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Effects of Different Agricultural Waste Composts on Cabbage Yield and Rhizosphere Environment

Jue Wang [1], Bo Zhang [1,2], Jie Wang [1], Guobin Zhang [1], Zhibin Yue [1], Linli Hu [1], Jihua Yu [1,3,*] and Zeci Liu [1,*]

[1] College of Horticulture, Gansu Agricultural University, Lanzhou 730070, China; m15689129070@163.com (J.W.); zhangbo@stgsau.edu.cn (B.Z.); wangjie@st.gau.edu.cn (J.W.); zhanggb@gsau.edu.cn (G.Z.); yuezb@st.gsau.edu.cn (Z.Y.); hull2022@163.com (L.H.)
[2] Dingxi Seed Station, Dingxi Academy of Agricultural Sciences, Dingxi 743000, China
[3] Gansu Provincial Key Laboratory of Arid Land Crop Science, Gansu Agricultural University, Lanzhou 730070, China
* Correspondence: yujihuagg@163.com (J.Y.); liuzc@gsau.edu.cn (Z.L.)

Abstract: The return of agricultural waste to the field is one of the most effective strategies of increasing crop yield, improving the soil's physicochemical properties, and improving the soil rhizosphere environment. In the present study, sheep manure (SM), cow manure (CM), tail vegetable (TV), mushroom residue (MR), and corn straw (CS) were used as raw materials, and no fertilization (CK1) and local commercial organic fertilizer (CK2) treatments were used as controls. Eight composts were set up using specific mass ratios of different compost materials. After fermentation, field experiments were conducted to determine the cabbage yield, soil's physicochemical properties, and soil rhizosphere conditions. The eight composts increased the soil organic matter and nutrient contents significantly. Among the eight fermentation formulas, T6 (CM:CS:TV:SM = 1:1:2:6), T7 (MR:CS:TV:SM = 1:1:2:6), and T8 (CM:MR:CS:TV:SM = 1:1:1:2:5) were relatively effective. Therefore, high-throughput sequencing was performed on T6, T7, T8, CK1, and CK2. T6, T7, and T8 exhibited increased relative abundance of Proteobacteria, Actinomycetes, and Firmicutes, while the Acidobacteria abundance was decreased. In addition, Ascomycota's and Basidiomycetes' relative abundance decreased, and the oil chytrid and mortierella increased. The microbial community structure was affected significantly by pH, electrical conductivity, available potassium, available nitrogen, and organic matter. In general, the three composts increased yield by improving the soil's physicochemical properties, fertility, and microbial community structure. Among them, T6 had the most significant effect and is the optimal formula for use as a local organic cabbage fertilizer, and it could facilitate sustainable agricultural development.

Keywords: planting and breeding waste; compost; yield; cabbage; soil environment

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1. Introduction

Agricultural waste is the non-product output of agricultural production and processing. It is potentially toxic to plants, animals, and human beings in numerous direct and indirect ways and has become one of the main sources of agricultural non-point source pollution, threatening the environmental security of many countries globally. Today, most of the agricultural waste is in the form of crop straw and livestock manure [1–3]. In China, the annual output of livestock and poultry manure is up to 3.8 billion tons, and that of crop straw is up to 1 billion tons [4]. However, due to a lack of proper environmental regulations and poor waste treatment systems for agricultural waste, most of the agricultural waste is not disposed of properly, or may be simply thrown away, which not only causes environmental pollution but represents a waste of resources [5,6].

With an increase in people's environmental awareness, the use patterns of agricultural waste are changing, with carbonization, biodegradation, compost hydrolysis, and pyrolysis being increasingly adopted to create fertilizers, feed, energy, base material, and

other products. Such activities improve the economic value of agricultural waste by transforming it into useful products [7,8]. Among them, compost hydrolysis is a sustainable approach that can be used to fix organic matter into material that can be used to promote soil improvement.

Soil ecosystems are vital for the functioning of the Earth's biosphere [9]. The soil's microbial community is diverse, and the microbiome structure is one of the indexes for soil health. The microbiome plays vital roles in nutrient cycling and energy flows in soil ecosystems [10,11]. Moreover, soil's microbial community composition and diversity, which play key roles in soil's ecosystem function, are sensitive indexes of microenvironmental changes in soil. The functional diversity of the soil's microbial community is an index that can reflect the ecological characteristics of soil microorganisms, providing a reliable basis for understanding microbial diversity. Organic fertilizer can affect the function of various agroecosystems by altering the composition and abundance of functional genes [12,13].

Previous field studies have concluded that organic fertilizer can maintain soil structure, improve soil's nutrient contents, and promote pathogen antagonists [14]. In addition, soil's microbial community structure and diversity can improve following organic fertilizer application, and the amount of plant growth promoting rhizobacteria, such as Azospirillum [15], Enterobacter [16], Pseudomonas [17], Bacillus [18,19], and Trichoderma [20], increases. Organic fertilizer application has been considered a partial substitute for inorganic nitrogen (N) and to provide longer-term nutrient release [21]. Furthermore, organic fertilizer amendment to soil can improve the growth of plant roots and the absorption efficiency of nutrients and water [22,23]. Moreover, organic fertilizers can increase soil's organic matter contents and, in turn, available nutrients to support crop growth [24].

Previous studies on organic fertilizers have focused mainly on the application of organic fertilizer alone or increased organic fertilizer in combination with reduced chemical fertilizer application [25,26]. Only a few studies have investigated the effects of agricultural waste compost on crop yield and the rhizosphere. In addition, the interactions between crop yield and shifts in microbial community diversity and compost application systems, in addition to the underlying mechanisms, remain unclear.

Lanzhou, China, is an important summer vegetable production area at the northern margin of the Tibetan plateau. The region is also rich in agricultural waste resources. At present, local, commercial, and organic vegetable fertilizer is mainly produced by compost fermentation mixed with tail vegetable/sheep manure = 3.5:6.5 (mass ratio), and there are still other types of crop and animal waste that are not properly recycled. Therefore, in the present study, some of the agricultural waste resources (corn straw, CS; tail vegetable, TV; mushroom residue; MR; sheep manure, SM; cow manure, CM) were used as fermentation materials. The compost fermentation formulas were based on local, commercial, and organic fertilizer formulas. By studying the effects of different agricultural waste composts on cabbage yield and the rhizosphere, the organic fertilizer production formula was optimized, which could provide a reference formula for application in the cultivation of cabbage or other vegetables. The results of the present study could provide a theoretical basis for the sustainable disposal and exploitation of agricultural waste and environmental management.

2. Materials and Methods

2.1. Experimental Site Condition

The present study was conducted in Yuzhong, Gansu Province, China. Average annual temperature, precipitation, and evaporation are 6.6 °C, 300~400 mm, and 1343 mm, respectively. The pH and electrical conductivity (EC) of the surface soil (0~20 cm depth) were 8.12 and 0.242 $\mu S \cdot cm^{-1}$, respectively. In addition, the alkali-hydrolyzable N (AHN), available phosphorus (P; AP), available potassium (K; AK), and organic matter (OM) contents were 76.42 $mg \cdot kg^{-1}$, 117.40 $mg \cdot kg^{-1}$, 237.70 $mg \cdot kg^{-1}$, and 14.03 $g \cdot kg^{-1}$, respectively.

2.2. Composting

Agricultural waste raw materials (corn straw, CS; tail vegetable (leafy vegetable), TV; mushroom residue; MR; sheep manure, SM; cow manure, CM) were crushed and weighed and mixed at specific mass ratios. The basic physicochemical properties of the composted agricultural waste are listed in Table 1. Before composting, the water content of the composting pile was adjusted to 60~65%. Subsequently, 1 kg of compost bacteria (colony forming unit [CFU] $\geq$ 50 billion/g, protease activity $\geq$ 70 μg/g, cellulase activity $\geq$ 60 μg/g) purchased from Renyuan biotechnology company (Hebi, China) was added to every 15 tons of agricultural waste. After the composting materials and bacteria were mixed completely, the mixture was stacked into strip ridges with widths of 1.5~3.0 m and heights of 0.8~1.5 m. During the composting process, the temperature 25~30 cm away from the top of the pile was monitored. After the temperature reached 55~60 °C, stacks were turned for the first time. Subsequently, the stacks were turned every 5~7 d until composting was complete, when the color of the stack was dark brown. The measured composting temperature was close to room temperature (20~30 °C), and the smell of rotten soil was perceived, which took about 38~40 d. The basic physicochemical properties of compost fertilizers with different agricultural waste are listed in Table 2.

Table 1. Basic chemical properties of different agricultural waste raw materials. Note: AN (available nitrogen) = AHN (alkali-hydrolyzable nitrogen)

Raw Material	TN (g/kg)	TP (g/kg)	TK (g/kg)	AN (mg/kg)	AP (mg/kg)	AK (mg/kg)	OM (g/kg)
Sheep Manure	8.99	6.61	11.8	658.58	304.87	9320	945.67
Cow Manure	9	5.71	13.3	686.58	383.29	6786.67	510.76
Tail Vegetable	11.09	5.41	139.6	971.25	391.25	13,886.67	614.43
Mushroom Residue	9.1	6.65	11.4	630.58	284.33	9253.33	470.31
Corn Straw	10.04	7.79	15.09	546.58	385.61	8246.67	998.77

Table 2. Basic physicochemical properties of compost with different agricultural waste formulations. Note: AN (available nitrogen) = AHN (alkali-hydrolyzable nitrogen)

Treatments	TN (g/kg)	TP (g/kg)	TK (g/kg)	AN (mg/kg)	AP (mg/kg)	AK (mg/kg)	OM (g/kg)	pH Value	EC Value (ms/cm)
CK2	9.19	4.27	14.60	434.58	122.11	7596.67	227.57	8.14	4.81
T1	8.09	3.40	15.35	429.92	143.29	8123.33	195.33	7.95	4.92
T2	9.37	4.12	13.76	415.92	100.87	7013.33	132.75	8.07	5.33
T3	9.19	4.38	11.68	476.58	93.33	6856.67	176.37	8.03	5.63
T4	10.13	4.54	14.99	504.58	165.40	8860.00	394.45	8.25	6.35
T5	10.17	4.27	10.11	411.25	96.54	7453.33	195.33	8.08	5.32
T6	10.49	4.50	14.28	415.92	166.01	8240.00	244.64	8.13	5.91
T7	11.34	4.86	13.77	555.92	161.93	9746.67	384.97	8.18	6.19
T8	10.90	4.64	14.00	448.58	173.55	8530.00	252.22	8.24	6.65

2.3. Test Materials and Field Management

"Shuangkang 58" cabbage (an early-maturing variety), purchased from Tianjin Shuofeng Seed Industry Co., Ltd. (Tianjin, China), was used as the experimental material. Seedlings were raised on 15 June 2022 and planted on 25 July 2022.

The field trial was conducted based on a random block design with three replicates. Two control groups were set up, with eight treatments: CK1 (no fertilizer), CK2 (local organic fertilizer fermentation formula, TV:SM = 3.5:6.5), T1 (TV:SM = 4.5:5.5), T2 (CM:TV:SM = 1:3:6), T3 (MR:TV:SM = 1:3:6), T4 (CS:TV:SM = 1:3:6), T5 (MR:CM:TV:SM = 1:1:2:6), T6 (CS:CM:TV:SM = 1:1:2:6), T7 (CS:MR:TV:SM = 1:1:2:6), and T8 (CS:MR:CM:TV:SM = 1:1:1:2:5). The application amounts of all the eight fermented organic fertilizer treatments and the CK2 were

6000 kg/ha. The organic fertilizer was evenly applied in strips, the soil on both sides was turned over for 25~30 cm to cover the base fertilizer, and ridges were set up. Each experimental plot was 20 m long, 1.1 m wide, and 22 m^2 in area. The width of each planting row was covered with film, and the width of the planting row was 1 m. Two rows of cabbage were cultivated on each planting row, and the plant spacing and row spacing were 20~25 cm and 35~40 cm, respectively.

2.4. Measurement of Yield and Soil Sampling

The planted cabbage was harvested on 7 October 2022. During the harvest period, 75 cabbage plants from each treatment were selected randomly to measure yield, and the soil samples from the 15~20 cm depth of three labeled cabbages were collected and used for rhizosphere microbial diversity analysis. Soil samples from the three cabbage roots were mixed. Debris such as stones, roots, and film fragments were sieved and removed with a 2 mm sieve. Afterward, the soil was divided into two parts; one part was used for subsequent microbial DNA extraction, and the other part was air-dried and used for the determination of soil's physicochemical properties.

2.5. Composting Fertilizers and Soil Physicochemical Property Analysis

The pH and EC of the soil were determined using the soil filtrate [16]. PHS-3E (Jinko, Shanghai, China) was used to determine the filtrate pH, and the EC was determined using a DSJ-308A conductivity meter (Jinko, Shanghai, China). After oxidation with potassium dichromate ($K_2Cr_2O_7$), OM content was measured using the titration method. Before the determination of total N (TN), total P (TP), and total K (TK) contents, wet digestion was performed with the H_2SO_4-H_2O_2 method. Subsequently, the TN content was determined using an automatic Kjeldahl N analyzer K1100F, TP was determined using a UV-1780 spectrophotometer (Shimadzu, Suzhou, China), and TK was determined using a ZEEnit 700P flame atomic spectrophotometer (Analytik Jena, Jena, Germany). The determination of AN, AP, and AK contents are in accordance with the methods used in previous studies [27]. All the above indexes were measured in triplicate.

2.6. Soil DNA Extraction and PCR Amplification

Soil microbial DNA was extracted using the EZNA kit (Omega Bio-tek, Norcross, GA, USA). Primers ITS1F and ITS2R were used to amplify the ITS2 region of the fungal DNA, while the s338F and 806R primers were used to amplify the V3–V4 region of bacterial DNA. The reaction mixture volume was 20 μL, including 4 μL buffer, 2 μL dNTPs, 1.5 μL of each primer, 10 ng DNA, and sufficient ddH_2O. The ABI GeneAmp 9700 PCR amplifier (Applied Biosystems, Foster City, CA, USA) was used for PCR. The amplification procedure was initial denaturation at 95 °C for 3 min, then denaturation for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 45 s, and final extension at 72 °C for 10 min, and the amplification cycle was 27. After amplification, the procedure was terminated at 4 °C. PCR products were electrophoresed on 2% agarose gel, purified using an AxyPrep DNA gel extraction kit, and quantified using the Promega quantum fluorometer (Promega, Madison, WI, USA).

2.7. Illumina MiSeq Sequencing

Purified amplified PCR amplification fragments were collected and sequenced by Shanghai Meiji Biomedicine Technology (Shanghai, China) on the Illumina MiSeq sequencing platform. The original 16s rRNA and ITS gene were sequenced through multi-channel separation. Trimmomatic was used to perform quality filtering, and FLASH merge was used to merge the data according to the standard. Sequence similarity > 97% was specified as an Operational Taxonomic Unit and used for UPARSE clustering. The fungal ITS (Unite 8.0) sequences and bacterial 16S rRNA (Silva SSU128) sequences were evaluated using RDP classifier (confidence threshold = 0.7).

2.8. Data Analysis

Microbial data analysis was performed in R v.3.5.2 [28]. Shannon, Simpson, and Chao indexes were calculated using QIIME2, accessed on 11 July 2023 (https://qiime2.org/). Principal Coordinate Analysis (PCoA) was performed based on Bray–Curtis distance to evaluate similarity in microbial community composition. Relationships among physicochemical properties and soil microbial community were analyzed using redundancy analysis (RDA) and Spearman rank correlation. Soil microbial communities in different treatments were evaluated by substitution multiple variance analysis (Per MANOVA). PCoA, RDA, and Per MANOVA analyses were implemented using the vegan package in R (version 2.0-5;) [29]. Circos-0.67-7 was accessed on 16 July 2023 (https://bioweb.pasteur.fr/packages/pack@circos@0.67-7) to draw Circos diagrams (version 0.67-7) [30]. One-way Analysis of Variance and Pearson correlation analysis were performed in IBM SPSS Statistics 21 (IBM Corp., Armonk, NY, USA). $p \leq 0.05$ indicated a significant difference among treatments.

3. Results

3.1. Soil's Physicochemical Properties under Different Composting Treatments

Different agricultural waste composts had significant effects on the physicochemical indexes of the cabbage rhizosphere soil (Figure 1). Compared with CK1 (no fertilizer), the total available and available nutrients in the soil were increased significantly after the organic fertilizer application. TN, TP, and TK contents were the highest under the T6 treatment, at 0.65 g/kg, 1.41 g/kg, and 11.48 g/kg, respectively. Compared with those in the CK2 (local commercial fertilizer) treatment, the TN, TP, and TK in the T6 treatment were 5.36%, 28.24%, and 15.49% higher, respectively. In addition, the AN, AP, and AK contents in T6 were the highest, at 89.86 mg/kg, 98.78 mg/kg, and 173.94 mg/kg, respectively, which were 5.26%, 11.97%, and 18.44% higher than those in the CK2 treatment, respectively.

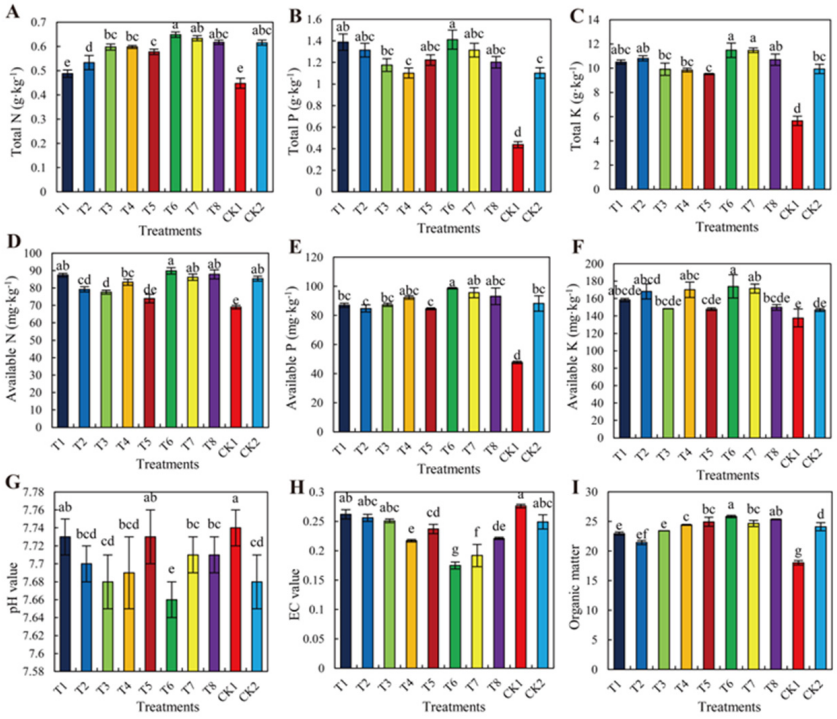

Figure 1. Physicochemical properties of cabbage rhizosphere soil under different compost treatments. (**A**): Total N; (**B**): total P; (**C**): total K; (**D**): available N; (**E**): available N; (**F**): available K; (**G**): pH value; (**H**): EC value; (**I**): organic matter. Note: T1~T8 represent the eight fermentation treatments. Different letters on the figure indicate significant differences ($p \leq 0.05$).

Both soil pH and EC were the highest under the CK1 treatment and the lowest under the T6 treatment, and the difference was significant. However, the total OM was the highest in the T6 treatment, and the lowest in the CK1 treatment, which was significantly lower than those in the other treatments.

3.2. Cabbage Yield under Different Composting Treatments

The yields of all agricultural waste compost treatments were significantly higher than that in the CK1 treatment. The biological yields (overground weight) and economic yields (sphere weight) of the T6 treatment were the highest, reaching 98.058 ton/ha and 71.263 ton/ha, followed by those in the T4 treatment. The biological and economic yields of the T6 treatment were significantly higher than those of the CK1 treatment, by 79.94% and 88.24%, respectively. In addition, compared with those of the CK2 treatment, the biological and economic yields of the T6 treatment were 7.18% and 5.38% higher, respectively (Figure 2).

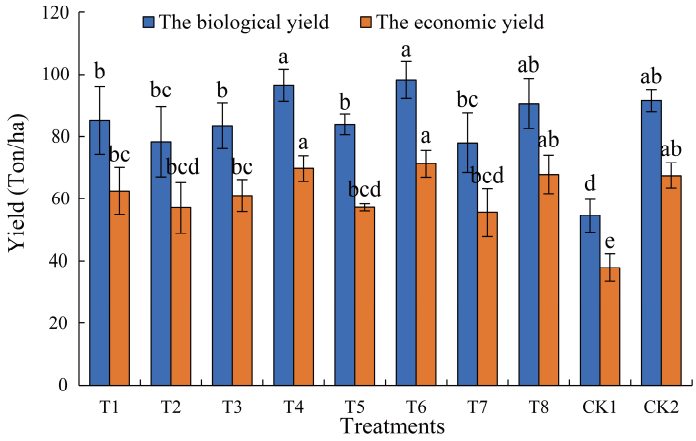

Figure 2. Average cabbage yield under different compost treatments. Different letters on the figure indicate significant differences ($p \leq 0.05$).

3.3. Soil's Microbial Diversity under Different Treatments

The ACE, Chao 1, Simpson, and Shannon indexes of fungi and bacteria under different treatments were measured to study the microbial community's diversity. The ACE and Chao 1 indexes were proportional to the microbial abundance, the Simpson index was inversely proportional to the diversity, and the Shannon index was proportional to the diversity.

The soil bacteria's ACE index of the T6 treatment was the highest, and there was no significant difference between T6 and the other treatments (Figure 3A). The T6 treatment had the highest Chao 1 index, which was 8.13% higher than that of the CK1 treatment, and the difference was significant (Figure 3B). Compared with that of the CK1 treatment, the Simpson index of the bacteria in the CK2, T6, T7, and T8 treatments decreased by 3.70, 12.00, 7.69, and 3.70%, respectively. In addition, the Simpson index in the T6 treatment was the lowest and significantly different from that of the CK1 treatment (Figure 3C). The Shannon index of the soil bacteria in the T6 treatment was the highest and was 2.22% higher than that of the CK1 treatment (Figure 3D).

T6 and T7 had the highest soil fungal ACE indexes, which were 19.12% and 20.36% higher than those in the CK1 treatment, respectively (Figure 3E). The Chao 1 index of soil fungi under the T6 treatment was the highest and 13.18% higher than that of the CK1 treatment (Figure 3F). T6 had the lowest Simpson index, but there were no significant differences among the treatments (Figure 3G). Compared with that of the CK1 treatment, the bacterial Shannon indexes of the CK2, T6, T7, and T8 treatments were 3.75, 4.50, 1.25, and 1.00% higher, respectively. The Shannon index of the T6 treatment was the highest, although there were no significant differences among the treatments (Figure 3H).

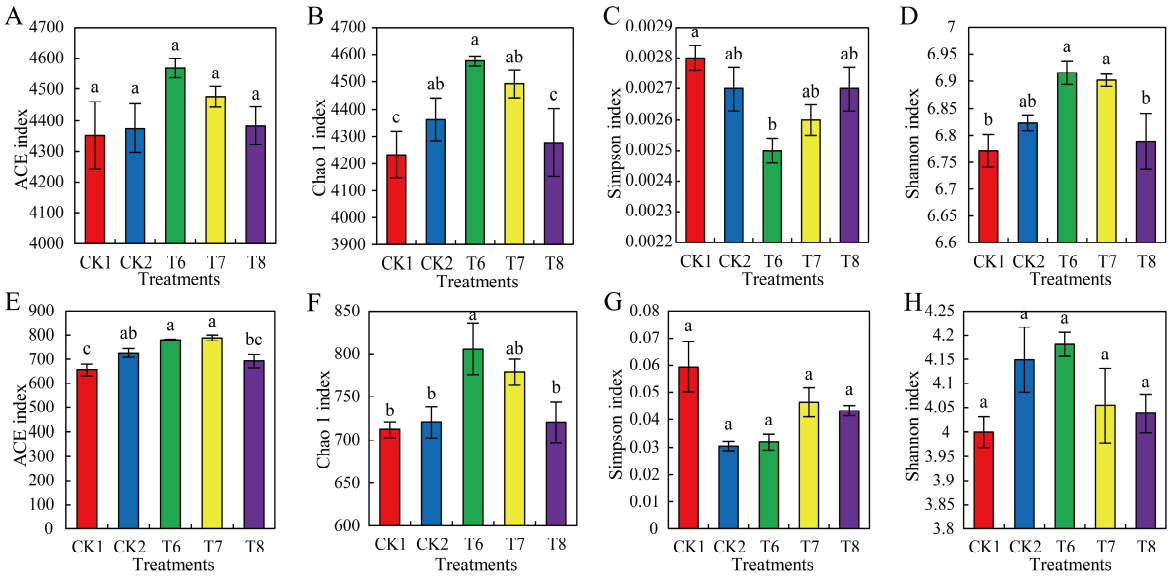

Figure 3. Bacterial (**A**–**D**) and fungal (**E**–**H**) diversity in rhizosphere soil of cabbage under different compost treatments. Different letters on the figure indicate significant differences ($p \leq 0.05$).

3.4. Soil's Microbial Community Structure under Different Fertilization Conditions

Different compost formulas altered the bacterial and fungal community's structure significantly. PCoA divided the bacterial community into two groups, namely, CK2, T6, and T7 and CK1 and T8 (Figure 4A). The bacterial community structures under the CK2, T6, and T7 treatments were clustered far from those of the other treatments, indicating that the bacterial community structure was changed significantly by compost application (Figure 4A). PCoA divided the fungal community into three groups, namely, CK2, T6, and T7; CK1; and T8 (Figure 4B). The fungal community structures in the CK2, T6, and T7 treatments were clustered at a distance from those of the other treatments (Figure 4B), while CK1 existed in one quadrant alone, indicating that compost application changed the fungal community structure significantly.

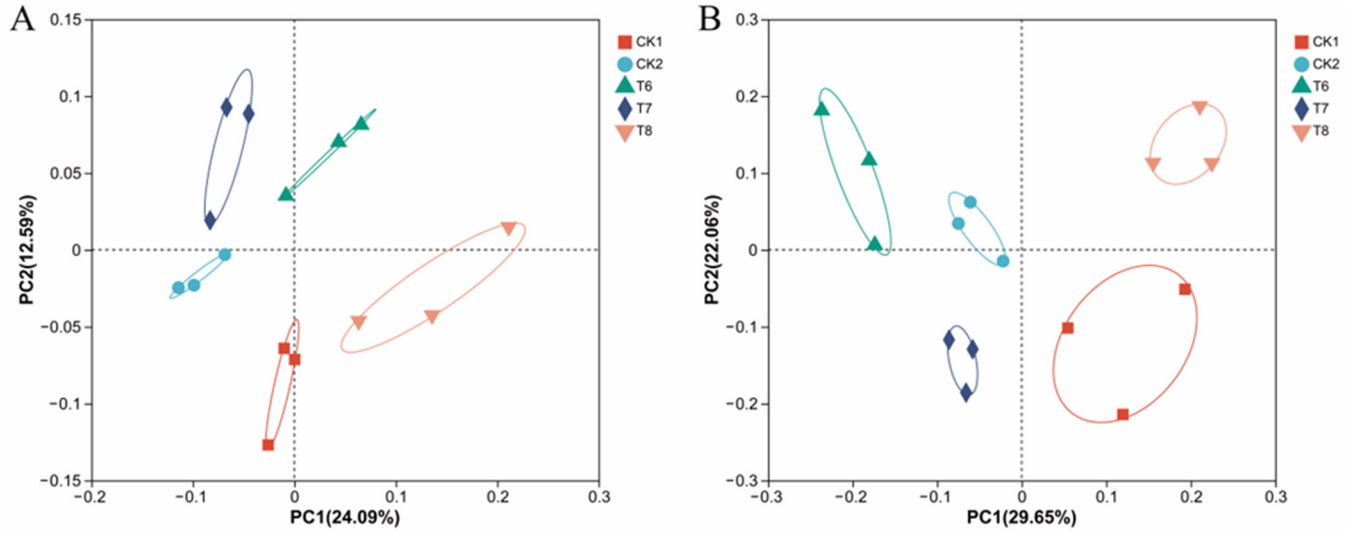

Figure 4. Principal Coordinate Analysis (PCoA) of bacterial (**A**) and fungal (**B**) communities.

3.5. Relative Abundance of Major Bacterial and Fungal Groups

As shown in Figure 5A,C, the main bacterial phyla under each treatment were Proteobacteria (25.22~29.49%), Actinobacteria (18.46~23.49%), Firmicutes (10.76~17.64%), and

Acidobacteria (10.29~14.48%), and their relative abundances in the treatments were in the 64.73~85.10% range. The other bacterial phyla were Chloroflexi (7.51~11.22%), Bacteroidota (3.82~5.10%), Myxococcota (2.89~3.87%), Gemmatimonadetes (2.30~2.77%), and Nitrospirota (1.02–1.24%). The abundances of Proteobacteria, Actinomycetes, and Firmicutes in the T6, T7, and T8 treatments were higher than that in the CK1 treatment, and the Acidobacteria abundances were lower than that in the CK1 treatment. Proteobacteria abundance was the highest in the T7 treatment, accounting for 29.49% of the total bacteria (TB), and its abundance was 16.93% higher than that in the CK1 treatment. The Actinomyces abundance was the highest in the T8 treatment, accounting for 23.49% of the TB, which was 21.96% higher than that in the CK1 treatment. The relative abundance of Firmicutes was the highest in the CK2 treatment, accounting for 17.64% of the TB, and it was 21.96% higher than that in the CK1 treatment. CK1 had the highest Acidobacteria abundance, which accounted for 14.48% of the TB, followed by those in the T8 and T6 treatments, accounting for 12.13% and 12.03% of the abundance, respectively.

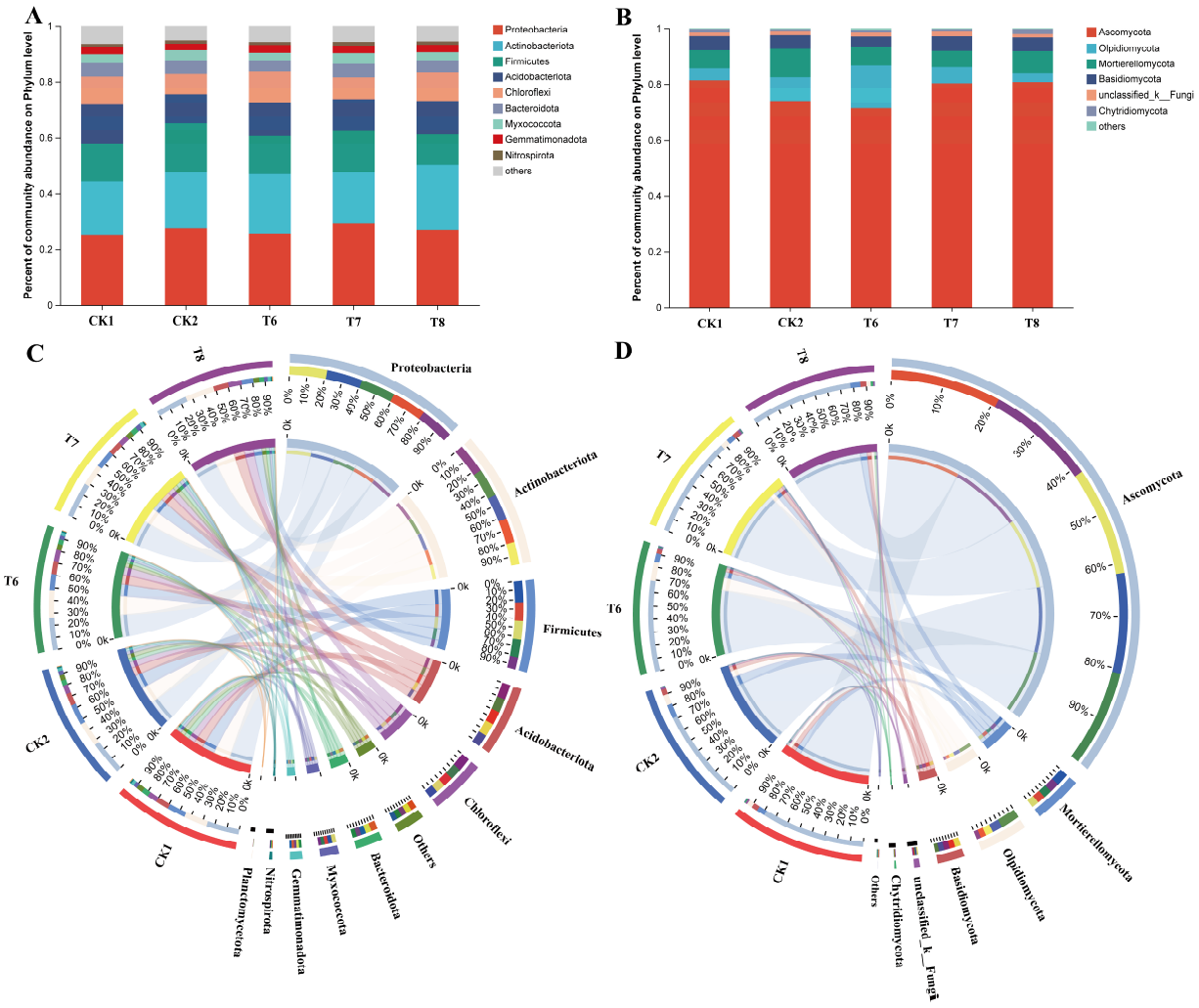

Figure 5. Relative abundances of major taxonomic groups of bacteria (**A**,**C**) and fungi (**B**,**D**) at the phylum level (others accounted for <0.01). The data are visualized using Circos, and the widths of bars indicate the relative abundance of the phyla.

The major fungal groups under different treatments were Ascomycota (71.61–81.34%), Olpidiomycota (3.44–15.19%), Mortierellomycota (5.89–10.44%), and Basidiomycota (5.89–10.44%). Basidiomycota (3.35–5.02%) was with lower concentrations in other unclassified phyla (Figure 5B,D). The abundances of Ascomycetes and Basidiomycetes under fertilization treatments were lower than those under the CK1 treatment, whereas Chytromycetes and

Sporoides abundances were higher than those under the CK1 treatment. Ascomycota abundances under the CK2, T6, T7, and T8 treatment were lower than those under the CK1 treatment and the lowest in the T6 treatment, with abundances that were 71.61% and 13.59% lower than that in the CK1 treatment. Basidiomycota abundances under the CK2, T6, and T8 treatments were lower than those of the CK1 treatment, and the lowest in the T6 treatment, which was 3.35% and 44.78% lower than that in the CK1 treatment. Ochrochytridia in the CK2, T6, and T7 treatments were higher than those in the CK1 treatment, and was the highest in the T6 treatment, being 15.19% and 238.31% higher than that in the CK1 treatment. Sporinae abundances in the CK2, T6, and T8 treatments were higher than those in the CK1 treatment and the highest in the CK2 treatment. The abundance in the CK2 treatment was 10.44% and 59.15% higher than that in the CK1 treatment.

3.6. Relationships among Soil Microbial Communities and Environmental Factors

The effects of environmental factors on the microbial community composition of the cabbage rhizosphere were evaluated using RDA (Figure 6). The soil properties under different agricultural waste compost applications influenced the microbial community structure. In Figure 6A, the first two axes of the RDA explain 47.37% and 20.81% of the total variation in bacterial community structure, respectively; for fungi, the first two axes explained 53.98% and 15.87% of the total variation, respectively (Figure 6C). Moreover, for bacteria, the first axis was positively correlated with TN, TP, TK, AN, AP, OM, and EC but negatively correlated with AK and pH; the second axis was positively correlated with AN, AK, and EC but negatively correlated with TN, TP, TK, AP, pH, and OM. In fungi, the first axis was positively correlated with TN, TP, TK, AN, AP, OM, and EC and negatively correlated with AK and pH. The second axis was positively correlated with TN, TP, TK, AN, AP, AK, pH, and OM and negatively correlated with EC. The environmental factors were significantly correlated to the bacterial and fungal community composition and were key factors influencing the bacterial community composition.

The relationships among physicochemical properties and bacterial communities were also assessed based on Spearman rank correlation (Figure 6B). We observed that Actinobacteriota was significantly positively correlated with EC, and Cyanobacteria was significantly positively correlated with AK ($p \leq 0.01$), whereas Myxococcota, Desulfobacterota, and Cyanobacteria were negatively correlated with EC. In addition, the microbes were correlated with other soil factors. Desulfobacterota was significantly positively correlated with AK and OM; Dependentiae was significantly negatively correlated with AN; Bacteroidota had a negative correlation with AN; Armatimonadota, Abditibacteriota, and Entotheonellaeota were positively correlated with pH; Hydrogenedentes and Dependentiae were negatively correlated with OM and TK; Hydrogenedentes were negatively correlated with AP; Dependentiae was negatively correlated with TN; and Dependentiae and Bacteroidota were negatively correlated with TP.

The Spearman correlation between the fungal community and physicochemical properties showed that unclassified fungi and AK were significantly positively correlated (Figure 6D). Unclassified-k-Fungi and Ascomycota were significantly negatively correlated with EC; Kickxellomycota was positively correlated with EC. Blastocladiomycota and Rozellomycota were negatively correlated with EC. Glomeromycota was positively correlated with pH and negatively correlated with TN, TK, AN, AP, TP, and OM. AK were positively correlated with Blastocladiomycota, Rozellomycota, and Aphelidiomycota.

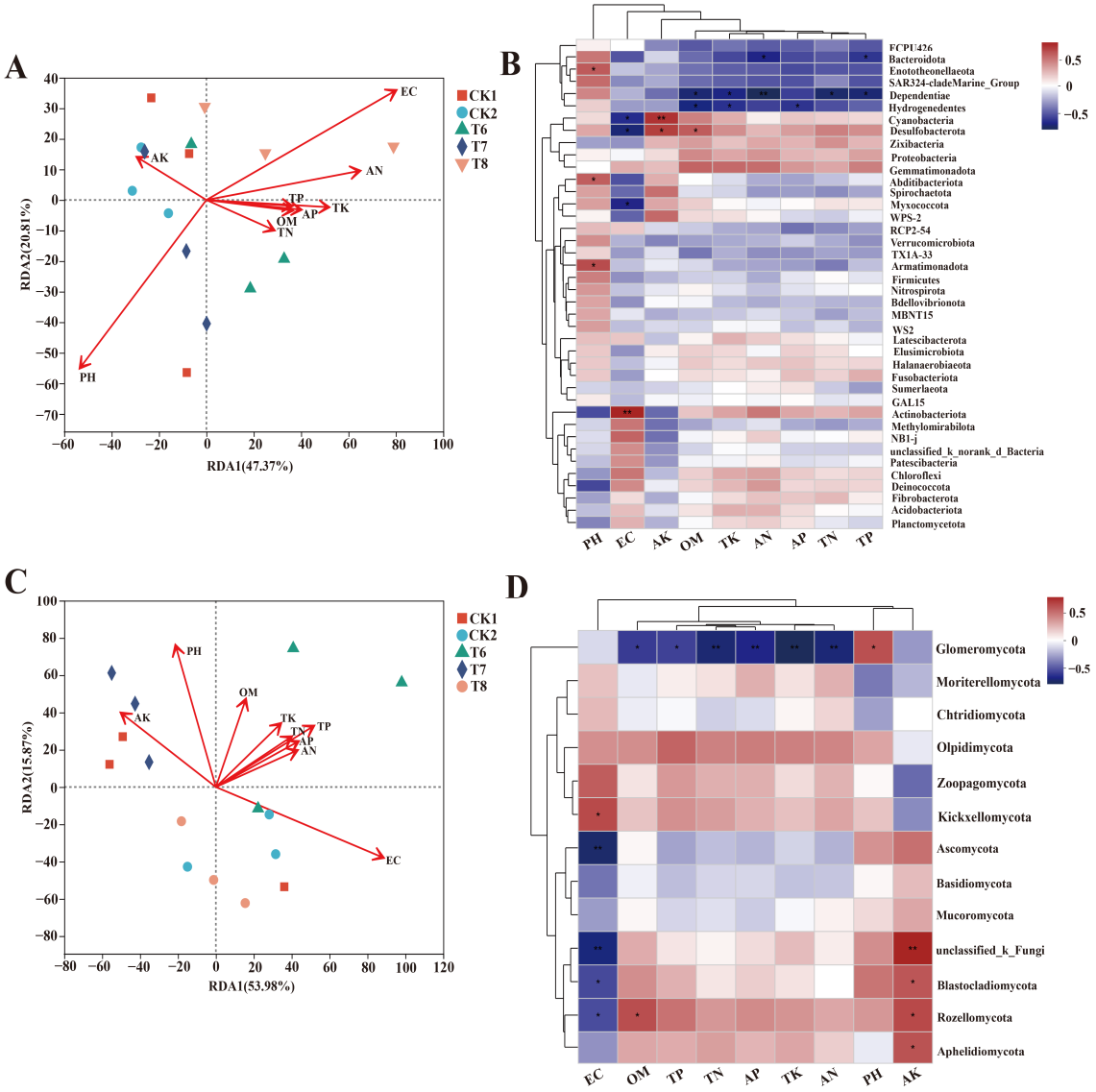

Figure 6. Redundancy analysis (RDA) of correlations between bacterial (**A**,**B**) and fungal (**C**,**D**) microbial communities and physicochemical properties and Spearman rank correlation heatmap ($p \leq 0.05$ *, $p \leq 0.01$ **).

3.7. Bacterial Function in Agricultural Waste Compost Soil

Tax4Fun transforms the 16S taxonomic lineages based on the Silva database into taxonomic lineages of prokaryotes in the KEGG database and predicts the KEGG function of prokaryote microbial communities by combining the correspondence between the two databases. The first level of the metabolic pathway database classifies biological metabolic pathways into six broad types: cellular processes, environmental information processing, genetic information processing, human diseases, metabolism, and organismal systems. The second level divides the 6 categories into 40 subcategories, and the 21 subclasses in Figure 7 are derived from 4 major classes and selected according to the second-level biological metabolic pathways.

In the genetic information processing pathway, there were four subcategories: cell growth and death, cell motility, cell community—prokaryote, transport, and catabolism. Bacterial communities under the T7 and T8 treatments had the highest functional abundance in the four subcategories. Bacterial communities under the CK2 treatment had the highest functional abundance in cellular motility. There were 11 subclasses of metabolic pathways, and the bacterial community under the CK2 treatment had the highest functional

abundance in carbohydrate metabolism, glycan biosynthesis metabolism, and nucleotide metabolism; the bacterial community under the T8 treatment had the highest functional abundance in biosynthesis of other secondary metabolites, energy metabolism, metabolism of other amino acids, and biodegradation and metabolism of heterotrophic organisms. The bacterial community under the T7 treatment had the highest functional predictive abundance in amino acid metabolism, energy metabolism, and cofactor and vitamin metabolism, while carbohydrate metabolism, terpenes, and polyketones metabolism were the highest under the T6 treatment. The results indicated that soil bacteria accounted for the highest proportion and functional abundance in biological metabolic pathways. Meanwhile, the application of agricultural waste compost improved the abundance of cellular processes, genetic information processing, and soil bacteria metabolism significantly.

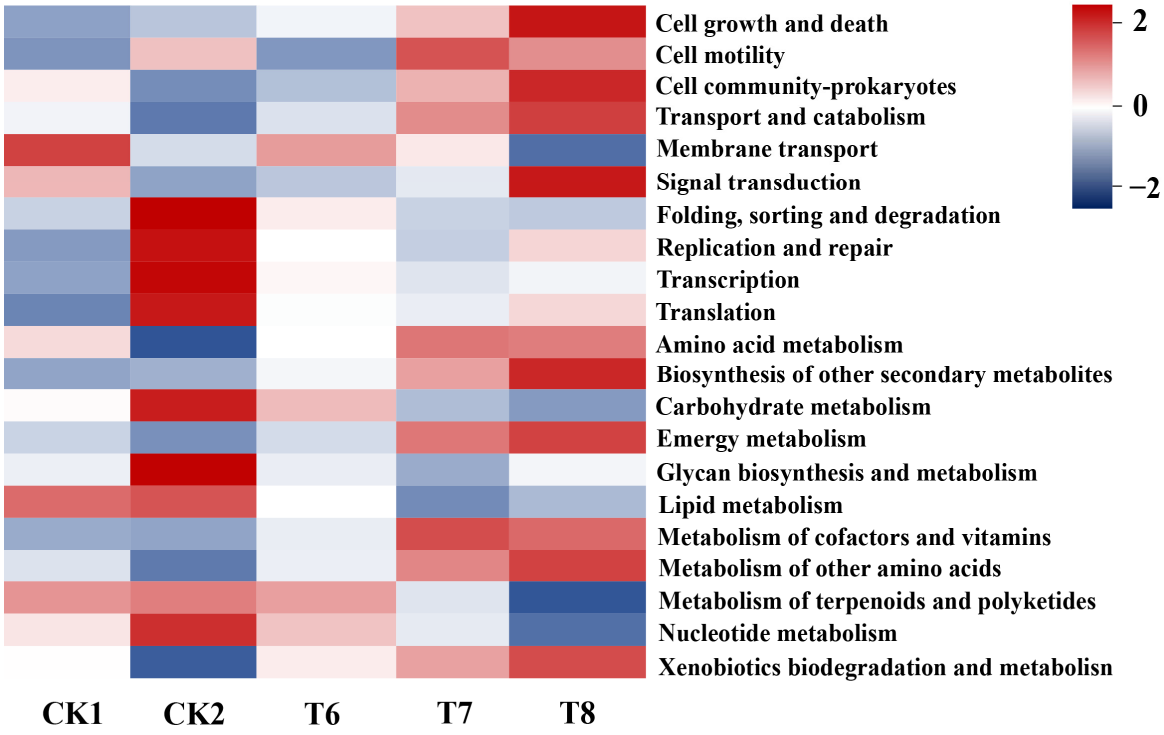

Figure 7. Heatmaps predicting bacterial function under different treatments. The colors from blue to red represent the relative abundances of the functions from low to high.

3.8. Fungal Function in Soil Treated with Agricultural Waste Composts

FUNGuild (Fungi Functional Guild) can classify fungal community function based on the trophic level, and functional prediction was conducted in the present study by associating species classification and functional guild classification using bioinformatics methods. Fungal communities can be divided into seven classes (saprotrophs, pathotrophs, saprotroph-symbiotrophs, symbiotrophs, pathotroph-symbiotrophs, pathotroph-saprotrophs, and pathotroph-saprotroph-symbiotrophs) according to the nutrition mode. A total of 81 functional groups were detected through functional classification and identification. According to the abundance ratio > 0.01 principle, 14 functional groups were identified. FUNGuild was used to predict changes in the composition of functional groups of fungi under different treatments (Figure 8).

Compared with the no fertilization CK1 treatment, the abundances of a variety of microbes changed after fertilization. The undefined saprotroph abundance in the CK2, T7, and T8 treatments increased by 19.81%, 4.98%, and 7.92%, respectively. The plant pathogen abundance in the CK2, T6, and T8 treatments decreased by 22.47%, 16.51%, and 56.77%, respectively. The abundances of Animal Pathogen–Endophyte–Plant Pathogen–Wood in the CK2, T6, and T7 treatments decreased by 223.38%, 289.06%, and 362.83%, respec-

tively. The Animal Parasite–Fungal Parasite abundances increased by 73.16%, 340.52%, and 82.34%, respectively. Moreover, the abundances of Animal Pathogen–Dung Saprotroph–Endophyte–Epiphyte–Plant Saprotroph–Wood Saprotroph under the CK2, T6, T7, and T8 treatments increased by 56.19%, 146.32%, 26.30%, and 85.12%, dung Saprotroph abundances increased by 97.19%, 405.62%, 444.28%, and 140.60%, while the Saprotroph–Wood Saprotroph abundances decreased by 580.44%, 491.26%, 523.23%, and 55.04%, respectively. In addition, Dung Saprotroph–Ectomycorrhizal–Soil Animal Pathogen–Endophyte–Lichen Parasite–Plant Pathogen–Soil Saprotroph–Wood Saprotroph abundances in the T6 and T7 treatments increased by 0.43% and 114.69%, respectively. According to the results, the agricultural waste compost application increased the number of saprophytic bacteria and saprophytic–symbiotic fungi significantly and reduced the number of pathogenic bacteria and pathogenic fungi to some extent.

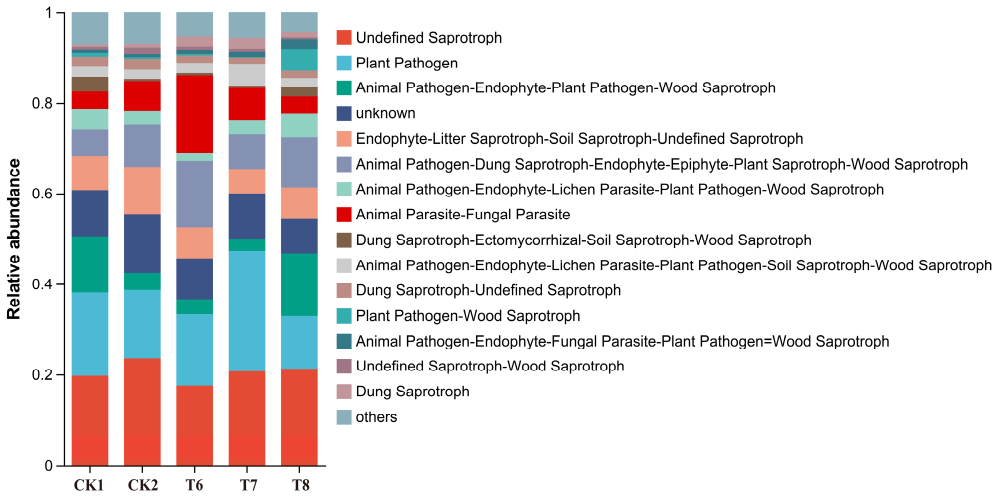

Figure 8. FUNGuild prediction of functional groups of fungi under different treatments.

4. Discussion

4.1. Effects of Agricultural Waste Composts on Cabbage Yield and Soil's Physicochemical Properties

Fertilization is critical for sustainable agricultural development. The rational application of crop waste compost improves soil's OM, which influences plant growth and yield by directly providing nutrients or indirectly by altering soil's physicochemical properties [31,32]. In the present study, the OM content was the highest under the T6 treatment and the lowest under the CK1 (no fertilizer) treatment, which was significantly lower than those in the other treatments, indicating that compost can increase the OM content significantly. Compared with the status in the CK1 treatment, the OM, total available nutrients, and available nutrient contents in the soil were significantly increased following the application of crop waste compost. Organic fertilizer can stimulate the production of root exudates and promote the activation of insoluble nutrients. In addition, organic fertilizers contain high amounts of nutrients, and the constituent carbon (C) and N can be decomposed and released relatively easily [33]. Moreover, biological organic fertilizers have high OM contents, which enhance microbial activities and can promote nutrient transformation and cycling [34]. Compared with those in the CK2 treatment, the OM, total available nutrient, and available nutrient contents in the T6, T7, and T8 treatments were increased significantly. The compost formulas in the T6, T7, and T8 treatments contained corn straw, and the OM, TN, and TP contents of corn straw are high, which could increase soil's N and P contents, indicating that the addition of appropriate amounts of corn straw can improve soil's N content and soil's N fixation ability [35]. After organic materials (including crop residues and organic fertilizers) are applied to the soil, mineral N is fixed by microbes due to the addition of energy materials, and soil N will increase correspondingly [36,37].

pH is one of the key indexes influencing soil's microbial community diversity; the closer the soil value is to a neutral pH (pH = 7), the greater the bacterial diversity is [38]. In

the present study, the soil pH was the lowest under the T6 treatment and the highest under the CK1 treatment. The pH in the CK1 treatment was higher than those in other waste compost fertilization treatments, indicating that compost fertilizer application could reduce soil's pH, prevent soil salinization, and improve bacterial diversity. In addition to pH, soil's EC in the present study was the lowest under the T6 treatment and the highest under the CK1 treatment, which was higher than those in other fertilization treatments, indicating that compost application could effectively decrease soil's EC value, reduce salt ions, decrease reverse osmotic pressure in soil, and minimize the toxic effect of soluble minerals on cabbage yield. Among all treatments, the T6 treatment had the most significant effect.

4.2. Effects of Agricultural Waste Compost on Soil's Microbial Richness and Diversity

Soil's microbial richness and diversity are two key indexes of soil quality, and they can be increased by inorganic or organic fertilizer application [39,40]. Organic fertilizer application enhances acid phosphatase and dehydrogenase enzyme activity in the maize rhizosphere, in addition to bacterial abundance and mycorrhizal infection [41]. In the present study, the ACE, Chao1, and Shannon indexes were the highest in the T6 treatment, while the Simpson index was the lowest in the T6 treatment. Opposite trends were observed in the CK1 treatment, indicating that T6 could improve the bacterial richness and diversity significantly. Similar to the T6 treatment, the T7 treatment increased the soil's microbial richness significantly. In addition, similar to the findings of Ji et al. [42], we observed that organic fertilizer application improved the soil's bacterial community diversity and evenness. The results could be attributed to the addition of corn straw to the T6 and T7 formulas, which decomposed and provided C and N sources for microorganisms, which facilitate microbial growth and reproduction [43,44]. The straw application can improve soil's physicochemical properties and structure, which in turn promotes microbial metabolic activities in soil [45]. Some studies have shown that the application of biochar that is produced from straw to a field can reduce competition among microorganisms, protect beneficial soil microbes, and improve the soil's microbial community structure [46].

Bacterial abundance, community structure, and diversity affect soil's sustainability and productivity [47,48]. Soil bacteria facilitate nutrient absorption and soil-borne disease resistance, and they activate plant defense systems against pathogens [49,50]. In the present study, Proteobacteria, Actinomyces, Firmicutes, and Acidobacteria were the dominant bacterial populations. The Proteobacteria abundance was the highest under the T7 treatment, followed by the T8 treatment. This may be due to differences in the OM content between the T7 and T8 formulas. Under higher OM and nutrient conditions, Proteobacteria, which are eutrophic bacteria, can grow and reproduce rapidly [51].

The T8 treatment had the highest Actinomycetes richness, followed by T6. Actinomycetes can produce numerous substances that can promote plant and animal residue decomposition and influence soil's microbial community structure and diversity [52]. In addition, some Actinomycetes can secrete hormone substances in soil and stimulate the release of more root secretions [53], providing rich energy resources for the growth and propagation of microbes and promoting the proliferation of beneficial bacteria. This is consistent with the results of related studies showing that organic fertilizer alters the bacterial and fungal community composition and increases the relative abundance of dominant bacterial phyla (e.g., Bacteroidetes, Blastomonas, and Myxococcus) and fungal phyla (e.g., Basidiomycetes and Mycetes) [54]. Acidobacteria represent a group of bacteria that grow slowly and accumulate in environments with low nutrient contents and that can degrade complex organic materials [55–57]. In the present study, the Acidobacteria abundance was the highest in the CK1 treatment, followed by the T6 and T8 treatments, indicating that T6 had a higher OM content and longer slow-release than the other treatments.

The Rhizosphere fungal community's structure is affected by temperature, soil moisture, and soil's microbial sources, with interactions among microbial sources and abiotic environments [44]. In the present study, the dominant fungal populations were Ascomycota, Echinomycota, Sporoidiae, and Basidiomycota, which is consistent with the conclusion that

the long-term application of inorganic and organic fertilizers could promote the succession of fungal communities toward Ascomycota, Zygomycota, and Basidiomycota [58]. Basidiomycota and Olpidiomycota reportedly increased significantly in pig manure and sludge compost treatments [59]. The Ascomycota abundance in the CK2, T6, T7, and T8 treatments was lower than that in the CK1 treatment, with the lowest being identified for the T6 treatment. The highest relative abundance of Ascomycota being in the CK1 treatment may be due to its saprophytic fungi, which are affected by plant species and fertilizer.

4.3. Relationships between Microbial Communities and Soil Environmental Factors

Soil's microbial diversity and composition are key indexes of soil's physicochemical properties. Soil's microbial diversity and composition are sensitive to shifts in soil's environmental factors such as the pH and OM content [60]. Bacterial and fungal growth and activity varied with crop yield, soil's physicochemical properties, and soil's biological properties. pH is one of the key factors influencing the microbial community structure [61], which is consistent with our results. In the present study, the RDA analysis results showed that the major factors driving community differences among treatments were the pH, EC, AK, AN, and OM. Although the pH varied over a small range, it still affected the microbial community structure significantly. On the one hand, pH can affect the types of soil microbes directly, and environmental pressures can screen out and retain species that have adapted to a certain pH level [62]. On the other hand, pH affects physicochemical activities such as enzyme activity, enzyme formation, membrane permeability, or metabolic pathways. In addition, compared with fungi, bacteria are more responsive to pH [63,64]. Cyanobacteria is a type of active N-fixing phylum that is critical for soil productivity improvement and maintenance, and several studies have reported the biological N-fixing potential of cyanobacteria (e.g., P bacteria) in dryland wheat fields [65]. The application of inorganic fertilizer, especially phosphate fertilizer, can stimulate Cyanobacteria growth [66], which is consistent with the results of the present study showing a significant positive correlation between cyanobacteria and AK. Consistent with previous studies that have reported that organic fertilizer can increase the relative abundance of Proteobacteria, Betaproteobacteria, and Deltaproteobacteria significantly, high N environments are favorable for symbiotic bacteria, and unfavorable for oligotrophic bacteria, whose capacity for OM degradation is relatively low [51]. Proteobacteria, especially Betaproteobacteria, are favored by high OM and high C contents in eutrophic environments [67], which is similar to our results.

As far as the compost formula is concerned, the addition of corn straw affected the soil's environmental factors significantly, and some studies have found that adding corn straw alters the fungal community structure [68,69]. In the present study, T6 had significant effects on the soil environment, which mainly changed the OM, AHN, and AP of the soil. Therefore, it is hypothesized that compost formulas containing corn straw alter soil's physicochemical properties, thereby affecting soil's microbial community structure and diversity.

4.4. Effects of Waste Compost on Soil Microbial Community's Function

In the present study, 4 major and 21 minor soil microbial community functions were predicted using Tax4Fun. According to the results, the application of agricultural waste compost enhanced cellular processes, genetic information processing, and soil bacterial metabolism functions significantly. Previous studies have shown that the enhancement of metabolic function improves a microbial community's decomposition activities and metabolic compound accumulation [70]. Amino acids and carbohydrates are the two main C sources that are utilized by microorganisms, and the increased metabolism of the two types of carbohydrates indicates that the microbial function diversity has increased [71]. It also indicates that OM decomposition and leaching have increased the substrate that is required for bacterial metabolic activities, providing a more suitable habitat for microbial metabolic activity [72,73]. An improvement in cellular processes and genetic information processing functions will enhance gene expression, and the expression of some functional

genes in turn enhances metabolic processes. In the present study, the addition of corn straw in compost enhanced energy metabolism, amino acid metabolism, and carbohydrate metabolism, which is consistent with the findings of previous research [74]. Such changes in bacterial groups and functional genes may drive nutrient cycling in soil, in turn promoting plant growth.

FUNGuild predicted that 12 out of 14 functional groups contained saprophytic fungi with increased abundance. The application of agricultural waste composts increased the number of saprophytic fungi and decreased the number of pathological fungi, and the above results also indicated that compost enhanced the decomposition capacity of soil fungi.

The Animal Pathogen–Dung Saprotroph–Endophyte–Epiphyte–Plant Saprotroph–Wood Saprotroph and Animal Parasite–Fungal Parasite abundances in the T6 treatment were significantly higher than those in the other treatments, indicating that that the T6 treatment could also increase the abundance of symbiotic fungi significantly. Some studies have shown that the decrease in ectomycorrhizal fungi following N application is offset by an increase in saprophytic fungi, and the saprophytic fungi are positively affected by soil's N content [75,76]. In the present study, the organic C input and change in soil aggregate size distribution played important roles in fungi development. In addition, increasing the OM content could increase the abundance of various fungi, improve the nutrient content and nutrient utilization, and reduce the spread of soil-borne diseases [77], which is consistent with the highest AN and OM contents being observed in soil that was treated with T6.

5. Conclusions

In conclusion, the use of agricultural waste composts can improve cabbage soil's environmental conditions and soil fertility and facilitate agricultural waste recycling. In the eight experimental formulas, T6 (corn straw/cow manure/tail vegetable/sheep manure = 1:1:2:6) was the optimal formula, which increased the contents of AK, AHN, and soil OM, reduced the soil's saline alkalinity, regulated the soil's microbial community structure, and increased the cabbage yield. The results of the present study could facilitate sustainable vegetable production and exploitation of agricultural waste resources.

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Data Availability Statement: The datasets (SRP483858 and SRP484084) presented in this study can be found in the NCBI Sequence Read Archive "https://www.ncbi.nlm.nih.gov/sra/?term=SRP483858 and https://www.ncbi.nlm.nih.gov/sra/?term=SRP484084 (accessed on 17 January 2014)". Data not included within the manuscript are available upon written request to the corresponding author.

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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