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Bioorganic Fertilizer Can Improve Potato Yield by Replacing Fertilizer with Isonitrogenous Content to Improve Microbial Community Composition

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Abstract: The application of bio-organic fertilizers can significantly improve soil fertility and crop yield. This study explored how replacing bio-organic fertilizer with equal nitrogen affected potato quality, yield, and soil microbial diversity after a 4-year positioning experiment. The results showed that the application of bio-organic fertilizer instead of 70% chemical fertilizer could significantly increase potato yield by 10.4–155.4% but had no significant effect on quality. Furthermore, replacing chemical fertilizers with bio-organic fertilizers could decrease the number of soil bacterial species, but it did not influence the diversity of soil bacterial and fungal communities. At the phylum level, bio-organic fertilizer application was directly proportional to the abundance of *Gemmatimonadota* and *Ascomycota*, but inversely proportional to the abundance of *Acidobacteriota* and *Basidiomycota*. At the genus level, *Longimicrobiaceae*, *Lysobacter*, and *Nocardioides* were higher, whereas *Vicinamibacteraceae*, *Gaiella*, and *Solirubrobacter* were lower. *Arthrobacter*, *Parcubacteria*, *Lautropia*, *Luteimonas*, and *Brunneochlamydosporium* were the signatures of bio-organic fertilizer treatment and were positively correlated with the potato yield. Thus, in dry climates with little rainfall, partial substitution of chemical fertilizer with higher bioorganic fertilizers can alter the composition of microbial communities in potato rhizosphere soil, thus significantly improving potato yield.

Keywords: potato; rhizosphere soil; bacterial communities; fungal communities; bioorganic fertilizer

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1. Introduction

Potatoes (*Solanum tuberosum* L.), belonging to the Solanaceae family, are known for their adaptability, are the fourth most important crop in the world after rice, wheat and corn, and are grown in more than 150 countries worldwide [1]. China is the largest producer of potatoes in the world, accounting for 32% (5.8 million hectares) of the world's total area harvest, and 25% (94.4 million tons) of the world's production in 2021 [2]. Nearly 40% of potato cultivation area in China is distributed in northern regions, greatly promoting local food diversification, income, and employment [2]. However, due to the low fertility of the sandy soil, the potato yield in northern China is lower than the world average level [3].

An important measure that can be used to quickly improve soil fertility is the application of manures, such as chemical fertilizers and organic fertilizers [4]. However, excessive application of chemical fertilizers during planting can adversely affect soil ecology and food security. This practice can degrade soil quality, cause nutrient depletion, and lead to elevated nitrite levels in crops [5]. As a result, organic fertilizers, especially bioorganic fertilizers, have recently received a lot of attention as a promising alternative strategy [6,7]. Wang et al.'s [8] study demonstrated that the application of bioorganic

fertilizers can significantly alter the composition of soil microbial communities and increase the levels of available potassium and pH, thereby enhancing the yield of *Brassica chinensis* L. Another study indicated that the integrated use of chemical and bioorganic fertilizers can substantially enhance soil carbon and nitrogen pool reserves, as well as nutrient content. This approach also improves the nutrient uptake efficiency of crops, ultimately leading to increased yields [9]. Nevertheless, the soil improvement effect of the combination of bioorganic fertilizers and chemical fertilizers may be limited by various factors, including soil type, the type of bioorganic fertilizers used, and the application ratio of chemical fertilizers and bioorganic fertilizers [10–12]. These factors make the promotion and application of this improvement measure in production practice challenging. Therefore, it is crucial to seek a combination application method of bioorganic fertilizer and chemical fertilizer with an optimal ratio and easy popularization for potato production.

Microorganisms are pivotal components of soil ecosystems, playing a crucial role in soil nutrient cycling and system stability, which is essential for the sustainability of soil microecology [13]. Furthermore, soil microbial communities supply essential nutrients for crop growth through diverse mechanisms, thereby stimulating crop development and influencing yield [14]. Zhang et al. [15] demonstrated that corn yield and individual plant biomass showed a strong positive correlation with the soil microorganism count. Yin et al. [16] reported that the substitution of organic fertilizer for part of chemical fertilizer significantly promoted potato growth and soil fertility. However, there are few studies on the effect of bioorganic fertilizer substitution on potatoes. Therefore, reasonable fertilization can increase the number of soil microorganisms and soil enzyme activity, effectively promote soil fertility and nutrients required for crop growth, and achieve the result of an increased crop yield.

Bioorganic fertilizers, collections of organic fertilizers and probiotic microorganisms, not only activate various microorganisms in soil, but also play an increasingly pivotal role in promoting crop production, restoring soil fertility, and inhibiting soil diseases [17]. Shi et al. [18] showed that bioorganic fertilizers significantly enhance soil health by mitigating soil acidification and enriching organic matter. These treatments also promote the establishment of specific rhizosphere microbiota, alter soil metabolic functions, and facilitate nutrient cycling and disease resistance in *Panax notoginseng*. Another study demonstrated that long-term application of bioorganic fertilizers could increase biocontrol bacteria (such as *Lecanicillium*, *Xanthomonadales*, *Pseudomonas*, *Ilyonectria*, *Lysobacter*, and *Bacillus*) and reduce harmful bacteria (*Acidobacteria*, *Sphaerobacter*, and *Chloroflexi*) to enhance the activity of catalase and invertase in soil, thereby boosting the yield of apples [19]. In addition, organic fertilizers can also influence the functions of microorganisms. It has been reported that organic nitrogen fertilizers increased nitrogen mineralization, ammonification, and nitrification, and that they enhanced the activity of ammonia-oxidizing bacteria and archaea [20]. However, the impact of bioorganic fertilizer substitution with equal nitrogen inputs on potato quality, yield, and soil microecological environment are still unclear.

Gansu is a major potato producing province, but its low soil fertility is an existing problem limiting the potato yield [21]. Mackiewicz and Lori et al.'s [22,23] studies have proved that fertilization can improve soil microbiota and soil nutrients, thereby achieving the goal of increasing crop yields. However, the response of soil microbial diversity in the potato rhizosphere to the replacement of bioorganic fertilizers with equal amounts of N sources has not been reported. In this study, gradient experiments on four mixed ratios of chemical fertilizers and bioorganic fertilizers were carried out in arid or semi-arid loamy soil to evaluate the quality, yield, and soil microbial characteristics of potato, mainly aiming to address the following problems: (1) identifying the optimal mixed ratio of bioorganic fertilizers and chemical fertilizers under equal nitrogen inputs; (2) determining the effects of different mixed ratios of bioorganic fertilizers and chemical fertilizers on potato yield and quality; and (3) analyzing the roles of different mixed ratios of bioorganic fertilizers and chemical fertilizers in the diversity and distribution of bacterial and fungal communities in potato rhizosphere soil. These research results will contribute to the scientific application of

bioorganic fertilizers, and in turn will help protect the ecological environment and ensure the safety of agricultural products.

2. Materials and Methods

2.1. Overview of Experimental Sites

The experiment was conducted at the National Soil Quality Anding Observation and Experiment Station (35°47′ N, 104°60′ E) of Gansu Academy of Agricultural Sciences, Dingxi, Gansu, China from 2020 to 2023. The annual precipitation of 420 mm, mainly concentrated in July to September. The annual average evaporation was 1530 mm, the frost-free period was 140 d, and the accumulated temperature of ≥10 °C was only 2075 °C. The soil texture in the experimental sites was loamy soil with a pH of 8.21, soil organic matter of 7.5 g kg^{-1}, total nitrogen of 0.73 g kg^{-1}, total phosphorus of 0.67 g kg^{-1}, total potassium of 19.9 g kg^{-1}, available nitrogen of 15.12 mg kg^{-1}, and available potassium of 174.81 mg kg^{-1}. Additionally, the effective rainfall in the potato growing season was 286.92 mm.

2.2. Experimental Design

Long-term positioning experiments have been deployed since 2020. In our field experiments, a single-factor completely randomized block design was adopted, and four groups were set up (n = 3 for each group), as follows: CK0 (without chemical fertilizer and organic fertilizer), CK1 (single application of chemical fertilizer with optimal nitrogen application), OFL (70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen), and OFH (30% chemical nitrogen fertilizer with 70% bioorganic fertilizer nitrogen) (Table 1). The area of the experimental plot is 42 m^2. The fertilizer for each treatment group was uniformly applied to the soil as a base dressing concurrently. In order to be consistent with conventional N fertilizer substitution methods, bioorganic fertilizer use was estimated as required. The chemical fertilizer contained urea (N 46%), superphosphate (P_2O_5 16%), and potassium sulfate (K_2O 50%). Bioorganic fertilizers, comprising cow manure and sheep manure, were sourced from Shanxi Boqin Biological Engineering Co., Ltd., located in Sanyuan, Shanxi, China. These fertilizers are characterized by a high organic matter content of at least 40%, nitrogen levels of no less than 4%, and an effective viable bacterial count exceeding 0.2 million g^{-1}. The ratio of cattle and sheep manure to bacterial agent was 100:1 to make bioorganic fertilizer. Cattle and sheep dung from Wuzhong, Ningxia, China, possessed the following values: soil organic matter (7.5 g kg^{-1}), total nitrogen (0.73 g kg^{-1}), total potassium (19.9 g kg^{-1}), total phosphorus (0.67 g kg^{-1}), fast-acting potassium (174.81 mg kg^{-1}), fast-acting nitrogen (15.12 mg kg^{-1}), and pH (8.21). The application amount of phosphorus and potassium fertilizer in all treatment groups was consistent.

Table 1. The amount of fertilizer in each group.

Group	Treatment	The Amount of Fertilizer (kg ha^{-1})			
		N	P_2O_5	K_2O	Bioorganic Fertilizer
CK0	Without chemical nitrogen fertilizer and organic fertilizer	0	0	0	0
CK1	Single application of chemical nitrogen fertilizer with optimal nitrogen application	180	90	90	0
OFL	70% chemical nitrogen fertilizer with 30% bioorganic fertilizer nitrogen	126	90	90	1325
OFH	30% chemical nitrogen fertilizer with 70% bioorganic fertilizer nitrogen	54	90	90	3150

CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen.

The potato variety tested was "Qingshu No.9", and this was provided by the green field potato farmers' professional cooperative in Dingxi, Gansu, China. The potato seeds were sown on 25 April and harvested on 20 October. This study employed a full-film-covered ridge and furrow planting, characterized by a ridge width of 60 cm, a furrow width

of 40 cm, and a band width of 100 cm. Potatoes were cultivated on both sides of the ridge at a density of 49,500 plants ha^{-1}.

2.3. Determination of Soil Physical and Chemical Properties

In 2020, soil samples were collected from each treatment for analysis of pH, organic matter, total nitrogen, total potassium, total phosphorus, available potassium, and available nitrogen, with three replicates for each treatment.

The determination of soil pH was conducted using a pH meter (pH-3C, Shanghai Yidian Scientific Instrument Co., Ltd., Shanghai, China) by directly inserting the pH meter electrode into the soil suspension to measure the acidity or alkalinity of the soil [24].

The content of soil organic matter was determined by the dichromate oxidation method [25]. In simple terms, soil samples were mixed with 0.8 M potassium dichromate solution and heated under acidic conditions with 96% sulfuric acid for digestion, followed by the determination of the remaining dichromate concentration using a UV spectrophotometer (UV-48025, Jiangsu Changcan Photoelectric Technology Co., Ltd., Wuxi, China), from which the organic matter content was calculated.

Total nitrogen was measured using the semi-micro Kjeldahl method [26]. This method involves mixing soil samples with 96% sulfuric acid and a catalyst, heating to digest and convert organic nitrogen to ammonia, then absorbing the ammonia with a boric acid solution, and finally determining the concentration of ammonia by titration using a Kjeldahl nitrogen analyzer (K9840, Haineng Future Technology Group Co., Ltd., Jinan, China).

Total potassium was determined by the alkali fusion–flame photometry method [27], which involves mixing soil samples with an alkaline flux, fusing at high temperatures, and then measuring the potassium concentration using a flame photometer (M410, SHERWOOD Company, Cambridge, UK).

Total phosphorus levels were ascertained employing the molybdenum blue spectrophotometry technique, as referenced in [26]. This procedure entails the combination of soil samples with molybdate and a reducing agent to produce a molybdenum blue complex, followed by the quantification of its concentration utilizing a spectrophotometer (UV-48025, Jiangsu Changcan Photoelectric Technology Co., Ltd., Wuxi, China).

Available potassium was measured using the flame photometry method (M410, SHERWOOD Company, Cambridge, UK) [27], which is a method for directly determining the concentration of soluble potassium ions in the soil.

Available nitrogen was determined by the diffusion absorption method, which involves contacting soil samples with an alkaline solution to allow ammoniacal nitrogen to diffuse into the alkaline solution, and then measuring the concentration of ammonia using a UV spectrophotometer (UV-48025, Jiangsu Changcan Photoelectric Technology Co., Ltd., Wuxi, China) [26].

2.4. Determination of Plant Height

Ten potato plants were randomly selected from each replicate, and plant height (cm) was measured using a ruler. These measurements were recorded at harvest time (20 October). After measurement and recording, the mean of five randomly selected plants was determined as a replicate.

2.5. Determination of Potato Yield

At harvest time (20 October), potatoes were harvested from each plot and weighed; yield data from each plot were recorded in detail, and statistical analysis was performed to assess the level of potato production. The number of potatoes, weight of potatoes, number of large potatoes, number of medium potatoes, and number of small potatoes were determined as follows.

Number of potato determination: In each treatment, 10 potato plants were randomly selected, and each potato plant was fully harvested, and the potato number of 10 plants was calculated. Weight of potato determination: The tubers harvested from 10 plants were

weighed to record the total weight of tubers. Number of large potatoes determination: The harvested tubers were categorized by weight, with large tubers defined as those exceeding 150 g in weight. The number of large tubers per 10 plants was counted. Number of medium potato determination: Medium tubers typically refer to those weighing between 100 g and 150 g. The number of medium tubers per 10 plants was counted. Number of small potato determination: Small tubers are those weighing less than 100 g. The number of small tubers per 10 plants was counted.

2.6. Determination of Potato Quality

At harvest time (20 October), the quality of potatoes was assessed for 10 strains per treatment. The process began with the thorough cleaning of the sample container and measurement window. Subsequently, we filled the designated container with peeled and diced potato samples, ensuring a minimum thickness of 1 cm at the bottom to maintain a uniform layer. The container, now laden with samples, was positioned within the measurement window, and the DS2500 Iris was employed for analysis.

Utilizing a near-infrared spectrum analyzer (DS 2500, FOSS Co., Ltd., Hillerød, Denmark), we captured the sample spectrum and then translated the spectral data into detailed chemical composition information. This included the percentage of water content, protein content, and starch content, as well as the concentration of various minerals and vitamins in milligrams per kilogram: water content (%), protein content (%), starch content (%), calcium content (mg kg^{-1}), iron content (mg kg^{-1}), fiber content (%), potassium content (mg kg^{-1}), magnesium content (mg kg^{-1}), reducing sugar content (%), vitamin C content (mg kg^{-1}), and zinc content (mg kg^{-1}) among others. These conversions were facilitated by pre-established calibration models.

Ultimately, we developed and validated a prediction model using partial least squares regression to ensure the precision and reliability of our measurement outcomes.

2.7. 16S rRNA Gene Sequencing and Internal Transcribed Spacer (ITS) Sequencing

During the tuber swelling stage of the potato plants, soil closely attached to potato roots (<2 mm) was collected as rhizosphere soil. The rhizosphere soil of 6 holes of potato plants in each plot was evenly mixed as a soil sample, and 3 soil samples were harvested for each treatment group. The collected soil samples were stored at −80 °C until subsequent sequencing.

The soil samples in the CK0, CK1, OFL, and OFH groups were subjected to Personalbio Technology Co., Ltd. (Shanghai, China) for 16S rRNA gene sequencing and ITS sequencing. In brief, the total DNA was extracted from soil by the OMEGA Soil DNA Kit (cat. no. D5625-01, Omega Bio-Tek, Norcross, GA, USA) based on the protocols of the manufacturer, and then qualified and quantified by an ultraviolet spectrophotometer and 0.8% agarose gel electrophoresis, respectively. After that, one group of DNA samples was amplified with the primers of the V3-V4 region of 16S rRNA gene (338F: 5′-barcode+ACTCCTACGGGAGGCAGCA-3′; 806R: 5′-GGACTACHVGGGTWTCTAAT-3′), while another group of DNA samples were amplified with the primers of the V1 region of ITS (F: GGAAGTAAAAGTCGTAACAAGG; R: GCTGCGTTCTTCATCGATGC). The PCR amplified products were submitted for 2% agarose gel electrophoresis, and then recovered and purified using a gel recovery kit from AXYGEN. Thereafter, the recovered products were quantified by a Quant-iT PicoGreen dsDNA Assay Kit on a microplate reader (FLx800, BioTek, Winooski, VT, USA), and then pooled into equal amounts. Subsequently, the TruSeq Nano DNA LT Library Prep Kit was employed for preparation of sequencing libraries, and an Agilent High Sensitivity DNA Kit was applied to evaluate the prepared sequencing libraries on an Agilent bioanalyzer. A Quant-iT PicoGreen dsDNA Assay Kit with the Promega QuantiFluor system was used to quantify the prepared libraries. Finally, for the qualified libraries, the Illlumina NovaSeq platform with a NovaSeq 6000 SP Reagent Kit (500 cycles) was employed for 16S rRNA gene sequencing and ITS sequencing.

2.8. Sequencing Data Analysis

The sequencing data were analyzed using the QIIME2 software (version 2019.4) and R language (version 3.2.0). Briefly, the sequencing original data were quality filtered, denoised, merged, and chimera were removed using the DATA2 method, and unique amplicon sequence variants (ASVs) were generated. Subsequently, utilized the classify-sklearn algorithm to annotate amplicon sequence variants (ASVs) derived from 16S rRNA gene sequencing with the Greengenes reference database classifier (version 13.8) and from ITS sequencing with the UNITE reference database classifier (version 8.0). Then, the alpha diversity. including Chao1, observed species, Shannon, Simpson, Faith's PD, Pielou's evenness and Good's coverage was calculated in the QIIME2 software. The differentially presented bacterial taxa in the different groups were assessed by PERMANOVA (permutational multivariate analysis of variance) using QIIME2, and the crucial phyla/genera in the groups were identified using linear discriminant analysis effect size (LEfSe) analysis in the QIIME2 software. Finally, the biological functions of the identified soil microbial communities were predicted using the PICRUSt2 software 2.5.3, and analyzed using the metagenomeSeq package in R software (version 3.3.1). Ultimately, the correlation between the top 50 bacterial and fungal genera, as well as key genera identified by LEfSe analysis, and the yield, weight of potato, or quality of potatoes, was assessed using Spearman's rank correlation coefficient.

2.9. Statistical Analysis

The data are reported as the mean ± standard deviation of three replicates. All statistical analyses were conducted using IBM SPSS Statistics 27 (SPSS, Chicago, IL, USA). For comparisons among multiple groups, an analysis of variance (ANOVA) was conducted, supplemented by Duncan's multiple range test. A p-value less than 0.05 was considered to indicate a statistically significant difference.

3. Results

3.1. Precipitation and Temperature

From 25 April–20 October 2020, the total precipitation was 452.2 mm, with an average temperature of 14.6 °C. From 25 April–20 October 2021, the total precipitation was 311.6 mm, with an average temperature of 15.4 °C. From 25 April–20 October 2022, the total precipitation was 208.2 mm, with an average temperature of 16.2 °C. From 25 April–20 October 2023, the total precipitation was 286.92 mm, with an average temperature of 15.8 °C (Figure S1). These data suggest that the experimental sites experienced reduced rainfall and a dry climate during the potato growing season in 2022 and 2023.

3.2. Effects of Different Fertilizing Methods on Potato Yield, Agronomic Traits, and Quality of Potatoes

Different fertilization methods had significant effects on potato agronomic traits and yield. It was found the potato yields in the CK0, CK1, OFL, and OFH groups were, respectively, 8115 ± 693 kg ha^{-1}, 9918 ± 1434 kg ha^{-1}, 14,787 ± 2481 kg ha^{-1}, and 20,724 ± 2748 kg ha^{-1} in 2023, which indicated that the application of alternative bioorganic fertilizers significantly enhanced the potato yield compared to the CK0 and CK1 groups ($p < 0.05$), with the highest for OFH, followed by OFL (Table 2). The optimal results from the OFH treatment were notably observed during the period of 2022–2023. In this timeframe, the OFH treatment demonstrated a significant increase in yield compared to the CK0 treatment, with enhancements of 68.2% and 155.4%, respectively. When contrasted with the CK1 treatment, the OFH treatment registered a significant increase of 10.4% and 109.0%, respectively. The OFL treatment, in comparison to the CK0 treatment, showed a significant increase of 51.93% and 82.22%, respectively. However, when compared with the CK1 treatment, the OFL treatment resulted in a significant increase of 49.09%, yet experienced a slight decrease of 0.26% in 2022 (Figure 1). As detailed in Table 2, in comparison with CK0, the CK1 treatment led to increases in plant height, number of potatoes, weight of potatoes,

and number of medium potatoes by 2.44%, 30.77%, 24.04%, and 53.33%, respectively. Under the OFL treatment, these parameters increased by 8.12%, 30.77%, 92.85%, and 53.33%, respectively. The OFH treatment yielded even more substantial increases, with 16.32%, 50.0%, 175.88%, and 146.67%, respectively. These findings suggest that the application of higher amounts of alternative bioorganic fertilizers (3150 kg ha^{-1}) could significantly boost potato yield and enhance the agronomic characteristics of potato plants.

Table 2. Effects of different fertilization methods on the agronomic characteristics of potatoes.

Treatments	Plant Height (cm)	Number of Potatoes (No 10 holes^{-1})	Weight of Potatoes (g 10 holes^{-1})	Number of Large Potatoes (No 10 holes^{-1})	Number of Medium Potatoes (No 10 holes^{-1})	Number of Small Potatoes (No 10 holes^{-1})
CK0	57.3 ± 0.42 ^{b}	26 ^{a}	1252 ± 15 ^{c}	0 ^{c}	7 ^{b}	19 ^{a}
CK1	58.7 ± 6.36 ^{b}	34 ^{a}	1553 ± 139 ^{c}	0 ^{c}	12 ^{ab}	22 ^{a}
OFL	61.95 ± 4.65 ^{ab}	34 ^{a}	2415 ± 363 ^{b}	2 ^{b}	19 ^{a}	13 ^{a}
OFH	66.65 ± 1.25 ^{a}	39 ^{a}	3454 ± 458 ^{a}	7 ^{a}	18 ^{a}	14 ^{a}

CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen. Different lowercase letters in the table indicated significant differences among fertilization treatments ($p < 0.05$).

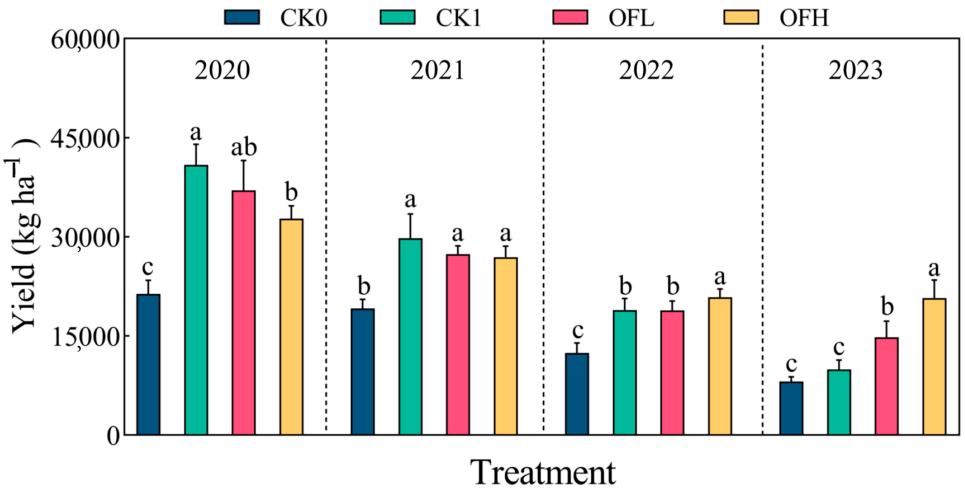

Figure 1. Effects of different amounts of bioorganic fertilizer substitution on potato yield. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen. Different lowercase letters in the figure indicate significant differences among fertilization treatments ($p < 0.05$).

After that, the effects of different fertilizing methods on the quality of potato were analyzed. The results showed that the water, calcium, magnesium, reducing sugar, and vitamin C of CK1-treated plants increased by 2.16%, 22.90%, 4.72%, 14.17%, and 0.35, respectively, compared with CK0-treated plants. Under OFL treatment, these factors increased by 1.19%, 28.09%, 0.15%, 22.50%, and 6.27, respectively. Under OFH treatment, these factors increased by 1.10%, 19.16%, 7.32%, 21.67%, and 5.76, respectively ($p > 0.05$, Table 3). These results suggest that the four different fertilization methods did not significantly affect the quality of the potatoes.

Table 3. Effect of different fertilization methods on potato quality.

Treatments	CK0	CK1	OFL	OFH
Water (%)	80.90 ± 0.78 [a]	2.65 ± 1.07 [a]	81.86 ± 1.73 [a]	81.79 ± 0.30 [a]
Protein (%)	2.36 ± 0.39 [a]	2.45 ± 0.24 [a]	2.26 ± 0.45 [a]	2.30 ± 0.49 [a]
Starch (%)	14.76 ± 1.73 [a]	14.13 ± 0.37 [a]	13.49 ± 1.05 [a]	14.24 ± 0.56 [a]
Calcium (mg kg^{-1})	115.70 ± 36.60 [a]	142.20 ± 23.55 [a]	148.20 ± 1.69 [a]	137.89 ± 27.98 [a]
Iron (mg kg^{-1})	18.37 ± 5.99 [a]	17.07 ± 1.03 [a]	18.83 ± 3.51 [a]	17.20 ± 1.53 [a]
Fiber (%)	0.96 ± 0.14 [a]	0.88 ± 0.03 [a]	0.90 ± 0.09 [a]	0.84 ± 0.04 [a]
Potassium (mg kg^{-1})	4118.17 ± 533.15 [a]	3700.50 ± 106.35 [a]	3819.13 ± 434.65 [a]	4115.27 ± 218.40 [a]
Magnesium (mg kg^{-1})	129.87 ± 21.13 [a]	136.00 ± 7.11 [a]	130.07 ± 8.38 [a]	139.37 ± 7.82 [a]
Reducing sugar (%)	0.40 ± 0.16 [a]	0.46 ± 0.17 [a]	0.49 ± 0.05 [a]	0.49 ± 0.11 [a]
Vitamin C (mg kg^{-1})	123.33 ± 31.51 [a]	123.77 ± 15.11 [a]	131.07 ± 23.77 [a]	130.43 ± 23.47 [a]
Zinc (mg kg^{1})	54.70 ± 3.50 [a]	54.50 ± 3.18 [a]	51.03 ± 4.69 [a]	55.97 ± 1.83 [a]

CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen. Different lowercase letters in the table indicated significant differences among fertilization treatments ($p < 0.05$).

3.3. Effects of Different Fertilizing Methods on the Overall Structure of Soil Bacterial Communities Through 16S rRNA Gene Sequencing

In order to understand the response of potato rhizosphere soil microbial communities to bioorganic fertilizer substitution, 16S rRNA gene sequencing and ITS sequencing were performed on the potato rhizosphere soil with different fertilizing methods. Based on the results of 16S rRNA gene sequencing, a total of 4376 ASVs, 3791 ASVs, 4142 ASVs. and 3633 ASVs were observed in the CK0, CK1, OFL, and OFH groups, respectively, with 1414 overlapped ASVs (Figure 2A). Principal coordinate analysis (PCoA) showed that the samples in each group were better clustered, and the four different groups could be distinguished from each other at the PCo1 level (Figure 2B). Additionally, the Good's coverage indexes in the CK0, CK1, OFL, and OFH groups were, respectively, 0.993 ± 0.001, 0.994 ± 0.001, 0.994 ± 0.0004, and 0.996 ± 0.0003, which suggested that the sequencing results of each sample basically covered all of the soil bacterial communities. All these results implied a high depth and reliability of the sequencing results, which could be employed for subsequent analysis.

Subsequently, the α-diversity indices for the CK0, CK1, OFL and OFH groups were determined, encompassing metrics such as Chao1, Simpson, Pielou's evenness, Faith's PD, Shannon, and observed species values. The analysis revealed no significant disparities in the Chao1, Simpson, Pielou's evenness, Faith's PD, and Shannon among the CK0, CK1, OFL, and OFH groups ($p > 0.05$). However, the observed species count in the OFH group was significantly lower than that in the CK0 group ($p = 0.049 < 0.05$, Figure 2C). These findings indicate that the application of higher rates of alternative bioorganic fertilizers (3150 kg ha^{-1}) could lead to a notable decrease in species richness within the rhizosphere soil of potatoes, while not impacting the other α-diversity indices such as Chao1, Simpson, Pielou's evenness, Faith's PD, or Shannon.

3.4. Effects of Different Fertilizing Methods on the Specific Soil Bacterial Communities

After analyzing the diversity of soil bacterial communities in the different groups, we further investigated the impacts of different fertilizing methods on the specific soil bacterial communities at the phylum and genus levels. From the aspect of the phylum level, the annotated ASVs primarily belonged to *Proteobacteria*, *Gemmatimonadota*, *Actinobacteriota*, *Acidobacteriota*, and *Chloroflexi* (Figure 2D). Among the groups, the relative abundance of *Proteobacteria* was approximately 26.12% in CK0, 28.26% in CK1, 25.50% in OFL, and 27.87% in OFH. The *Gemmatimonadota* abundance in the CK0, CK1, OFL, and OFH groups was, respectively, 19.01%, 20.02%, 22.57%, and 23.29%; the *Acidobacteriota* abundance in the CK0, CK1, OFL, and OFH groups was approximately 15.02%, 11.32%, 8.52%, and 7.53%, respectively. These results indicated that the application of fertilizers increased

the abundance of *Gemmatimonadota* and decreased the abundance of *Acidobacteriota*, with particularly notable effects in the OFH group.

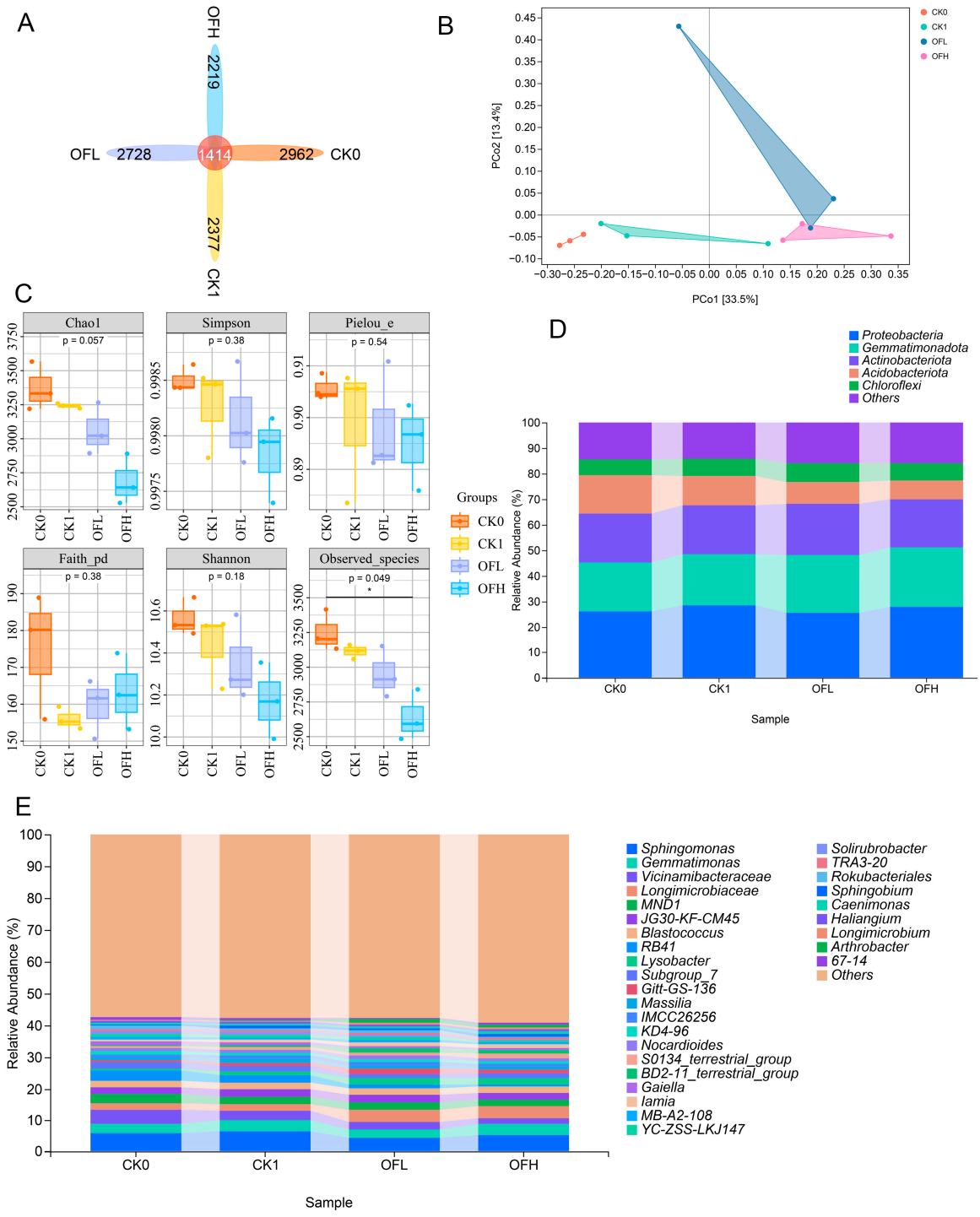

Figure 2. Effects of different fertilizing methods on the overall composition of soil bacterial communities through 16S rRNA gene sequencing. (**A**) The Venn diagram of the annotated soil bacterial communities (ASVs) in the different groups. (**B**) The principal coordinate analysis of the samples in the different groups. (**C**) The α-diversity of the soil bacterial communities, including Chao1, Simpson, Pielou's evenness, Faith's PD, Shannon, and observed species values in the different groups. (**D**) The distribution of top5 dominant phyla of soil bacterial communities in the different groups. (**E**) The distribution of top30 dominant genera of soil bacterial communities in the different

groups. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen. Significant levels at $p < 0.05$ were indicated by *.

At the genus level, top30 soil bacterial genera were displayed, including *Sphingomonas*, *Gemmatimonas*, *Vicinamibacteraceae*, *Longimicrobiaceae*, *MND1*, *JG30-KF-CM45*, *Blastococcus*, *RB41*, *Lysobacter*, *Gitt-GS-136*, *Massilia*, *Nocardioides*, *Gaiella*, *Solirubrobacter*, and *Arthrobacter* (Figure 2E). The *Sphingomonas* abundance in the CK0, CK1, OFL, and OFH groups was, respectively, 6.06%, 6.59%, 4.43%, and 5.36%, while the *Gemmatimonas* abundance in the CK0, CK1, OFL, and OFH groups was 2.86%, 3.47%, 2.77% and 3.47%, respectively. The abundance of *Vicinamibacteraceae* was highest in the CK0 group (4.56%), followed by the CK1 (2.94%), OFL (2.36%), and OFH (1.86%) groups, whereas the abundance of *Longimicrobiaceae* was higher in the OFH (3.85%) and OFL (3.94%) groups, followed by the CK1 (2.01%) and CK0 (1.82%) groups. Furthermore, compared with the CK0 group, the abundance values of *MND1*, *RB41*, *Gaiella*, and *Solirubrobacter* were lower, whereas the abundance values of *Lysobacter*, *Gitt-GS-136*, *Nocardioides*, and *Arthrobacter* were higher, in the other three groups, especially in the OFH group. These indicated that the application of bioorganic fertilizers could increase the abundance of *Longimicrobiaceae*, *Lysobacter*, *Gitt-GS-136*, *Nocardioides*, and *Arthrobacter*, but such a treatment could decrease the abundance of *Vicinamibacteraceae*, *MND1*, *RB41*, *Gaiella*, and *Solirubrobacter*.

LEfSe analysis employed to identify biomarkers across various groups and taxonomic levels. At the phylum level, *Acidobacteriota*, *Entotheonellaeota*, and *MBNT15* were specific to the CK0 group (Figure 3A). Delving into the genus level, *Subgroup-10*, *Vicinamibacteraceae*, *Entotheonellaceae*, *MBNT15*, and *SC-I-84* emerged as the defining bacterial communities characteristic of the CK0 group. In contrast, the OFL group was notably marked by the presence of *BD2-11-terrestrial-group* and *Methylobacillus* as key genera. Meanwhile, the OFH group was distinguished by significant genera such as *Arthrobacter*, *Parcubacteria*, *Lautropia*, *Luteimonas*, and *Allorhizobium-Neorhizobium-Parahizobium-Rhizobium* (Figure 3A).

The functions of the identified soil communities were then investigated, and it was observed that these soil bacterial communities were related to "cell motility", "membrane transport", "replication and repair", "amino acid metabolism", "carbohydrate metabolism", "glycan biosynthesis and metabolism", "lipid metabolism", "metabolism of cofactors and vitamins", and "metabolism of terpenoids and polyketides" functions (Figure 3B). Then, the metagenomeSeq method was employed to determine the significantly different metabolic pathways among the different groups. In the comparison group of OFL and CK0, ko03022 (basal transcription factors), ko04144 (endocytosis), and ko04976 (bile secretion) were the differential functional pathways. Additionally, ko00622 (xylene degradation) and ko04974 (protein digestion and absorption) were the differentially expressed pathways between the OFH and CK0 groups (Figure 4). The differential functional pathways between the OFH and CK1 were ko04621 (NOD-like receptor signaling pathway), ko04320 (dorsoventral axis formation) and ko04310 (Wnt signaling pathway). Additionally, ko03022 (basal transcription factors) and PWY-5507 (adenosylcobalamin biosynthesis I (early cobalt insertion)) were, respectively, the differential functional pathways in the comparison groups of OFL vs. CK1 and OFH vs. OFL (Figure 4).

3.5. Effects of Different Fertilizing Methods on the Overall Structure of Soil Fungal Communities Through ITS Sequencing

ITS sequencing results displayed that 447 ASVs, 424 ASVs, 394 ASVs, and 408 ASVs were, respectively, found in the CK0, CK1, OFL and OFH groups, and that there were 118 overlapped ASVs in the 4 groups (Figure 5A). The PCoA results displayed that the values of PCo1 and PCo2 were, respectively, 11% and 10.6%, and the samples in each group were not significantly separated from each other (Figure 5B). Additionally, the Good's coverage index of each group was about 0.99998, which reflected that the sequencing results of each sample basically included all the soil fungal communities. Thereafter,

theα-diversity parameters (Chao1, Simpson, Pielou's evenness, Shannon, and observed species) of the soil fungal communities in the different groups were calculated. As shown in Figure 5C, no significant differences were observed in the indexes of Chao1, Simpson, Pielou's evenness, Shannon, and observed species among the CK0, CK1, OFL, and OFH groups ($p > 0.05$), which reflected that the application of fertilizers (CK1, OFL, and OFH) could not significantly influence the α-diversity of potato soil fungal communities.

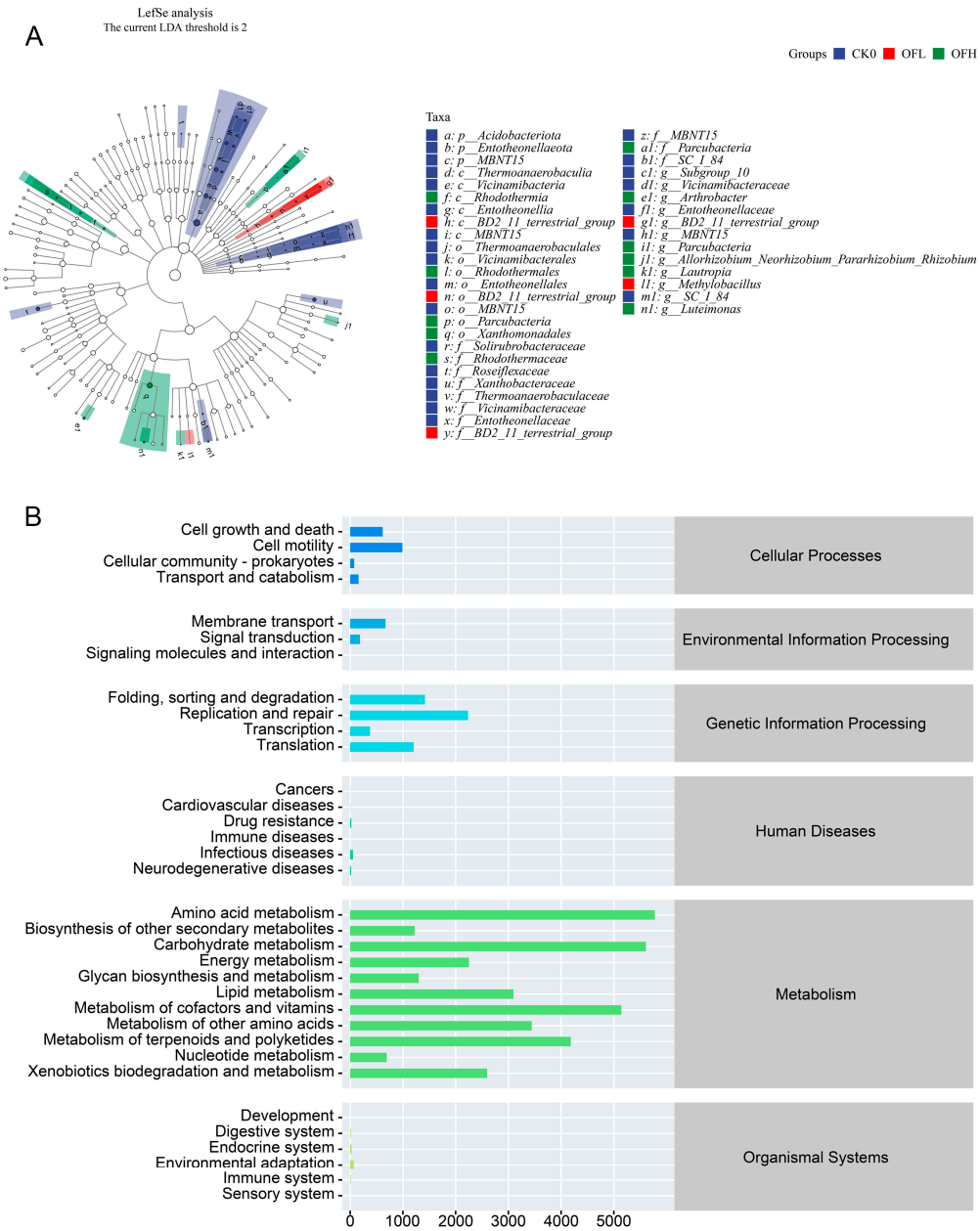

Figure 3. Identification of the soil bacterial biomarkers among the different groups and functional analysis of the identified soil bacterial communities. (**A**) The biomarkers of bacterial communities in the different groups using linear discriminant analysis effect size (LEfSe) analysis at different levels. (**B**) The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways predicted by the identified soil bacterial communities. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen.

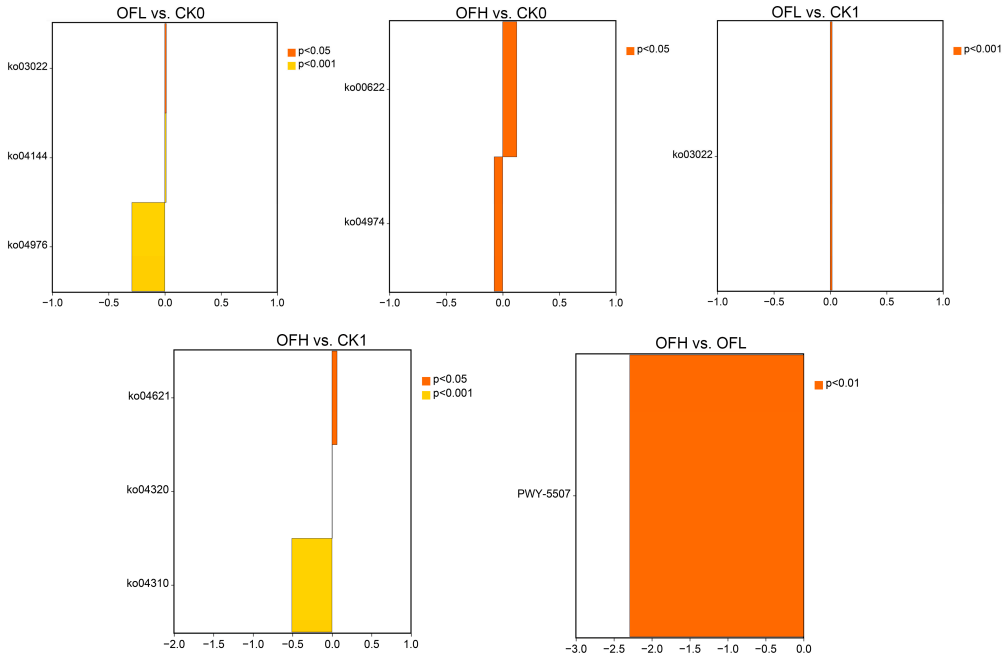

Figure 4. The differential pathways in the comparison groups of OFL vs. CK0, OFH vs. CK0, OFL vs. CK1, OFH vs. CK1, and OFH vs. OFL using the metagenomeSeq method. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen.

3.6. Effects of Different Fertilizing Methods on the Specific Soil Fungal Communities

Furthermore, we analyzed the alterations in the composition of specific soil fungal communities in the different groups at the phylum and genus levels. At the phylum level, the top5 phyla of potato soil fungal communities were *Ascomycota*, *Basidiomycota*, *Mortierellomycota*, *Chytridiomycota*, and *Glomeromycota* (Figure 5D). It was observed that *Ascomycota* was the dominant phylum in all four groups, with an average abundance of approximately 90%. In comparison with the CK0 group (88.24% for *Ascomycota*, and 11.07% for *Basidiomycota*), the *Ascomycota* abundance was higher in the CK1 (96.29%), OFL (97.94%), and OFH groups (98.49%), whereas the *Basidiomycota* abundance was lower in the CK1 (2.65%), OFL (0.66%), and OFH groups (0.61%). Then, the top30 fungal genera in the different groups were analyzed, including *Plectosphaerella*, *Botryotrichum*, *Cladosporium*, *Lectera*, *Alternaria*, *Humicola*, *Bisifusarium*, *Paramyrothecium*, *Pseudopeyronellaea*, *Coprinellus*, *Filobasidium*, *Furcasterigmium*, and *Arthrographis* (Figure 5E). The *Plectosphaerella* abundance values in the CK0, CK1, OFL, and OFH groups were 7.86%, 10.33%, 8.47%, and 12.81%, respectively. The *Botryotrichum* abundance values in the CK0, CK1, OFL, and OFH groups were, respectively, 3.15%, 8.49%, 13.11%, and 14.15%. However, the *Cladosporium*, *Lectera*, and *Alternaria* abundance values were the highest in the CK0 group (14.15% for *Cladosporium*, 9.96% for *Lectera*, and 12.55% for *Alternaria*), and their abundance values were lower in the other three groups. However, within the OFH group, the relative abundance of *Humicola* and *Bisifusarium* in the OFH group reached 13.65% and 10.95%, respectively. In contrast, the relative abundance of *Pseudopeyronellaea*, *Coprinellus*, *Filobasidium* and *Furcasterigmium* was found to be lower following various fertilizer treatments when compared to the CK0 group. As for *Arthrographis*, it was undetected in the CK0 group but was present in the CK1, OFL, and OFH groups, with particularly higher levels observed in the groups treated with bioorganic fertilizers, namely OFL and OFH.

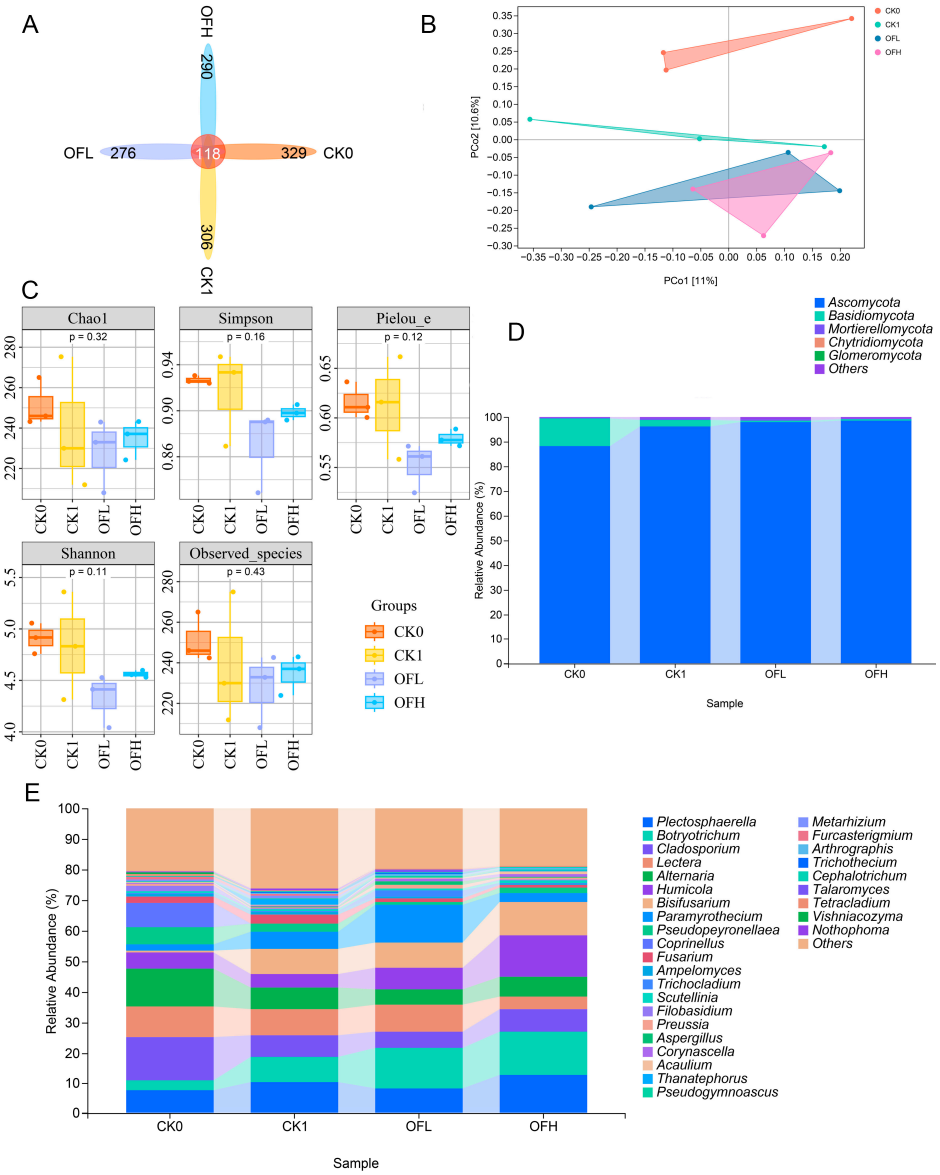

Figure 5. Effects of different fertilizing methods on the overall composition of soil fungal communities through internal transcribed spacer (ITS) sequencing. (**A**) The Venn diagram of the annotated soil fungal communities (ASVs) in the different groups. (**B**) The principal coordinate analysis of the samples in the different groups. (**C**) The α-diversity of the soil fungal communities. including Chao1, Simpson, Pielou's evenness, Shannon, and observed species values in the different groups. (**D**) The distribution of top5 dominant phyla of soil fungal communities in the different groups. (**E**) The distribution of top30 dominant genera of soil fungal communities in the different groups. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen.

According to the results of the LEfSe analysis, we observed that *Comoclathris* was the crucial fungal genus for the CK0 group; furthermore, the biomarker fungal genus identified in the OFH group was *Brunneochlamydosporium* (Figure 6A).

Eventually, the functions of the identified potato soil rhizosphere fungal communities were predicted, and the "fatty acid and lipid biosynthesis", "nucleoside and nucleotide biosynthesis", "cofactor, prosthetic group, electron carrier, and vitamin biosynthesis", "carbohydrate degradation", "electron transfer", "respiration", "TCA cycle", "pentose

phosphate pathways", and "tRNA charging" functions were obtained (Figure 5B). Afterwards, the significantly differential functions were compared among the CK0, CK1, OFL, and OFH groups ($p < 0.05$). In the comparison of CK1 vs. CK0, PWY-7420 (monoacylglycerol metabolism (yeast)), GLUCOSE1PMETAB-PWY (glucose and glucose-1-phosphate degradation), PWY-7269 (NAD/NADP-NADH/NADPH mitochondrial interconversion (yeast)), PWY3O-355 (stearate biosynthesis III (fungi)), PWY-7268 (NAD/NADP-NADH/NADPH cytosolic interconversion (yeast)), PWY-621 (sucrose degradation III (sucrose invertase)), and SO4ASSIM-PWY (sulfate reduction I (assimilatory)) were identified as the significantly differential pathways (Figure 5C). PWY-5651 (L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde) and PWY-5994 (palmitate biosynthesis I (animals and fungi) were the differential pathways in the comparison of OFL vs. CK0. After comparing the OFH and CK0 groups, the significantly differential pathways were PWY-7007 (methyl ketone biosynthesis), PWY-7288 (fatty acid and beta-oxidation (peroxisome, yeast)), PWY-6609 (adenine and adenosine salvage III), and P221-PWY (octane oxidation) (Figure 6C).

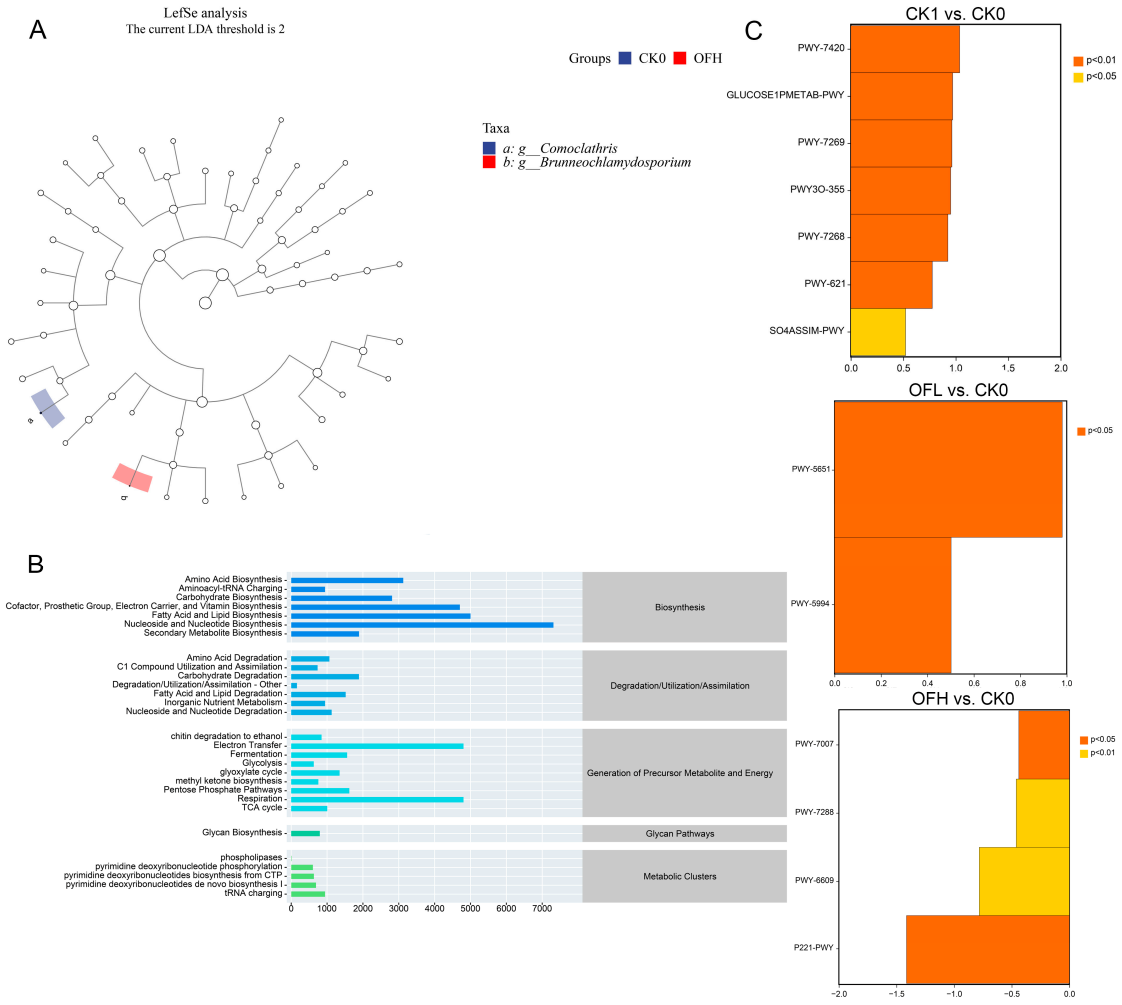

Figure 6. Identification of the soil fungal biomarkers among the different groups, and functional analysis of the identified soil fungal communities. (**A**) The biomarker of fungal communities in the different groups using LEfSe analysis at different levels. (**B**) The MetaCyc pathways predicted by the annotated soil fungal communities. (**C**) The differential pathways in the comparison groups of CK1 vs. CK0, OFL vs. CK0, and OFH vs. CK0 using the metagenomeSeq method. CK0: without chemical nitrogen fertilizer and organic fertilizer; CK1: single application of chemical nitrogen fertilizer with optimal nitrogen application; OFL: 70% chemical nitrogen fertilizer combined with 30% bioorganic fertilizer nitrogen; OFH: 30% chemical nitrogen fertilizer combined with 70% bioorganic fertilizer nitrogen.

3.7. Relationships Between the Identified Soil Bacterial/Fungal Genera and Potato Quality and Yield

In order to further explore the relationship between the identified important bacterial or fungal communities and potato quality, yield, or weight of the potatoes, Spearman correlation coefficient analysis was conducted. In terms of soil bacterial communities, *Longimicrobiaceae*, *BD2-11-terrestrial-group*, *Caenimonas*, *Arthrobacter*, *Altererythrobacter*, *Luteimonas*, *Parcubacteria*, and *Lautropia* were significantly positively correlated with potato yield and weight of potato, whereas *Vicinamibacteraceae*, *RB41*, *KD4-96*, *Solirubrobacter*, *TRA3-20*, *Rokubacteriales*, *Subgroup-10*, *Flavisolibacter*, *Subgroup-17*, *Microvirga* and *Entotheonellaceae* were evidently negatively related to potato yield and the weight of potatoes (Figure 7A). Through ITS sequencing, we discovered that *Plectosphaerella* showed a significantly positive correlation with potato yield, while it exhibited a markedly negative correlation with the starch and potassium (K) content in potatoes. *Botryotrichum* was only significantly correlated with the iron (Fe) content (Figure 7B). *Bisifusarium* was found to be positively related to the weight of potatoes, but *Fusarium* was negatively correlated with the potato yield (Figure 7B). Furthermore, the potato yield and weight of potatoes were negatively correlated with *Tetracladium* and *Microdochium*, but were positively correlated with *Scopulariopsis* and *Brunneochlamydosporium* (Figure 7B).

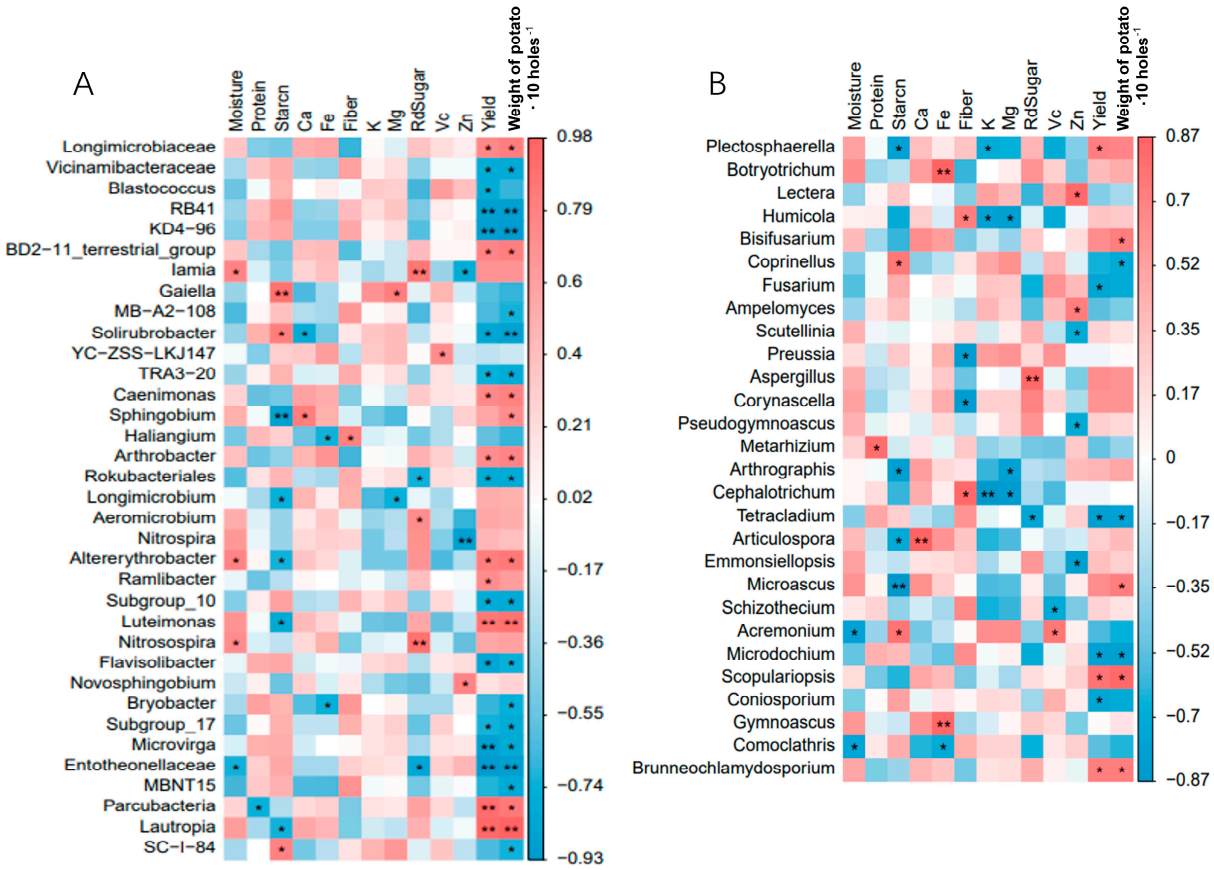

Figure 7. The correlation heatmaps between the crucial bacterial or fungal communities at the genus level and potato quality, yield, or weight using Spearman correlation coefficient analysis. (**A**) The associated heatmap between the soil bacterial genera and potato quality, yield, or weight. (**B**) The correlated heatmap between the soil fungal genera and potato quality, yield, or weight. Red indicates a positive correlation, and blue indicates a negative correlation. The darker the color, the higher the correlation. *: $0.01 < p < 0.05$; **: $p < 0.01$.

4. Discussion

Bioorganic fertilizers, which include organic fertilizer and beneficial microorganisms, have been shown to increase soil vitality, organic matter content, and the effectiveness of pest biocontrol agents [28]. This study assessed the effects of varying ratios of bioorganic to chemical fertilizers on potato yield, quality, and soil microbial communities. We found that increasing the application of bioorganic fertilizers over chemical fertilizers improved potato plant height, potato weight, and yield, particularly by increasing the number of larger tubers. This aligns with Xiao et al.'s [29] findings that balanced fertilizers, reduced by 30% in chemical content and combined with bioorganic fertilizers, can enhance cauliflower yield by improving soil biochemical properties, such as by increasing organic matter and enzyme activity. Brenzinger et al. [30] also demonstrated that combining balanced fertilizers with bioorganic fertilizers can increase crop yields. In addition, this study found that the application of bioorganic fertilizer instead of chemical fertilizer had no significant effect on potato quality. This effect takes a certain duration to emerge, and short-term experiments may not fully capture the long-term effects of bioorganic fertilizers on potato quality. Thus, in arid regions with limited rainfall, substituting 70% of chemical fertilizers with bioorganic fertilizers can significantly increase potato yield, characterized by a higher number of larger tubers, without compromising potato quality. The application of bioorganic fertilizers appears to enhance crop yields by improving the structure and function of soil microbial communities.

Bishnoi et al. [31] believes that bioorganic fertilizers have a significant impact on microbial communities. Ding et al. [32] found that combining organic and inorganic fertilizers enhances soil microbial diversity. Our study, however, suggests that reducing chemical fertilizers and using bioorganic ones might reduce soil bacterial species numbers without impacting the diversity and richness of bacterial and fungal communities. This could be due to the additional bioorganic fertilizers, rich in beneficial bacteria and organic matter, fostering competition for nutrients among microbes, where dominant species suppress the reproduction of others [33]. In addition, the composition and function of microbial communities may also be influenced by various factors, such as nutrient availability, soil pH, and organic matter content [34].

The impact of bioorganic fertilizers on soil microbial community structure is significant, particularly in terms of how microbial species at different phylum levels respond to their application. In the OFH group, we observed increased abundance of *Gemmatimonadota* and *Ascomycota* were more abundant, whereas the abundance of *Acidobacteriota* and *Basidiomycota* were decreased. This aligns with Lebedev et al. [35], who found that using bioorganic fertilizers instead of chemical fertilizers could evidently reduce *Acidobacteriota* abundance in the soil of the red raspberry orchard. *Ascomycota* is an important driver of carbon and nitrogen cycling in arid ecosystems, and also plays roles in soil stability, the decomposition of plant biomass, and endogenous interactions with plants [36]. *Basidiomycota* is one of the dominant fungal phyla in soil, and its abundance decreased with the accumulation of soil nutrients [37]. Wu et al. [38] elaborated that the application of increased organic fertilizers and reduced chemical fertilizers could improve the quality of grape berries while increasing *Ascomycota* abundance decreasing the *Basidiomycota* abundance on the surface of grape berries. Our findings partially diverge; bioorganic fertilizers in the place of chemical fertilizers did not significantly affect potato quality but increased *Ascomycete* and decreased *Basidiomycete* abundance. Differences in crop types, soil microbial community structures, environmental and management factors, fertilization strategies, and microbial community functions may account for the discrepancies between Wu et al. [34] and our results. Future studies should explore how these factors influence the response of different crops to bioorganic fertilizers. In summary, we hypothesized that the increased application of bioorganic fertilizers in place of chemical fertilizers could enhance potato yield and potato weight by influencing the abundance of *Gemmatimonadota*, *Acidobacteriota*, *Ascomycota*, and *Basidiomycota*.

The application of bioorganic fertilizers is closely associated with microbial species at the genus level and significantly impacts soil microbial community structure. Our study found that the abundance of *Longimicrobiaceae*, *Lysobacter*, *Nocardioides*, *Arthrobacter*, *Plectosphaerella*, *Humicola*, and *Botryotrichum* increased, while *Vicinamibacteraceae*, *Gaiella*, *Solirubrobacter*, *Cladosporium*, *Lectera*, *Alternaria*, and *Coprinellus* decreased under bioorganic fertilizer treatments. This is consistent with a study by Shi et al. [18], which reported that bioorganic fertilizers enrich beneficial microorganisms, such as *Lysobacter*, *Arthrobacter*, *Sphingomonas*, and *Luteimonas*, thereby accelerating the growth and yield of Panax notoginseng. Additionally, Humicola is a prolific source of diverse metabolites with biological activities and possesses thermal stability, indicating its biotechnological and industrial potential [39]. Pu et al. [40] found that bioorganic fertilizers enhance microbial diversity and the relative abundance of beneficial soil bacteria, like *Humicola*, *Bacillus*, and *Mortierellomycota*, improving soil fertility and the quality and yield of Panax notoginseng. Similarly, replacing a part of chemical fertilizers with bioorganic ones increased the abundance of *Botryotrichum*, *Gemmatimonas*, and *Trichoderma*, which are potentially correlated with litchi yield [41]. These findings align with our results, showing that bioorganic fertilizers promote soil microbial diversity and significantly increase potato yield. Zhang et al. [42] demonstrated that the application of cow manure significantly altered the relative abundance of *Gaiella*, *Entotheonellaceae*, *Solirubrobacter*, and *Halomonas*, which is consistent with our observation of changes in these genera in potato soil under bioorganic fertilizer treatments. *Cladosporium*, *Alternaria*, and *Coprinellus*, important soil fungal genera, were found by [43] to decrease in abundance with bioorganic fertilizer application, enhancing oat yield in saline–alkali environments. This is in line with our study, where bioorganic fertilizer application significantly reduced the abundance of *Cladosporium*, *Alternaria*, and *Coprinellus*, thereby increasing potato yield. Integrating these literature findings with our results, we infer that increased bioorganic fertilizers replacing chemical fertilizers may enrich beneficial soil microorganisms (*Longimicrobiaceae*, *Lysobacter*, *Nocardioides*, *Arthrobacter*, *Humicola*, and *Botryotrichum*) and inhibit harmful soil pathogens (*Vicinamibacteraceae*, *Gaiella*, *Solirubrobacter*, *Cladosporium*, *Lectera*, *Alternaria*, and *Coprinellus*), thus enhancing potato yield.

LEfSe can analyze the differences in microorganisms among groups and determine the essential microbiota specific to each group, helping to uncover potential biomarkers. A previous study of Gu et al. [44] employed LEfSe analysis to point out that *Gitt-GS-136*, *KD4-96*, *Thermomicrobiales*, *MB-A2-108*, *Dehalococcoidia*, and *S0134_terrestrial_group* were significantly enriched in soil after treatment with bioorganic fertilizers, which indicated that these taxa with differential abundance values could be considered as potential biomarkers of treatment of bioorganic fertilizers. Another study also utilized sequencing and LEFSe analysis to show that *Gammaproteobacteria*, *Proteobacteria*, *Deltaproteobacteria*, *Alphaproteobacteria*, and *Nitrospirae* were the most significant contributors in rice soil after bioorganic fertilizer treatments [29]. In this study, the signature taxa in the OFH group were *Arthrobacter*, *Parcubacteria*, *Lautropia*, *Luteimonas* and *Brunneochlamydosporium*, which had significantly positive correlations with the potato yield and potato weight through Spearman correlation analysis. Therefore, we speculated that *Arthrobacter*, *Parcubacteria*, *Lautropia*, *Luteimonas*, and *Brunneochlamydosporium* may be the potential biomarkers in the potato soil after higher bioorganic fertilizer treatment. However, the specific roles of these signature microorganisms in potato planting should be further investigated.

5. Conclusions

In conclusion, under the condition of a total nitrogen application of 180 kg ha^{-1}, the use of bioorganic fertilizer to replace 30% and 70% of the nitrogen fertilizer can significantly increase both the number and weight of large potatoes, thereby achieving yield increases. Specifically, during the 2022–2023 period, the OFH treatment (70% replacement) showed a significant increase 10.4–109.0% in yield, compared to the CK1 treatment. However, the OFL treatment (30% replacement) exhibited year-to-year variation, with a decrease of 0.26% in 2022 and a significant increase in yield of 49.09% in 2023, both compared

to the CK1 treatment. It can be seen that under the same nitrogen fertilizer conditions, bioorganic fertilizer replacing 70% of the chemical fertilizer is the optimal strategy for potato planting in the northwest dry area. *Arthrobacter*, *Parcubacteria*, *Lautropia*, *Luteimonas*, and *Brunneochlamydosporium* were the signatures of bioorganic fertilizers treatment, and were positively correlated with the potato yield. The diversity of soil microorganisms is improved through an increase in beneficial microorganisms and a reduction in harmful pathogens, and, ultimately, the loss of yield is minimized. Therefore, the changes in the potato rhizosphere soil environment under different fertilization methods provided a scientific basis for establishing green agriculture and environment-friendly fertilization technology to improve the potato yield in dry land. Future studies should explore further optimization strategies, such as long-term effects under different soil and climate conditions, mechanisms and strategies for microbial migration, and targeted fertilization and precision agriculture techniques.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy14122881/s1, Figure S1: The daily precipitation and average air temperature in 2003.

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Data Availability Statement: The original contributions presented in the study are included in the article. The microbial and nematode DNA sequences from the 12 soil samples have been deposited in the Sequence Read Archive (SRA) of the NCBI database under Accession numbers NCBI: PRJNA1179710.

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Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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