump to control solvent delivery, an SIL-16 automatic sampler for precise injection, a CTO-16 column oven to maintain optimal separation temperature, an SPDM-40 diode array detector for UV-visible detection, and an RF-20A fluorescence detector for enhanced sensitivity of amino acid derivatives.

For separation, a Hypersil BDS C18 column (150 mm × 4.6 mm, 3 μm, Dalian Yili Analytical Instrument Co., Ltd.) was used. The mobile phase consisted of 0.016 mol/L phosphate buffer (pH 8.2), methanol, and acetonitrile, which were degassed and filtered through a 0.45 μm membrane before use. The flow rate was maintained at 1.0 mL/min, and the column temperature was set to 50°C.

Before injection into the chromatograph, 5.0 μL of each cabbage extract was mixed with 2.0 μL of borate buffer and 1.0 μL of OPA derivatization reagent, allowing amino acids to react and form fluorescent derivatives. The fluorescence detector was set to an excitation wavelength of 340 nm and an emission wavelength of 450 nm to maximize sensitivity. The quantification of amino acids was achieved by comparing sample retention times and peak areas against calibration curves generated using standard amino acid solutions.

Experimental order

After transplanting four-leaf-stage cabbage seedlings into plots, fertilization treatments were applied by mixing high-potassium organic fertilizer (3000 kg/ha) with subsoil. Soil samples (0–20 cm depth) were collected post-harvest using a soil auger at five random points per plot. These were homogenized, sieved (2 mm), and divided into two aliquots: one stored at 4°C for microbial analysis and the other air-dried for physicochemical testing. Concurrently, cabbage leaves (100 g per plot) were harvested, freeze-dried, and ground for amino acid quantification.

Experimental design

The study was conducted in Anning City, Yunnan Province (altitude: 1800 m; latitude: 24°31'3"N; longitude: 102°62'12"E). The area is characterized by a dry-hot valley climate, with an annual average temperature of 15–22°C, average relative humidity of 60%, and annual precipitation of approximately 900 mm. The soil type in the experimental field is sandy loam, with an initial pH of 6.8 and an organic matter content of 18.5 g/kg. The experiment followed a randomized block design, with five fertilization treatments (T1–T5) and three replicates per treatment. The selection of treatments and their levels was based on previous agronomic studies and local farming practices, aiming to improve soil fertility, enhance microbial diversity, and optimize Chinese cabbage quality (*Table 1*).

1. T1 (Control): No fertilization, used as a baseline to assess the effects of fertilization treatments.
2. T2 (High-potassium organic fertilizer, 3000 kg/ha): Organic fertilizer was applied to improve soil organic matter content and nutrient availability, as organic amendments have been shown to enhance soil microbial diversity and plant growth.

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3. T3 (T2 + Y2 functional bacterial agent, 150 g/ha): A bacterial inoculant was included to assess its impact on soil microbial structure and nutrient cycling, as functional bacteria can enhance nitrogen fixation and phosphorus solubilization.
4. T4 (T2 + aminobutyric acid, 750 g/ha + polyglutamate, 15 kg/ha): Aminobutyric acid was used to investigate its role in stress tolerance and quality improvement, while polyglutamate was applied as a biostimulant to enhance nutrient uptake efficiency.
5. T5 (T3 + aminobutyric acid, 750 g/ha + polyglutamate, 15 kg/ha): This combination was designed to evaluate the synergistic effects of organic fertilizer, microbial agents, and biostimulants on soil fertility and plant quality.

Table 1. *Treatment of Fertilization combination of each Chinese cabbage*

Treatments	Fertilization combination
T1	No fertilize
T2	High-potassium organic fertilizer: 3000 kg/ha
T3	High potassium organic fertilizer 3000 kg/ha + Y2 functional bacterial agent 150 g/ha
T4	High potassium organic fertilizer 3000 kg/ha + aminobutyric acid 750 g/ha + polyglutamate 15 kg/ha
T5	High potassium organic fertilizer 3000 kg/ha + Y2 functional bacterial agent 150 g/ha + aminobutyric acid 750 g/ha + polyglutamate 15 kg/ha

The levels of organic fertilizer (3000 kg/ha), aminobutyric acid (750 g/ha), and polyglutamate (15 kg/ha) were selected based on preliminary experiments and recommendations from previous studies on leafy vegetables grown under similar climatic conditions (Zhang et al., 2019; Li et al., 2022). The bacterial agent level (150 g/ha) was chosen according to manufacturer guidelines and previous applications in vegetable production. These treatments were expected to provide insights into optimizing fertilization strategies for sustainable cabbage cultivation.

Each experimental plot measured 10 m² (2 m × 5 m), and each plot contained 40 Chinese cabbage plants, resulting in a total of 600 plants across all treatments. Fertilization treatments were applied before transplanting, and cabbage seedlings at the four-leaf stage were transplanted into the plots at a spacing of 30 cm × 40 cm (row × plant distance). Field management, including irrigation, pest control, and weeding, was carried out uniformly across all treatments to ensure comparability as follows:

Except for different fertilization formulas, other field management measures were consistent. Before transplanting, the fertilizer was mixed with the subsoil according to the design of the experimental area, and then transplanted into cabbage seedlings.

Preparation of reagents

For chromatographic separation, mobile phase A was prepared as a 0.016 mol/L phosphate buffer (pH 8.2) by dissolving 1.81 g of anhydrous sodium hydrogen phosphate and 4.75 g of sodium tetraborate in 1000 mL of ultrapure water. The pH was adjusted to 8.2 using concentrated hydrochloric acid to ensure optimal amino acid derivatization, pass 0.45 μ m filter membrane, ultrasonic degassing. Mix 450 mL of methanol, 450 mL of acetonitrile and 100 mL of water, pass through 0.45 μ m filter membrane and ultrasonic degassing.0.4 mol/L borate buffer (pH=10): weigh 2.45 g of boric acid in 100 mL of water and adjust pH to 10 with 0.4 mol/L sodium hydroxide. Derivative reagent: weigh OPA 80 mg, dissolve in 1.0 mL acetonitrile, add 7.0 mL borate buffer and 125 μ L 3-mercapto propylene to weigh 17 amino acid standards, place in 1000 mL volumetric flask, dissolve in 0.1 mol/L hydrochloric acid solution and prepare amino acid standard working solution.

Preparation of the test solution

Accurately weigh 0.1000 g tea sample in a triangular bottle, add 100 mL of boiling water, extract in a boiling water bath for 25 min (shake every 5 min), cool to room temperature, including all tea residue transferred to 250 mL volumetric flask, shake after fixed volume, the supernatant over 0.45 μm microporous filter film.1.3.4 Derivation of the derivative reactions. The autosampler absorbs 5.0 μL of borate buffer and 2.0 μL of tested solution, absorbs and spits 5.0 μL of air at 15 μL/s for 4 times; 1.0 μL of OPA derivative at 15 μL/s 55 and 5.0 μL air 4 times, wait for 30 s; absorbs 10.5% of 1.5% H_3PO_4 solution and 5.0 μL air at 15 μL / s, inject the derived sample into the liquid chromatograph.

The chromatographic conditions

Mobile phase: 0.016 mol/L phosphate buffer gradient in phase A Procedure: 06 min, 5%B→10%B; 68 min, 10%B; 8~10 min, 10%B→16%B; 10~23 min, 16%B→40%B; 23~30 min, 40%B→50%B; 30~32 min, 50%B; 32~33 min, 50%B→100%B; 33~35 min, 100%B; 35~36 min, 100%B→5%B; 36~44 min, 5%B; Flow rate of 1.0 mL/min; Column temperature box: 50°C; The fluorescence detector used excitation 340 nm and emission 450 nm.

Sample collection and analysis methods

Collection of soil samples

After harvesting the Chinese cabbage, soil samples were collected from each village using a soil drill at a depth of 0–20 cm. A total of 1.0 kg of mixed soil samples were taken from five different locations within each area. The samples were carefully processed by removing any fresh soil, gravel, and plant debris. The five samples were then thoroughly mixed and divided into two equal portions. One portion was stored in a refrigerator at 4°C for microbial analysis, while the other was air-dried for further analysis of soil physical and chemical properties, organic carbon content, and soil enzyme activity.

Determination of soil physical and chemical properties

The physico-chemical properties of the soil tested included pH, organic matter, available nitrogen, available phosphorus, and available potassium. Soil pH was measured using a pH meter. Organic matter content was determined using the $K_2Cr_2O_7$ (Potassium dichromate) method with heat capacity. Available nitrogen was quantified by alkali diffusion of nitrogen. Available phosphorus was measured through photoelectric colorimetry, while available potassium was determined using NH_4OAc (Ammonium acetate) extraction followed by flame photometry. Soil pH was measured using a pHS-3C acidity meter (Shanghai Magnetic Instrument Factory). The pH electrode was calibrated using buffer solutions (pH 4.0, 7.0, and 9.2) before immersing it in a 1:2.5 soil-to-water suspension for measurement. Organic matter content was determined by the potassium dichromate oxidation method, which involved titration with ferrous sulfate to quantify the oxidized organic carbon. Hydrolytic nitrogen was measured using alkali diffusion, where soil samples were treated with sodium hydroxide and absorbed ammonia was quantified using boric acid indicators. Available phosphorus was analyzed via molybdenum blue spectrophotometry, with absorbance readings taken at 880 nm to calculate phosphate concentrations. Available potassium was extracted using ammonium acetate and measured by flame photometry using a BSA24S electronic balance (Sadis Scientific Instrument, Beijing, China) for precise weighing.

Measurement of physical and chemical properties of Chinese cabbage

After the test, about 100g each of cabbage was collected from each cell for detecting composition, mainly for the detection of vitamin C, soluble sugar, soluble protein, nitrate, and so forth.

Analysis of the functional diversity of soil microorganisms

Soil microbial genomic DNA was extracted using the TM kit following the manufacturer's instructions. The quality of the extracted genomic DNA was assessed through 80% agarose gel electrophoresis, and the DNA concentration was measured using a UV spectrophotometer. For bacterial 16S rRNA gene amplification, the primer sequences used were: 338F: ACTCCTACGGGAGGCAGCA and 806R: GGACTACHVGGGTWTCTAAT. For fungal internal transcribed spacer (ITS) region amplification, the primer sequences were: ITS 5F: GGAAGTAAAAGTCGTAACAAGG and ITS 1R: GCTGCGTTCTTCATCGATGC. The PCR reaction system consisted of a total volume of 25 μL, which included 12.5 μL of 2x Taq-PCR-MasterMix, 3 μL of BSA (2 ng/μL), 1 μL of primers (5 μmol/L each), 2 μL of template DNA, and 5.5 μL of ddH2O. The amplification was carried out using a Mastercycler gradient PCR instrument with the following program: initial denaturation at 95°C for 5 minutes, followed by 30 cycles of denaturation at 95°C for 50 seconds, annealing at 58°C for 50 seconds, and extension at 72°C for 45 seconds. A final extension step was performed at 72°C for 10 minutes, followed by a hold at 4°C. The PCR products were analyzed by electrophoresis on a 1.0% agarose gel. For recovery, the products were purified using the AxyPrepDNA gel recovery kit with elution in Tris-HCl buffer. The purified PCR products from each sample were pooled and confirmed through 2% agarose gel electrophoresis. The PCR products were purified using a gel extraction kit, sequenced on an Illumina MiSeq platform, and analyzed using MOTHUR software to compute microbial diversity indices such as Chao1, Shannon, and Simpson indices. Taxonomic classification was conducted by comparing sequences against the Silva 16S and UNITE ITS databases.

Data analysis

All data were analyzed using WPS Office and IBM SPSS Statistics 27 software, with a significance level set at 0.05. Data entry was performed in WPS Office, followed by calculation of the mean and standard deviation for each cell. Data points with large errors were excluded based on the ±1.96 standard deviation (SD) rule, corresponding to a 95% confidence interval (CI). Any values falling outside this range were considered outliers and removed before statistical analysis. After processing three sets of data, one-way ANOVA was applied to assess significant differences between treatments. All statistical analyses were performed using SPSS (IBM Corp., Armonk, NY, USA). One-way ANOVA was conducted to assess differences among groups. Prior to ANOVA, the homogeneity of variances was tested using Levene’s test. For data meeting the homogeneity assumption, Gabriel’s post-hoc test (s-b) and Tukey’s HSD test (W) were applied for multiple comparisons. When the assumption of homogeneity was violated, the Tamhane's T2 test (M) was used as a robust alternative. The significance level was set at $p < 0.05$ for all tests. After calculating means and standard errors, outliers were removed based on the ±1.96 standard deviation (95% confidence interval). One-way ANOVA was applied to test for overall differences among the five fertilization treatments. When a significant treatment effect was detected, multiple comparisons were performed using appropriate post-hoc tests. Specifically, for variables meeting the assumption of homogeneity (as assessed by Levene's test), both Tukey's HSD test and Gabriel's post-hoc test were employed to compare treatment means. For variables where the homogeneity assumption was violated, the Tamhane's T2 test was used. In the tables, different lowercase letters denote statistically significant differences ($P < 0.05$). The operational taxonomic units (OTUs) were annotated using taxonomic reference databases: the bacterial 16S rRNA Silva database and the fungal ITS UNITE database. Microbial diversity in each soil sample was assessed using MOTHUR software, which calculated OTU richness, Chao1 index, Shannon index, and phylogenetic diversity index.

Results

Effect of different fertilization combinations on the amino acid content of Chinese cabbage

The analysis of 17 kinds of amino acids, including threonine, valine, methionine, isoleucine, leucine, phenylalanine and lysine, histidine, glycine, tyrosine, arginine, six essential amino acid, 6 other amino acid, serine, glutamate, alanine, cystine and proline, the determination results are shown in *Table 2*.

Table 2. *Linear regression equations and correlations for the 17 amino acids*

Amino acids	Retention time/min	Regression equation (n =9)	r	Linearity range	Quantitative	Limit of detection	Interior label
Gly	1.712	Y=3.741 ×10-4X +0.0747	0.9995	0.32~8	0.32	0.096	Met - d3
Ala	1.977	Y=2.889×10-3X－0.0827	0.999	0.32~8	0.32	0.096	Ala - d4
Val	3.414	Y=4.896×10-3 X－0.100	0.9993	0.32~8	0.32	0.096	Phe - d5
Leu	5.347	Y=9.439 ×10-3X－0.00308	0.9997	0.32~8	0.32	0.096	Phe - d5
Ile	4.924	Y=9.066 ×10-3X －0.0800	0.9993	0.32~8	0.32	0.096	Phe - d5
Lys	2.821	Y=7.695×10 -4X－0. 0257	0.9995	0.32~8	0.32	0.096	Phe - d5
Met	3.466	Y=3.025×10-3X－0.157	0.9995	0.32~8	0.32	0.096	Met - d3
His	2.525	Y=2.462 ×10-3X +0. 439	0.9998	0.32~8	0.32	0.096	Ala - d4
Phe	6.507	Y =3.915 ×10-3X －0.0219	0.9998	0.32~8	0.32	0.096	Phe - d5
Arg	3.087	Y=9.159×10-4X +0.0918	0.9992	0.16~4	0.16	0.048	Phe - d5
Ser	1.678	Y=2.447 ×10-3X +1.98	0.9992	0.16~4	0.16	0.048	Met - d3
pro	2.204	Y=6.614 ×10 -3X +0. 207	0.9997	0.16~4	0.16	0.048	Phe - d5
Thr	1.873	Y=2.303×10-3X－0. 397	0.9995	0.16~4	0.16	0.048	Ala - d4
Orn	2.48	Y =1.315 ×10 -3X +0.174	0.9998	0.16~4	0.16	0.048	Ala - d4
Glu	1.915	Y =3.691 ×10- 3X +0. 593	0.999	0.16~4	0.16	0.048	Ala - d4
Aty	4.791	Y =1.188 ×10- 3X－0. 0364	0.9995	0.16~4	0.16	0.048	Phe - d5
Tyr	3.826	Y =2.217 ×10- 4X +0. 00754	0.9992	0.032~0.8	0.032	0.0096	Phe - d5

As can be seen from *Table 3*, for 7 kinds of human essential amino acids, threonine was not detected in cabbage, except valine was improved compared with the control group, the content of methionine and phenylalanine was increased compared with the control group, and the content of leucine was decreased in the control group. Relative to the control group, only treatment 4 increased the content of isoleucine and lysine.

Table 3. *Essential amino acid content (%) in Chinese cabbage under different fertilization treatments (T1: Control; T2: High-potassium organic fertilizer; T3: T2 + Y2 bacterial agent; T4: T2 + aminobutyric acid + polyglutamate; T5: T3 + aminobutyric acid + polyglutamate)*

Amino Acids	**T1**	**T2**	**T3**	**T4**	**T5**
Total number of free amino acids	1.18±0.1136a	1.24±0.1217a	1.28±0.1179a	1.16±0.1054a	1.19±0.1153a
Asp	0.0589±0.0053a	0.062±0.0056a	0.0548±0.0048ab	0.0453±0.004b	0.0542±0.0049ab
Thr	0	0	0	0	0
Ser	0.0124±0.0006b	0.0136±0.0007a	0.013±0.0007ab	0.0067±0.0003c	0.0066±0.0003c
α-aminoglutaric acid	0.009±0.0005e	0.0214±0.0011a	0.0171±0.0009b	0.013±0.0007c	0.0106±0.0005d
proline	0.433±0.022a	0.433±0.026a	0.438±0.022a	0.479±0.024a	0.458±0.023a
glycocoll	0.0089±0.0005a	0.0058±0.0003b	0.0054±0.0003b	0.0041±0.0002c	0.0036±0.0002c
Ala	0.0139±0.0013b	0.019±0.001a	0.0204±0.0009a	0±0c	0.0132±0.0012b
cystinol	0	0	0	0	0
Val	0.299±0.027ab	0.276±0.025b	0.344±0.031a	0.311±0.028ab	0.314±0.029ab
Met	0.19±0.017a	0.199±0.018a	0.212±0.019a	0.216±0.02a	0.2±0.018a
Ile	0.01±0.0009ab	0.0044±0.0004d	0.0087±0.0008b	0.0111±0.001a	0.0065±0.0006c
Leu	0.0148±0.0014a	0.0145±0.0013a	0.0142±0.0013a	0.0079±0.0007c	0.0102±0.0009b
p-hydroxy-phenylalanine	0.0614±0.0056ab	0.0636±0.0058ab	0.0678±0.0062a	0.0539±0.0049b	0.0572±0.0052ab
Phe	0.0091±0.0008d	0.0116±0.0011bc	0.019±0.0017a	0.0102±0.0009cd	0.0126±0.0012b
lysine	0.0127±0.0011b	0.0071±0.0006c	0.0072±0.0006c	0.0165±0.0015a	0.0068±0.0006c
His	0.029±0.0025bc	0.0458±0.0041a	0.0414±0.0037a	0.0236±0.002c	0.03±0.0025b
arginine	0.0132±0.0012b	0.0152±0.0013ab	0.0158±0.0014a	0.013±0.0007b	0.0089±0.0008c

Note: The data in the table are mean ± standard error, and different lowercase letters in the same column indicate significant difference ($P<0.05$)

Influence of different fertilization methods on soil physical and chemical properties

Nitrogen, phosphorus, and potassium are crucial nutrients for plant development, while pH levels and organic matter content play a significant role in determining the quality of Chinese cabbage. Based on the data in *Table 4*, the pH level in treatment 4 was notably higher than in treatments 1 and 2. Treatment 2 exhibited a significantly greater organic matter content compared to the other treatments, with no notable differences among the other groups. Hydrolytic nitrogen was found to be considerably higher in treatment 2 than in treatments 1, 3, 4, and 5. In terms of effective phosphorus, treatment 2 outperformed all other treatments, though no significant differences were observed between the remaining treatments. Finally, treatment 3 demonstrated a significantly higher level of rapid potassium compared to treatments 2, 4, and 5.

Table 4. *Effect of different fertilization methods on soil physical and chemical properties*

Treatments	P H	Organic matter	Hydrolytic nitrogen	Effective P	Quick effect potassium
T1	7.72±0.01 c	17.15±0.45 b	47.35±10.95 b	63.3±0.9 b	354±16 ab
T2	7.82±0.05 bc	19.85±0.05 a	69.1±3.6 a	74.65±2.75 a	307±4 c
T3	7.88±0.08 ab	17±1.8 b	45.65±12.85 b	76.2±3.6 a	370±32 a
T4	7.95±0.04 a	17.95±0.65 b	50.7±0.2 b	65.1±0.8 b	305±2 c
T5	7.92±0.05 ab	17.8±0.4 b	59±0.8 ab	65.2±1 b	328.5±5.5 bc

Note: The data in the table are mean ± standard error, and different lowercase letters in the same column indicate significant difference (P<0.05)

Effect of different fertilization methods on Chinese cabbage quality

According to *Table 5*, vitamin C content varied significantly among treatments (T1 > T4 > T2 > T5 > T3), and soluble sugar content was highest in T5. There was no statistically significant difference in soluble protein or nitrate content across treatments.

Table 5. *Effect of different fertilization methods on Chinese cabbage quality*

Treatments	Vitamin C mg / 100g	Soluble sugar %	Soluble protein %	Nitrate mg/kg
T1	49.9±0.5 a	0.79±0.01 d	0.44±0	54±0
T2	40.35±0.15 c	0.82±0 c	0.58±0	990±0
T3	26.2±0.4 e	0.34±0.01 e	0.62±0	1200±0
T4	46.9±0.5 b	0.92±0.01 b	0.44±0	240±0
T5	27.75±0.15 d	1.11±0.01 a	0.46±0	360±0

Note: The data in the table are mean ± standard error, and different lowercase letters in the same column indicate significant difference (P<0.05)

Post-hoc comparisons revealed several treatment-specific differences. For instance, *Table 3* shows that although the overall total free amino acid content did not differ significantly among treatments (all treatments are labeled “a”), the aspartate (Asp) level in T4 (0.0453 ± 0.004, “b”) was significantly lower than in T1 (0.0589 ± 0.0053, “a”). Similarly, for other amino acids, treatments T3 and T5 often shared intermediate significance levels (labeled “ab”) compared to T1 or T4. In the quality parameters (*Table 5*), vitamin C content in T1 (49.9 ± 0.5, “a”) was significantly higher than in T3 (26.2 ± 0.4, “e”), while soluble sugar content was highest in T5 (1.11 ± 0.01, “a”). These differences were confirmed using Tukey’s, Gabriel’s, and Tamhane’s T2 tests, depending on the specific variable’s variance characteristics. Such detailed post-hoc analyses underscore the impact of the various fertilization regimes on both amino acid composition and quality traits of Chinese cabbage.

Comparison of soil microbial diversity in different fertilization methods

After quality filtering, 1002925 fungal high-quality raw sequences with an average length of 240bps were obtained from the rhizosphere soil samples. The Sobs index at the OTU level for all samples was between 325 and 607. Similarly, for bacteria, 976,879 high-quality raw sequences with an average length of 415bps were obtained, and the Sobs index was between 2624 and 3236 across all samples. As the sequencing data approached saturation, the species dilution curve leveled, effectively capturing a high proportion of species in the cabbage rhizosphere soil microbial community (*Figure 1*) and achieving 99.00% coverage (*Table 6*). These data are considered as relatively reliable.

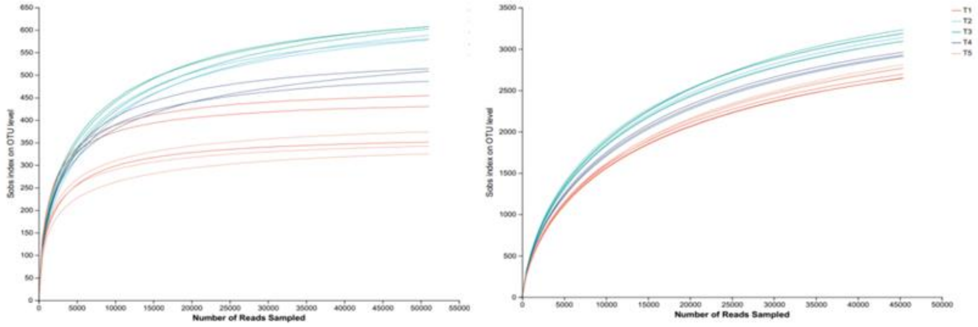

Figure 1. *Effect of different fertilization methods on the exponential dilution curves of fungal and bacterial Sobs (a) Fungal exponential dilution curve (b) Bacterial exponential dilution curve*

Table 6. *Effect of different fertilization methods on α diversity of bacterial and fungal communities in rhizosphere*

Class	Treatments	Shannon	Simpson	Ace	Chao	Coverage
Germ	T1	6.22±0.07a	0.0053±0.0003ab	2617.31±217.07a	2590.64±214.4a	0.99
	T2	6.21±0.03a	0.0056±0.0006a	2700.13±144.03a	2622.41±145.0a	0.99
	T3	6.3±0.04a	0.0048±0.0007bc	2685.22±93.98 a	2622.94±84.27 a	0.99
	T4	6.28±0.09a	0.0046±0.0002c	2554.67±80.78 a	2498.69±72.47 a	0.99
	T5	6.19±0.01a	0.0053±0.0003ab	2620.85±52.92 a	2566.9±44.21 a	0.99
Fungus	T1	4.16±0.01a	0.0388±0.0045a	569.51±91.78a	570.94±93.78a	0.99
	T2	3.82±0.55a	0.0694±0.0418a	623.17±89.14a	619.2±96.02a	0.99
	T3	4.27±0.03a	0.0312±0.003a	698.94±10.86a	695.09±13.9a	0.99
	T4	3.97±0.21a	0.0506±0.0194a	629.31±57.69a	627.63±60.58a	0.99
	T5	4.28±0.14a	0.0388±0.0053a	576.3±85.08a	570.15±80.59a	0.99

Note: The data in the table are mean ± standard error, and different lowercase letters in the same column indicate significant difference (P<0.05)

In this study α Diversity (including Shannon, Simpson, Ace, and Chao1 diversity) can reflect the richness and diversity of soil fungal and bacterial communities. For bacteria, there was no significant difference in Shannon, Ace, and Chao index for each treatment, while the Simpson index of T4 was significantly lower than the other treatments except T3. For fungi, none of the Shannon, Simpso, Ace, and Chao indexes of the five treatments showed significant differences.

The results of the principal component analysis showed that PC1 and PC2 contributed 16.381% / 14.656% (*Figure 2a*) and 15.468% / 14.186%, respectively (*Figure 2b*). Soil bacteria from treatments 5 and 3 were indistinguishable on the PC1 and PC2 axes, indicating that the bacterial microbial communities were similar between the two treatments, without the remaining treated bacteria and fungi. The results showed that different fertilization treatments affected the bacterial community structure in rhizosphere. Soil microbial communities varied between the five fertilization treatments.

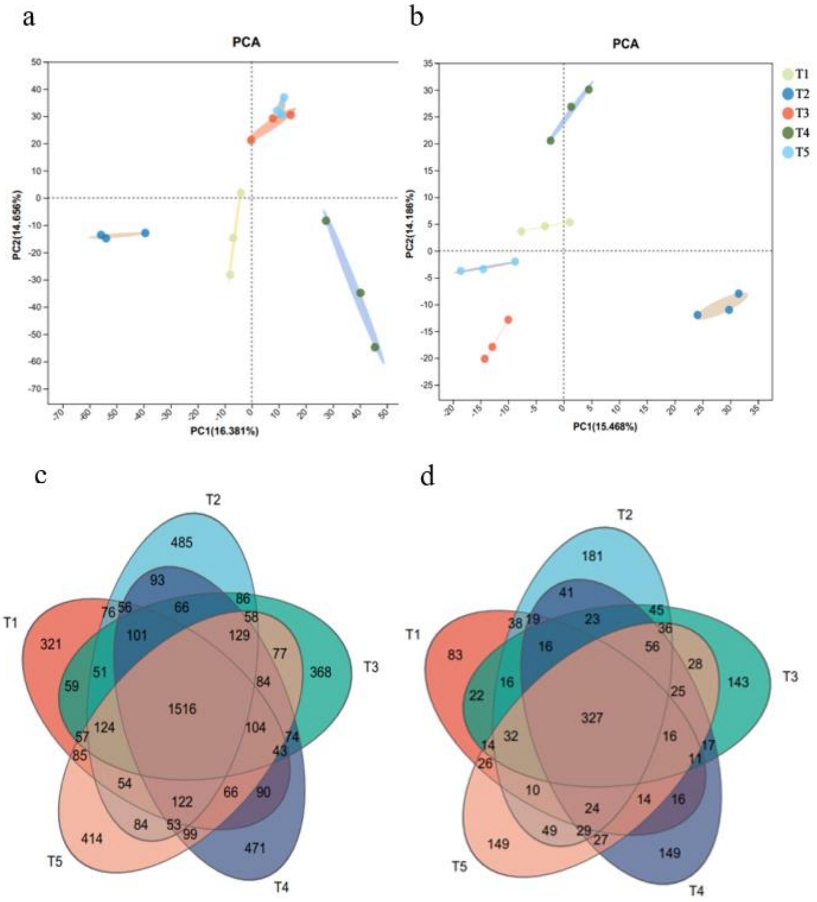

Figure 2. *Effect of different fertilization methods on the similarity and differentiation of fungal and bacterial communities. (a) PCA plot of the bacterial community at the ASV level (b) PCA plot of the fungal community at the ASV level (c) A Venn diagram of bacterial taxa at the genus level (d) A Venn diagram of fungal taxa at the genus level*

The Venn diagram shows that the number of OUT in each samples of bacteria (*Figure 2c*) was 1516, T1, T2, T3, T4, T5, and treatment-specific OUT numbers were 321,485,368,471,414. The number of OUT common to each treatment of the fungus (*Figure 2d*) was 327, and the number of OUT unique to T1, T2, T3, T4, and T5 treatments was 83,181,143,149,149. In the number of bacterial and fungal Feature, compared with no fertilization (T1), except for T5, and T2 and T4 treatment increased the most significant number of bacterial and fungal OUT.

As shown in *Figure 3a*, The predominant bacterial species whose gate-level relative abundance reaches more than 1% in different samples are, The Actinobacteria (Actinobacteriota, 27.88% ~ 30.68%), Chloroflexi (Chloroflexi, Accounted for 19.63% ~ 29.97%), Proteobacteria (Proteobacteria, 14.47% ~ 21.98%), acid bacteria (Acidobacteriota, 9.58%~11.48%), Firmicutes (Firmicutes, 3.78%~5.90%), Budulomonas (Gemmatimonadota, proportion. 3.05%~5.69%). Compared no fertilization, all fertilization treatments increased the relative abundance of Acibacter and Firmicutes in soil, by 1.63%, 2.22%, 1.21% and 2.41%, respectively. Firmicutes increased by 0.65%, 1.88%, 0.89%, and 1.32%, respectively. *Figure 3c* shows that the dominant genera in the taxa are Bryobacter, Sphingomonas, Bradyrhizobium,

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Streptomyces, Conexibacter, and Gemmatimonas. All treatments increased the relative abundance of Bryobacter and Conexibacter and decreased the relative abundance of Streptomyces, Sphingomonas and Gemmatimonas compared to no fertilization (T1).

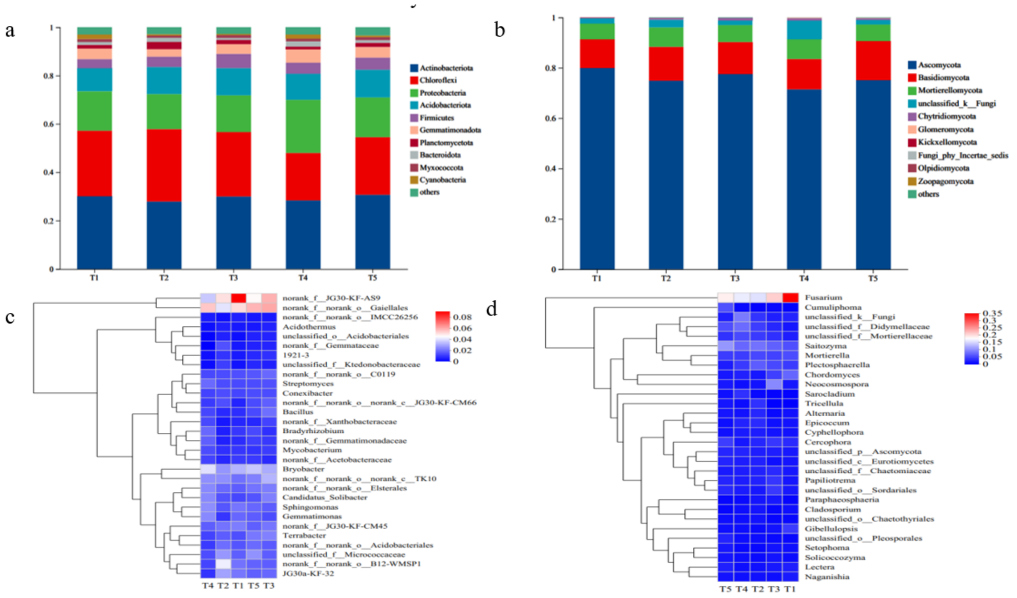

Figure 3. *Effect of different fertilization methods on fungal and bacterial composition in the soil rhizosphere (a) Relative abundance of the bacterial phylum (b) relative abundance of the fungal phylum (c) Heat map of the major bacterial genera (d) Heat map of the major fungal genera*

As can be seen from *Figure 3b*, the dominant fungal group in the soil is Ascomycota (Ascomycota), accounting for more than 70% of the total, followed by Basidiomycota (Basidiomycota 11.38%~15.34%), followed by 𝔵 (Mortierellomycota 6.23%~7.96%). Compared with no fertilization (T1), T2, T3, T4 and T5 all reduced the content of Ascomycota by 5.12%, 2.33%, 8.52% and 4.72%, respectively. Compared without fertilization (T1), all treatments increased the relative abundance of Basidiomycota (Basidiomycota) and Calpha, by 2.07%, 1.20%, 0.68%, and 3.95%, respectively, and by 1.50%, 0.48%, 1.72%, and 0.34%, respectively. As *Figure 3d* shows, the dominant genera in the taxa are Fusarium, Neocosmospora, Saitozyma, Chordomyces, Cercophora, Mortierella, and Plectosphaerella. Compared no fertilization (T1), all treatments reduced the relative abundance of Fusarium, Chordomyces, Mortierella and increased the relative abundance of Saitozyma.

Relationship between soil physicochemical properties and soil microorganisms in the rhizosphere

According to *Table 7*, each index of bacterial Alpha diversity was significantly correlated with soil phosphorus and potassium content, and soil organic matter content was significantly negatively correlated with Simpson index and positively correlated with Shannon index. Each index of fungal Alpha diversity was positively correlated with soil organic matter content, among which Chao1 index and Ace index were both very significantly correlated with organic matter content and with phosphorus and potassium content. The above data analysis showed that the physicochemical properties of Chinese cabbage soil were closely related with the microbial diversity.

Table 7. *Correlation coefficient between soil physicochemical properties and microbial diversity*

Microbe	Diversity coefficient	pH	Organic matter	Hydrolyzable nitrogen	Effective phosphorus	Quick effect potassium
germ	Chao1	0.103	0.49	0.139	0.650**	0.807**
	Simpson	0.049	-0.534*	-0.166	-0.68**	-0.738**
	Shannon	-0.069	0.626*	0.085	0.672**	0.712**
	Ace	0.096	0.499	0.186	0.692**	0.809**
fungus	Chao1	-0.152	0.651**	-0.097	0.534*	0.534*
	Simpson	0.209	0.181	0.117	0.406	0.291
	Shannon	-0.274	0.001	-0.275	-0.378	-0.341
	Ace	-0.144	0.664**	-0.091	0.545*	0.535*

Note: * indicates a significant difference (p <0.05), and * * means that the difference is highly significant (p <0.01)

To investigate the impact of environmental factors from different fertilization treatments on the microbial community composition at the phylum level, redundancy analysis (RDA) was performed to assess the relationship between microbial communities and environmental variables. The results showed that soil physicochemical properties accounted for 37.79% of the variation in the soil bacterial community structure. Specifically, the first and second axes of the RDA explained 21.03% and 16.76% of the changes in the bacterial community structure, respectively (*Figure 4a*). The relative abundance of Actinobacteria, Greenbay, and Firmicutes was significantly positively associated with organic matter, hydrolytic nitrogen, and fast phosphorus, and negatively associated with PH. Proteobacteria and Aciobacteria showed showed significant positive correlation with rapid potassium. The environmental factors that caused the structure of bacterial dominant community were PH, organic matter, hydrolytic nitrogen and effective phosphorus.

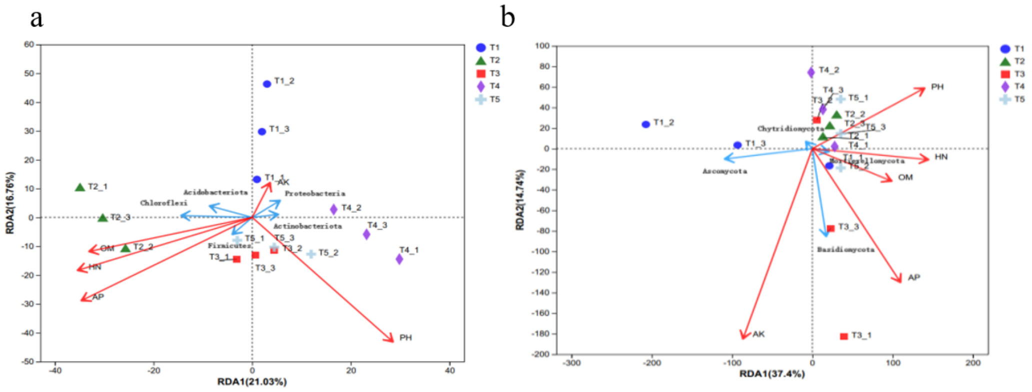

Figure 4. *Effect of soil physicochemical properties on fungal and bacterial composition in the soil rhizosphere. Soil physiochemical properties and predominant bacterial phylum (b) Soil physicochemical properties and predominant fungal phylum*

Soil physicochemical properties collectively explained 52.14% of the changes in soil fungal community structure, and the first and second axes explained 37.4% and 14.74% of the changes in fungal community structure, respectively. The relative abundance of

Ascomycota was positively correlated with fast K, and significantly negatively correlated with PH, organic matter, hydrolytic nitrogen, and fast P (*Figure 4b*), while the relative abundance of Basidiomycota was positively correlated with organic matter, fast K, and effective P, and negatively correlated with PH values. The environmental factors that caused the structure were organic matter and hydrolysis nitrogen, quick potassium, effective phosphorus and PH.

In order to study the influence of different fertilization treatments on the physical and chemical properties of Chinese cabbage, the relationship between microbial community and environmental factors was obtained by redundancy analysis (RDA). The physicochemical properties of cabbage explained 43.84% of the changes in soil bacterial community structure, and the first and second axes explained 26.26% of the changes in bacterial community structure, respectively (*Figure 5a*). Actinobacteria were positively associated with soluble sugars and vitamin C; Green fungi and Proteobacteria were positively associated with soluble protein and nitrate, and negatively associated with vitamin C; the main bacteria in green cabbage and Proteobacteria.

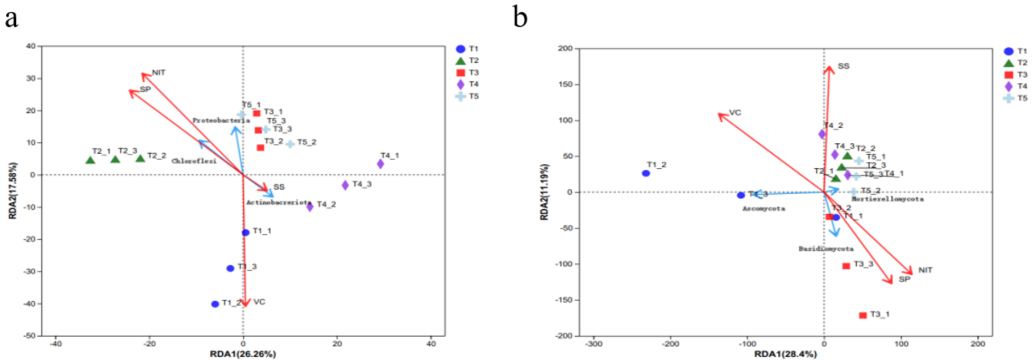

Figure 5. *Effect of fungal and bacterial composition on Chinese cabbage quality in the soil rhizosphere, Physical and chemical properties and dominant bacteria phylum (b) and fungal phylum*

The physical and chemical properties of cabbage explained 39.59% of the structure changes of soil fungal community, and the first and second axes explained 28.4% and 11.19% of the changes of fungal community structure, respectively (*Figure 5b*). The relative abundance of Ascomycota was positively correlated with vitamin C and negatively correlated with soluble protein and nitrate content; Basidiomycetes were positively correlated with hydrolytic protein and nitrate content, and negatively correlated with vitamin C and soluble sugar content. The main bacteria causing the changes in the physicochemical properties of cabbage are ascomycota and basidiomycota.

Correlation analysis of Chinese cabbage quality

According to *Table 8*, the physicochemical properties of Chinese cabbage are closely related to the microbial diversity. The Alpha diversity index of bacteria was negatively associated with the vitamin C content and positively correlated with the soluble sugar content program. The fungal ACE index and Chao1 index were significantly and positively correlated with soluble protein and nitrate content. The above data indicate that microorganisms are closely related to Chinese cabbage quality.

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Table 8. *Correlation coefficient between physicochemical properties and microbial diversity in Chinese cabbage*

Microbe	Diversity coefficient	VC	SS	SP	NIT
germ	Shannon	-0.346	0.411	0.269	0.393
	Simpson	-0.054	0.268	-0.045	-0.076
	Ace	-0.493	0.429	0.386	0.447
	Chao1	-0.496	0.496	0.353	0.415
fungus	Shannon	0.004	0.307	0.078	0.229
	Simpson	0.079	-0.196	-0.179	-0.306
	Ace	-0.5	0.168	0.577*	0.622*
	Chao1	-0.482	0.171	0.549*	0.6*

Note: * indicates a significant difference (p <0.05), and * * means that the difference is highly significant (p <0.01)

For the Spearman correlation analysis between the top ten bacteria and fungi in phyla-level relative abundance and soil physicochemical factors, the results are shown in *Figure 6*. At the level of bacterial phylum (*Figure 6a*), the content of soluble protein and nitrate in Chinese cabbage was positively correlated with chlorenobacteria, Aciobacteria, Firmicutes and Flomold. Blaomonas showed a significant negative correlation with soluble protein content. Acidoacter phylum showed a significant negative correlation with vitamin C content. At the level of fungal phylum (*Figure 6b*), the soluble sugar content was significantly positively correlated with the relative abundance of Balloinococcus (Glomeromycota) and negatively correlated with soluble protein and nitrate content.

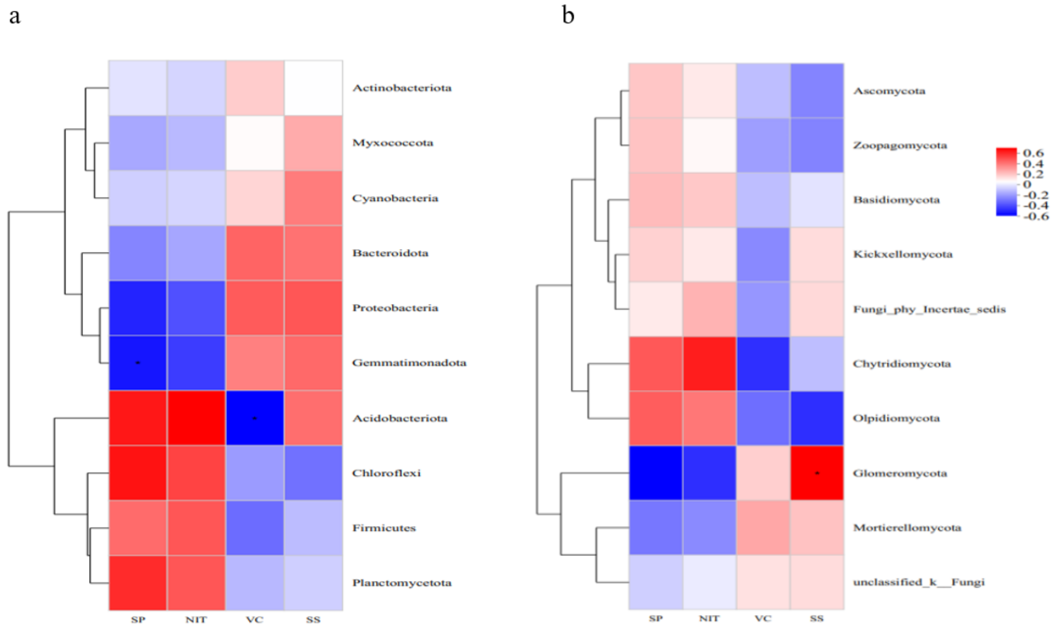

Figure 6. *Effects of fungal and bacterial dominant bacteria on cabbage quality in soil rhizosphere, (A) Physicochemical properties and predominant bacterial phylum (b) Physical and chemical properties and dominant bacterial phylum*

As shown in *Table 9*, the results of the correlation between soil physicochemical properties and cabbage growth showed that the effective phosphorus had a significant negative correlation (P <0.05) and the soluble protein and nitrate content (P <0.05). These results indicate that soil phosphorus content significantly influences cabbage quality.

Table 9. *Correlation between physicochemical properties and soil*

Treatments	**PH**	**Organic matter (g / kg)**	**Hydrolyzed nitrogen HN (mg / kg)**	**Effective Phosphate AP (mg / kg)**	**Quick effect potassium Ak (mg/ kg)**
Vitamin C (mg / 100g)	-0.413	0.134	-0.036	-0.486	-0.318
soluble sugar(%)	0.159	0.27	0.387	-0.667**	-0.616*
soluble protein (%)	0.003	0.192	0.143	0.943**	0.268
Nitrate (mg / kg)	0.131	0.23	0.19	0.944**	0.182

Note: * indicates a significant difference (p <0.05), and * * means that the difference is highly significant (p <0.01)

Discussion

Effects of fertilization and planting patterns on soil nutrient content

Soil quick-acting nutrients are converted from soil organic nutrients under the action of ecology and environment, and it is an important index to evaluate the soil fertilizer supply capacity (Sawyer et al., 2019; Li et al., 2022). Among them, the content of hydrolytic nitrogen and effective phosphorus represent the intensity of nitrogen and phosphorus supply in the soil respectively, and the amount of its content determines the absorption of nitrogen and phosphorus by crops, which is directly related to the growth, quality and yield of crops (Kumar et al., 2019; Li et al., 2022). This study revealed that, compared to T1, the soil content of hydrolytic nitrogen, effective phosphorus, and quick potassium was significantly higher in the other fertilization treatments. This indicates that both the planting method and fertilization strategies, as well as their interaction, had a substantial effect on soil nutrient content.

Effects of different fertilization treatments on soil microbial communities in the rhizosphere of Chinese cabbage

Studies show that an appropriate amount of fertilizer application can increase the diversity of soil bacteria and fungi (Rouphael et al., 2004; Rouphael et al., 2006; Zhang et al., 2019). This study also found that the diversity index (Shannon) and evenness index (Chao1 and Ace) of each fertilization treatment were higher than T1 except for the T5 treatment of fungi, indicating that the microbial diversity of the rhizosphere soil increased, which may be due to the change of the rhizosphere environment after fertilization, which increased the diversity of the soil microbial community compared with the unfertilized treatment. However, the diversity index of T5 treatment fungi decreased compared with T1 treatment, which may be due to the soil compaction caused by changes in the proportion of microbial fertilizer, Cause insufficient oxygen supply, affecting the survival of aerobic microorganisms, resulting in reduced diversity (Sun et al., 2012; Zhang et al., 2019).

In this study, it was found that the dominant bacteria of the rhizosphere bacterial communities in different fertilization treatments were proteobacteria, Actinobacteria, Actinobacteria, Chloranobacteria, Acidibacteria, Budomonas, Bacteroidetes, Firmicutes, and Myxococcus, and similar phenomena were also found in the rhizosphere soil of rice and tea plantations (Xun et al., 2016), This means that even in sandy soil, the dominant bacterial phylum is not unique, but its abundance varies in different fertilization treatments. The relative abundance of Proteobacteria, Budomomonas and Bacteroidetes was higher than that of T1, and the relative abundance of Chlorobacteria was lower than that of T1. The phylum is facultative anaerobic and is widely found in poor soil, While fertilization can cause increased soil fertility, which may be one of the main reasons for the decreased relative abundance of Chlorfungi (Huang et al., 2023; Afzal et al., 2024).

In this study, we found Ascomomycota as the dominant species of fungal communities, together with cucumber plots, Yellow mud field, Oil tea forest (Sun et al., 2021; Li et al., 2022). The rhizosphere soil fungal phylum level dominant bacteria is similar, indicating that ascomycota and basidiomycota have an important position in soil microorganisms. In this study, the relative abundance of Ascomycota in each regions was as high as 68.35 % to 87.00%, together with Ge et al. (2023) and Ahsan et al. (2024). The results of the rhizosphere microbes showed that ascomobacteria is the most dominant bacteria. Most of the fungi under Ascomycota are terrestrial, saprophytic, parasitic and symbiotic, most of which can decompose plant remnants (Peters et al., 2017). Some fungi under the Ascomycota are classified as plant-promoting fungi, which directly promote plant growth, but some fungi are harmful to plants and can cause a variety of diseases (Khalil et al., 2021; Baloch et al., 2024). The fungi under Ascomycota are suitable for survival in fertile and moist soil (Challacombe et al., 2019; Fatemi et al., 2023). The relative abundance of Ascomycota was higher than T1, probably because nitrogen enters the soil with fertilization, and improved soil conditions favor Ascomycota survival. However, the relative abundance of basidiomycota was lower than fertilization treatment T1.

Relationship between soil physico-chemical properties and soil microbes in the rhizosphere of Chinese cabbage in different fertilization treatments

The species and quantity of soil microorganisms are very sensitive to the changes of environmental factors and the response of human disturbance, which can reflect the changes of soil in time (Nannipieri et al., 2017), Soil microbial community structure and diversity are the result of the combination of multiple soil environmental factors. Among them, pH, organic matter, total nitrogen, quick nitrogen, total phosphorus and effective phosphorus content play an important role in the soil microbial diversity in the study area (Roesch et al., 2012), Which indicates that environmental factors are the main factors affecting the diversity of bacterial and fungal communities. In this study, PH showed little association with fungi and bacterial diversity, but Liu et al. (2014). We show that PH and organic matter have significant effects on soil microbial structure and diversity. However, some results show that PH has no significant effect on soil microorganisms (Nie et al., 2018), same as in the present study. This study showed a very significant positive relationship between soil organic matter and microbial diversity index, which is consistent with previous studies (Adams et al., 2020; Xue et al., 2021). This may be because fertilization facilitates the accumulation of aboveground biomass, resulting in increased import of organic matter into the soil, and the increase of organic matter provides better reproductive conditions for the soil flora, ultimately leading to increased microbial diversity. The main environmental factors affecting bacterial community structure in this study were soil effective phosphorus, fast-acting potassium, and organic matter. Studies have confirmed that only soil water and total phosphorus are significantly correlated with the bacterial community (Liu et al., 2016). The possible reason for the partial consistency with previous studies is the difference in soil conditions and the crop varieties planted, and the differences in soil physical and chemical properties between different soils (Su et al., 2014), and different crops roots on soil physical and chemical properties (Ghestem et al., 2011; Hejazi et al., 2025). Thus, bacterial community structure has different responses to soil physicochemical properties.

Conclusion

This study investigates the impact of different fertilization regimes on the amino acid composition of cabbage and the microbial community in the rhizosphere. Using high-throughput sequencing, the research shows that all fertilization treatments, compared to the unfertilized control, significantly improved soil pH, hydrolytic nitrogen, effective phosphorus, organic matter, and available phosphorus content. The microbial diversity was notably influenced by fertilization, affecting the availability of phosphorus, potassium, and organic matter. The bacterial community was dominated by Actinobacteria, Chloroans, Proteobacteria, Acidobacteria, Firmicutes, and Bacteroidetes, with increased relative abundance of Acidobacteria and Firmicutes in fertilized treatments. The fungal community primarily consisted of Ascomycota, Basidiomycota, and Entomophthoromycota, with fertilization reducing Ascomycota levels and boosting Basidiomycota and Zygomycota abundance. Soil pH, organic matter, hydrolytic nitrogen, and effective phosphorus were key factors influencing bacterial composition, while organic matter, hydrolytic nitrogen, available potassium, and pH affected fungal diversity. A strong correlation was observed between soluble protein and nitrate content with microbial diversity. The optimal fertilization strategy, combining high-potassium organic fertilizer (200 kg/m^2), aminobutyric acid (50 g/m^2), and polyglutamate (1 kg/m^2), enhanced soil health by improving organic matter, hydrolytic nitrogen, available phosphorus, and potassium content. This approach not only balanced cabbage quality factors but also increased amino acid content and microbial diversity, making it a promising fertilization method for improving both cabbage quality and soil fertility in local cultivation.

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