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Short-Term Effects of Different Organic Amendments on Soil Fungal Composition

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Abstract: Fungi play an essential role in recovering the quality and fertility of soil. There is a limited understating of the complex response of fungal diversity to different organic materials in clay loam soil. Here, we report the response of soil fungi toward the short-term application of manure (M), sugarcane straw (S), and sugarcane straw plus manure (MS), including no organic material control (CK) at two different time points (50 and 100 days after application). Illumina sequencing was used to examine the fungal communities. Our results reveal a significant shift among the soil fungal community structure associated with each organic material application. After both time points, amendments—especially M and MS—decreased the fungal richness and stimulated the copiotrophic fungal group (*Ascomycota*) compared to the control soil (CK) and S-amended soil. On the contrary, as compared to the M and MS-amended soils, the CK and S-amended soils at both time points increased the fungal richness and stimulated the oligotrophic fungal groups. Organic material use, especially M and MS, showed variable results regarding pathogenic fungi enhancing the abundance of *Lophodermium* and *Cercophora* and decreasing *Fusarium*. Concerning the abundance of plant-beneficial fungi, *Mortierella* was reduced, and *Podospora* was increased by M and MS input. FUNGuild showed that the amendment of organic materials efficiently declined the abundance of endophytes and plant pathogens, but also enhanced the animal pathogens in terms of abundance with respect to CK at two time points. This study could be useful to provide a novel understanding of the management of soil-borne pathogens by organic amendments for the sustainable production of short-term crops.

Keywords: short-term fertilization; soil fertility; sugarcane straw; goat manure; fungal community composition; soil-borne pathogens; high throughput sequencing

1. Introduction

Fertilization is a well-known agricultural strategy in which the mineral and organic amendments are commonly practiced to enhance soil fertility and crop yield [1]. One of the leading concerns is the growing demand for crop production to feed human beings around the globe [2]. Conventional

agriculture farming based on mineral fertilizers has made a significant contribution to meeting global food demands [3]. On the contrary, soil degradation and acidification are the significant obstacles attributed to the application of mineral fertilizers; the nitrogen especially contributes to a drastic reduction in soil fertility and crop yield [4,5]. In view of that, organic material application represents an alternative approach to mineral fertilizers in order to ensure human health, agricultural sustainability, food security, and crop yield [6,7]. Furthermore, organic materials frequently improve soil fertility and structure by enhancing soil organic matter contents and nutrient status, thereby increasing soil microbial biomass and activity [8–10]. Additionally, different types, amounts, and frequencies of soil amendments improve the soil physiochemical attributes, affecting soil fertility, and thus ensuring crop yields [1,8].

Fungi are the primary decomposers and carbon sequesters in soil and agroecosystems [11–13]. The shift in fungal community composition is not only due to the input of substrates but also the existence of fungi in the organic materials [14–16], which may be pathogenic to human and plant health [17,18]. However, most of the researchers have studied the response of fungal communities to organic materials in term of different types in soil ecosystems under long-term experiments [19,20]. Only a few studies were carried out in order to investigate the impacts of organic materials on soil fungal community structure and soil fertility under short-term experiments [21,22], which are supposed to be very different from long-term ones. In our previous study, we explored the impacts of sugarcane straw (S), goat manure (M), and goat manure plus sugarcane straw (MS) on soil fertility, soil enzymes activities, and bacterial composition at two different time points. The results revealed that M and MS amendments could effectively improve soil fertility and enzyme activities as well as enhance the plant beneficial bacteria [8]. However, the response of soil fungal communities to M, MS, and S-treated soil was not explored. Therefore, in this study, Illumina sequencing of the fungal ITS (Internal Transcribed Spacer) region was used to investigate the response of soil fungal communities to various organic materials (M, S, and MS) at two different time points (50 and 100 days after application). We assumed that variations in the fungal communities due to the application of different organic materials may change the abundance of various fungal taxa.

2. Material and Methods

2.1. Experimental Design and Soil Sample Scheme

A pot experiment was carried out from March to June in 2017 in Fujian Agriculture and Forestry, Fuzhou, Fujian, China (latitude: 26°05′9.60″ N; longitude: 119°14′3.60″ E). In this experiment, four different treatments were performed by amending S, M, and MS to soil in the pots (red PVC) with 120-mm diameter and 180-mm height. Soil without amendment was considered as control (CK). The collection of S was carried out from the university sugarcane field, chopped into small pieces, air dried for 20 days, and kept at room temperature. M was purchased from the market. The soil had a clay loam texture (43.1% silt, 36.6% sand, and 20.3% clay) with 0.97%, 0.07%, and 0.10% of total carbon (TC), total phosphorus (TP), and total nitrogen (TN), respectively. The physiochemical characteristics of S and M that were utilized in this experiment were as follows: (i) S:TN (0.45%), TC (44.15%), total potassium (TK) (0.5%), TP (0.04%), and C:N ratio (98.11); and (ii) M:TN (0.8%), TC (17%), TK (0.41%), TP (0.52%), and C:N ratio (21.25) [8]. For MS treatment, the 7.5% M, 7.5% S, and 85% soil were combined. For S and M amendments, the 15% of S and M respectively, was combined to 85% of soil [23]. During the experiment, the relative humidity of 75–80% and temperature of 18–30 °C were kept. Three repetitions were considered for each pot. On a weekly basis, one liter of distilled water was provided to each pot [24]. Soil sampling was carried out at two time points (50 and 100 days) after the amendment of organic materials [8,25], and then samples were sieved using two mm of mesh and kept at −80 °C until DNA extraction and molecular analyses were performed. Further details and information concerning this experiment have been described in our previous work [8].

2.2. DNA Extraction, Purification, and Fungal ITS Sequencing

For each sample, total genomic DNA was extracted by using a Fast DNA^{TM} Spin kit (MP Biomedical, Santa Ana, CA, USA) and purified through DNA purification kit (Tiangen Biotech Co., Ltd., Beijing, China), according to the manufacturer's recommendations. DNA was assessed for quantity and quality by using Nanodrop 2000c (Thermo Fisher Scientific, Middletown, VA, USA) and stored at −20 °C until sequencing. The primers ITS5-1737F and ITS2-110 2043R were used to amplify the fungal ITS1 region [26]. PCR reactions were conducted in 30-μL mixtures with each primer (0.2 μM), Phusion® High-Fidelity PCR Master Mix (15 μL) (New England BioLabs, Ipswich, MA, USA), and DNA templates (10 ng). PCRs conditions were (98 °C for one minute, followed by 30 cycles of 98 °C for 10 seconds, 50 °C for 30 seconds, and 72 °C for 60 seconds with a final extension at 72 °C for five minutes). The PCR products were purified by using QIAquik Gel Extraction Kit (QIAGEN, Düsseldorf, Germany). A TruSeq® DNA PCR-Free Sample Preparation Kit (Illumina, San Diego, CA, USA) was used to generate the sequencing libraries, and their qualities were further evaluated on the Qubit@ 2.0 Fluorometer (Thermo Scientific, Waltham, MA, USA) and Agilent Bioanalyzer 2100 system. Finally, the DNA libraries were sequenced on an Illumina HISeq2500 platform by external service (Novogen, Beijing, China).

2.3. Bioinformatic and Statistical Analysis

The paired-end reads from the original DNA fragments were merged using FLASH [27,28] and according to the unique barcodes that were assigned to each sample. Based on 97% similarity, sequences were assigned to the same operational taxonomic unit (OTU). The representative sequences were selected for each OTU and in order to annotate the taxonomic information for each representative sequence, the Ribosomal Database Project (RDP) classifier was used [29]. The diversity (Simpson and Shannon) [30] and richness (Chao1 and ACE) indexes [31,32] were used to analyze alpha diversity by Quantitative Insights into Microbial Ecology (QIIME) and displayed using R software (version 2.15.3) [33]. Based on the observed species richness, the rarefaction curves were constructed, and the Venn diagram was used in order to display the unique and common OTUs between the eight soil samples. For beta diversity analysis, unweighted UniFrac principal coordinate analysis (PCoA) and weighted Unifrac UPGMA (Unweighted Pair Group Method with Arithmetic Mean) was employed to examine the differences in species complexity between samples. In order to examine the interaction between the fungal community structure and environmental parameters, redundancy analysis (RDA) was performed on the soil's physiochemical characteristics that were analyzed in our previous work [8]. The RDA of soil properties and the relative abundance of dominant fungal phyla was performed by using the R software (version 2.15.3). Significant differences in the relative abundance of each fungal taxon among the amendments and within each sampling time were examined through one-way analysis of variance (ANOVA) using the DPS software (version 7.05, www.dpssoftware.co.uk).

2.4. Functional Assignment

FUNGuild v1.0 [34] was used in order to explore the fungal functional groups (guilds) in organically-amended soils at the two time points. In more detail, the OTUs were generally grouped based on the three main trophic modes as saprotrophs, pathotrophs, and symbiotrophs, while all of the OTUs that were not matching with any taxa in the database were categorized as "unassigned".

3. Results

3.1. Fungal Species Richness, Alpha and Beta Diversity Analysis

At both time points, a total of 1,897,648 (average 79,069) reads were obtained from all of the samples. According to the rarefaction analysis curve, the OTU numbers for ITS were plateaued at 97% similarity after the 45,000 sequences (Figure 1; Table S1). This confirmed that the sequence depth was sufficient to capture the richness and diversity of soil samples derived from CK, M, MS, and S

at both time points. A total of 1383, 940, 1087, and 1191 OTUs were found from the samples derived from CK, M, MS, and S after the first sampling (50 days) (Figure S1). In contrast, a total of 1238, 1133, 967, and 1054 OTUs were observed from CK, M, MS, and S after the second sampling (100 days) (Figure S1). The Chao1 and ACE indexes of S, M, and MS amendments decreased compared to CK at both time points (Figure 2a,b). The Shannon and Simpson alpha diversity indexes with M, MS, and S amendments increased at the first time point as compared with CK, while at the second time point, they increased by M, decreased by MS, and appeared equal in S, with respect to CK (Figure 2c,d). The results indicate that the species richness decreased and the diversity of fungi increased by the organic material input at both sampling times. According to cluster analysis, CK and S samples at both time points were clustered in the same groups (I and III, respectively), while M and MS samples of both time points were clustered in group II (Figure 3a). PCoA confirmed what was observed with the cluster analysis, demonstrating that the composition of fungal communities might be directly associated with different organic types (Figure 3b).

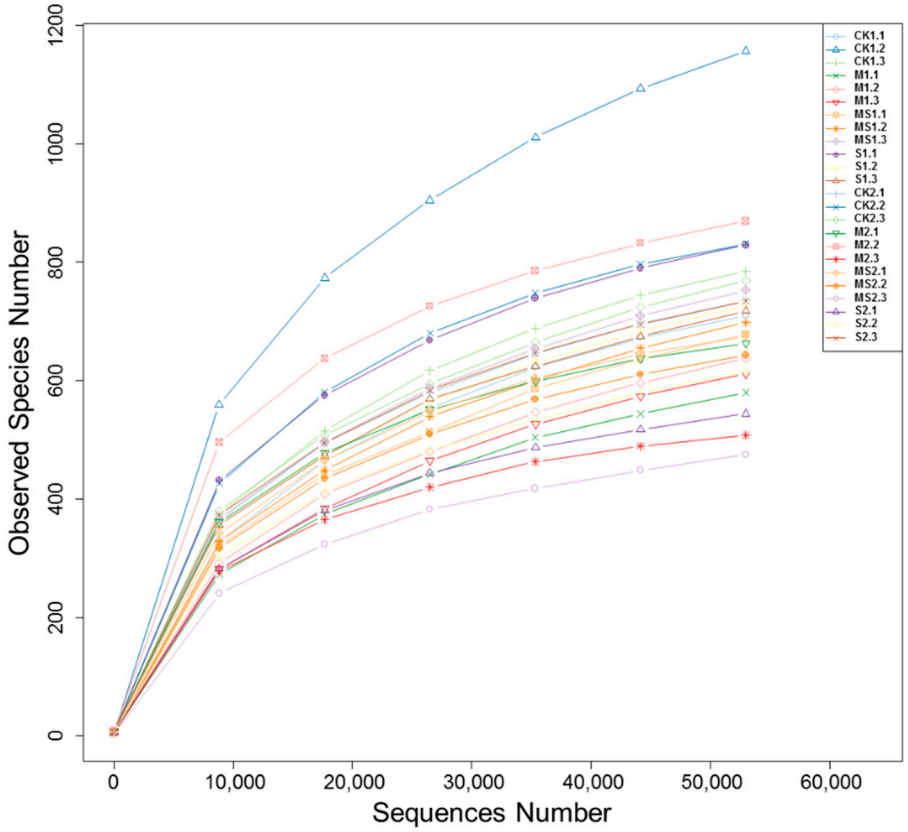

Figure 1. Rarefaction curves for organic-amended soil samples of two time points at an operational taxonomic unit (OTU) threshold of 97% sequence similarity. CK1.1, CK1.2, and CK1.3: control soil at 50 days; M1.1, M1.2, and M1.3: goat manure-treated soil at 50 days; MS1.1, MS1.2, and MS1.3: goat manure plus sugarcane straw-treated soil at 50 days; S1.1, S1.2, and S1.3: sugarcane straw-treated soil at 50 days. CK2.1, CK2.2, and CK2.3: control soil at 100 days; M2.1, M2.2, and M2.3: goat manure-treated soil at 100 days; MS2.1, MS2.2, and MS2.3: goat manure plus sugarcane straw-treated soil at 100 days; S1.1, S1.2, and S1.3: sugarcane straw-treated soil at 100 days.

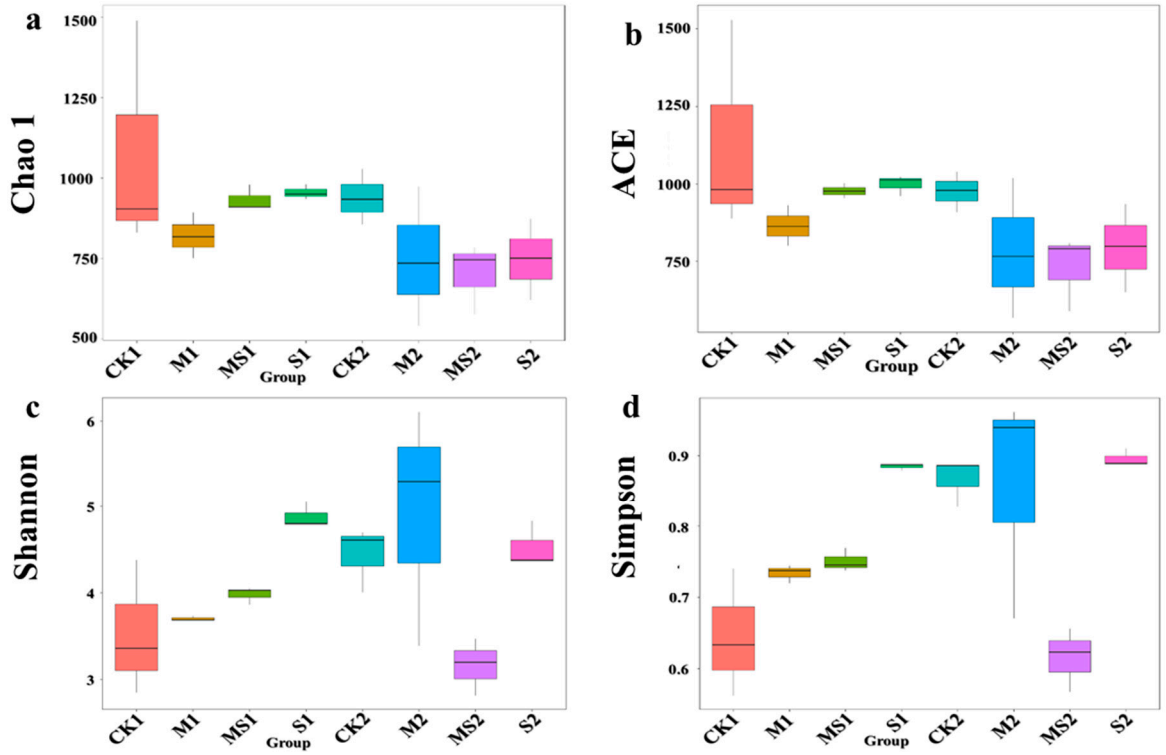

Figure 2. Box plots of the Chao1, ACE, Shannon and Simpson diversity indices of soil samples derived by various organic amendments at both time points. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days.

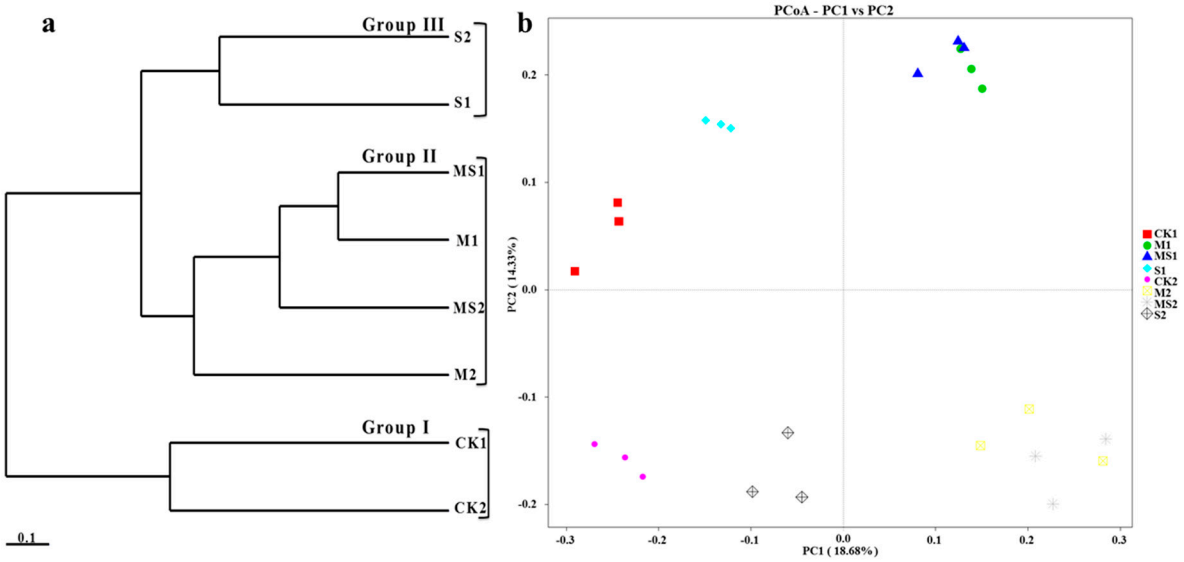

Figure 3. (**a**) Weighted Unifrac UPGMA clustering analysis of fungal communities associated with soil samples derived by various organic-amended soils at both time points. (**b**) Unweighted UniFrac (UUF) principal coordinate analysis (PCoA) plot based on the ITS sequencing genes from soil samples of both time points. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days.

3.2. Difference of Fungal Abundance by Different Organic Amendments

The most dominant phyla observed in all of the samples were *Ascomycota*, *Basidiomycota*, *Chytridiomycota*, *Zygomycota*, *Glomeromycota*, and *Neocallimastigomycota* representing the 90–96% of the fungal sequences (Figure 4; Table S2). At the first time point, in CK, the *Ascomycota* and *Zygomycota* were significantly represented as lower and higher with respect to the M, MS, and S-amended soils. At the second time point, the *Ascomycota* and *Zygomycota* were the highest and lowest in MS treatment, as compared with other treatments. At the same time point, *Basidiomycota* abundance in S treatment was significantly higher than the other treatments. At the first time point, *Podospora* abundance was significantly higher in M and MS amendments than CK, and S. *Cercophora* was significantly higher in M and MS with respect to S and CK amendments (Figure S2; Table S3), and the abundance of *Zopfiella* was higher in MS and S-amended soils rather than MS and CK. *Lophodermium* abundance was significantly higher in M-amended soil than that of CK, MS, and S. The *Mortierella* abundance was lower in M, MS, and S amendments as compared to CK. A lower abundance of *Fusarium* was observed in M, MS, and S amendments with respect to CK. Concerning the second time point, *Podospora* abundance was significantly higher in M and MS amendments than CK and S. The *Cercophora* abundance was higher in M and MS amendments as opposed to S and CK. A significantly higher abundance of *Zopfiella* was observed in S-amended soil than M, MS, and CK. As compared to CK, MS, and S amendments, *Lophodermium* showed higher abundance in M. Besides, a significantly higher abundance of *Mortierella* was observed in M-amended soil as compared to CK, MS, and S, while a lower *Fusarium* abundance was observed in M, MS, and S-amended soils with respect to CK.

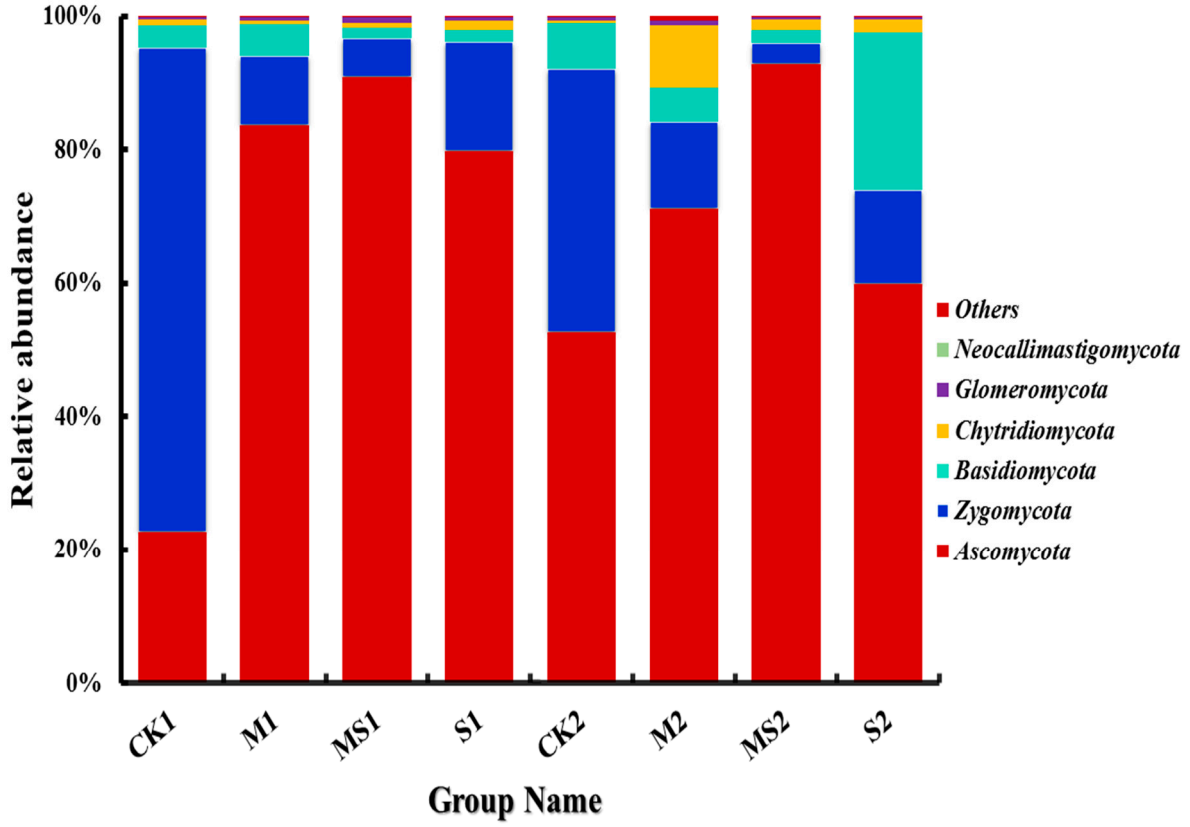

Figure 4. Fungi with high relative abundance at the phylum level in the soil samples derived from control and organic-amended soils at both time points. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days.

3.3. Functional Groups

The OTUs obtained from CK, M, MS, and S treatments during both time points were detected as trophic modes, symbiotrophs, pathotrophs, and saprotrophs, while all of the OTUs that were not matching with any taxa in the database were categorized as "unassigned" (Figure S3, Table S4). Concerning the first time point, the abundance of saprotrophs in CK (54.89%) and S (61.72%) was higher than M and MS amendments (44.33% and 50.46%, respectively). At the same time, significantly lower symbiotrophs were observed in M, MS, and S (15.87%, 16.97%, and 5.07%) amendments as opposed to CK (19.47%). Besides, a significantly higher proportion of pathotrophs was observed in M (11.14%) and S (14.31%) amendments as compared to CK (8.00%) and MS (7.24%). Concerning the second time point, the proportion of saprotrophs in S (78.54%) was significantly higher than that in the CK, M, and MS treatments (52.20%, 49.21%, and 58.41%, respectively). The proportion of symbiotrophs in M and MS-amended soils (13.87% and 19.69%, respectively) was higher than that of CK (12.19%). Finally, a significantly lower proportion of pathotrophs was observed in M (8.57%), S (7.51%), and MS (4.03%) amendments compared to CK (14.87%) at the second time point.

FUNGuild gave more detailed information on the trophic modes of fungal populations obtained from the selected soil (Figure 5; Table S5). Regarding the first time point, the relative abundance of endophytes in M, MS, and S treatments (15.29%, 15.85%, and 4.31%, respectively) was reduced compared to CK (18.43%). Animal pathogens increased in the M, MS, and S treatments (1.87%, 3.32%, and 10.11%, respectively) rather than CK (0.70%). The relative abundance of plant pathogens was enhanced in M (9.26%), while the MS and S treatments (3.89% and 4.09%, respectively) reduced compared to CK (7.29%). Control treatment (CK) was dominated by unidentified saprotrophs (27.78%), which was significantly higher than M, MS, and S (8.68%, 11.15%, and 15.32%, respectively). The proportion of wood saprotrophs in CK (21.94%) was higher than that of M, MS, and S (16.23%, 15.55%, and 7.21%, respectively). Compared with CK (1.78%), the dung saprotrophs was significantly higher in M, MS, and S treatments (18.33%, 22.03%, and 34.71%, respectively).

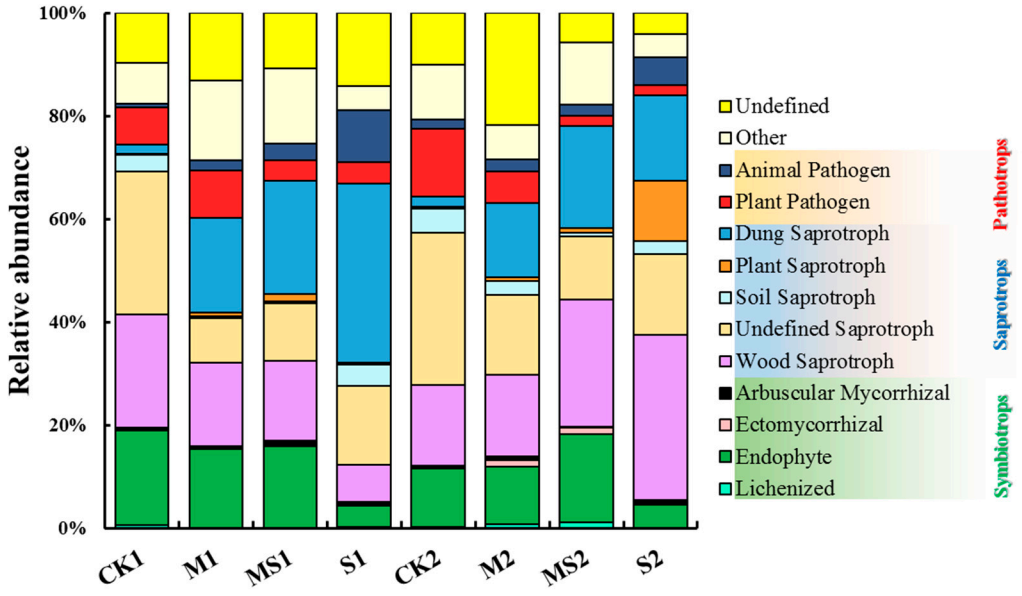

Figure 5. Variation in fungal function and the structure of the fungal functional groups (guilds) observed in this study. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days.

Regarding the second time point, the relative abundance of endophytes was reduced in M-amended soils (11.13%) and more strongly reduced in the S-amended soils (4.50%), while it increased

in the MS-amended soil (17.24%) compared to the CK-amended soils (11.45%). Animal pathogens increased in the M, MS, and S-amended soils (2.43%, 2.09%, and 5.49%, respectively) compared with CK (1.72%). An opposite trend was observed for plant pathogens in M, MS, and S-amended soils (respectively 6.01%, 1.89%, and 1.99%) compared with CK (13.13%). In the CK-amended soils, a high abundance of unidentified saprotrophs (29.39%) was observed with respect to the M, MS, and S-amended soils (15.45%, 12.29% and 15.63%). Wood saprotroph abundance was higher (15.96%, 24.67% and 32.20% respectively) in the M, MS, and S-amended soils as compared to CK (15.69%). Finally, a greater abundance of dung saprotrophs in the M, MS, and S-amended soils (14.51%, 19.90%, and 16.49%, respectively) was found compared to CK (1.96%).

3.4. Correlation Analysis between Soil Attributes and Fungal Community

Soil features can affect the fungal communities under different organic matter treatments. Of the analyzed soil features, C/N, NH_4^+, AK, TC, AP, and TN were significant conditional influences, while pH, TP, AN, and NO_3^- concentrations had an indicative influence on *Ascomycota*, *Glomeromycota*, *Chytridiomycota*, and *Neocalliumastigomycota*. Finally, all of these soil features were negatively correlated with *Zygomycota* (Figure 6).

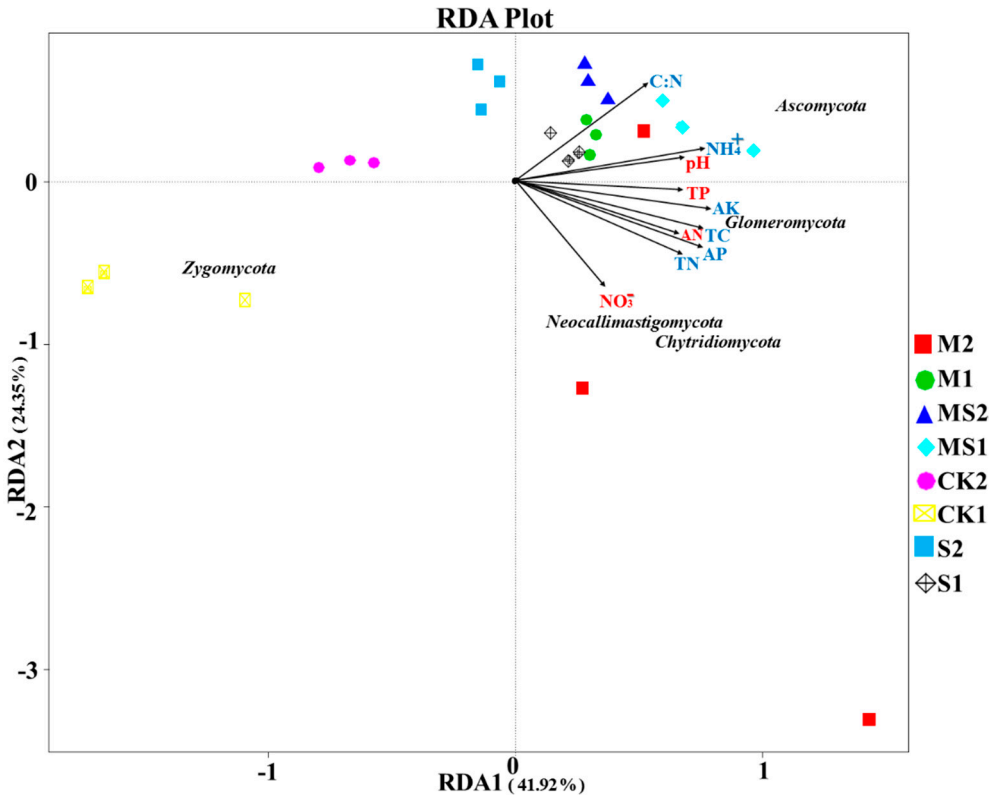

Figure 6. Redundancy analysis of soil properties and the relative abundance of dominant fungal phyla. These factors such as C/N, NH_4^+, AK, TC, AP, and TN, pH, AN, TP, and NO_3^- concentrations are shown in blue and red text. Soil properties' arrows in terms of length are showing the strength of interaction among the overall fungal community and soil properties. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days.

4. Discussion

The input of organic materials into the agricultural farming system has been recognized as a promising approach in order to enhance soil fertility. In our previous research, we have demonstrated that organic materials such as S, M, and MS were more effective at improving soil fertility in a short-term experiment (Table S6) [8]. Although S, M, and MS have a positive effect on soil fertility, their addition to soil could leave destructive or beneficial effects on soil health by increasing or suppressing pathogenic and beneficial fungi. Thus, with the current research, we studied the effects of S, M, and MS, focusing on the fungal communities in amended soil at two time points.

We observe a decrease in species richness in the M and MS-amended soils as compared to the CK and S-amended ones (Figure 2a,b), and the possible explanation could be due to the high availability of substrate incorporated in the soil affecting the oligotrophic fungal groups. Particularly, the higher oligotrophic population in CK and S-amended soils could be due to the lower nutrient availability, which in turn, enhanced the species richness in these treatments [35]. The destructive and beneficial impacts of fungal taxa later organic inputs have been widely reported [35–38]. It is likely that a higher availability of nutrients by M, MS, and S amendments may result in a shift of fungal taxa abundance that may be propitious or harmful to crop, human, and animals, thus influencing agroecosystem stability and performance.

Short-term organic fertilizers could have significant influences on soil fungal community structures. Clustering and PCoA analysis revealed visible changes in the fungal community compositions due to the different amendments (Figure 3a,b), which is consistent with previous results [21,22]. *Ascomycota* were significantly higher in term of relative abundance in soil amended with M and MS at both time points (Figure 4; Table S2). *Ascomycota* is known as the most ubiquitous and diverse phyla of eukaryotes as well as the decomposition of the organic substrates (e.g., leaf litter, wood, and manure), and has been found as the predominant fungal phyla in organic-amended soils [21]. At both time points, the relative abundance of *Zygomycota* in M, MS, and S-amended soils was significantly reduced, which is consistent with previous findings [21,39]. At first time point, the relative abundance of *Basidiomycota* in the soil amended with MS and S was lower, while an opposite pattern was observed in response to the amendment with S at the second time point. However, *Basidiomycota* usually degrades plant litter in forests with high lignin content [40]. It is likely that the high lignin content delivered by the S has led toward the increase in their abundance in the second time point.

Pathogenic fungi commonly acquire nutrients invading the host cells, so they are considered to have an adverse influence on other members of the fungal community [41]. The symbiotrophic fungi could lead to benefits for crop quality, health, and nutrition [42,43]. At the first time point, a lower abundance of symbiotrophs was found in organically-amended soils than CK, while the reverse pattern was observed in M and MS2-amended soils at the second time point. At the first time point, a considerably higher proportion of pathotrophs was observed on M and S amended soil as compared to CK and this trend was opposed in organically-amended soils at the second time point (Figure S3; Table S4). The results of FUNGuild showed that the amendment of organic materials efficiently decreased the abundance of endophytes and plant pathogens, but also enhanced the animal pathogens in terms of the abundance compared with CK at two time points. Additionally, goat manure input not only enhanced the proportion of endophytes at the second time point, but also enhanced the plant pathogens at the first time point (Figure 5; Table S5).

When investigating the data obtained through Illumina sequencing, we considered for unique fungal taxa (beneficial or pathogenic) that are suppressed or promoted by various management approaches. Thus, we can also report on the environmental role of fungal taxa regarding their behaviors in other systems [35]. In this contest, our study contributes to understanding how the input of organic materials may increase the proliferation of pathogenic and beneficial fungal taxa. *Lophodermium* spp. cause needle cast disease in a wide range of plants, and it was [44], enhanced significantly in M-amended soils at the first time point compared to the second time

point (Figure S2; Table S3). *Cercophora* were highly abundant genus in M and MS-amended soils rather than S and CK soil at both time points. Plant diseases such as leaf spots in various crops are attributed to *Cercophora* [45–48], which is consistent with the previous study under long-term organic amendment [35]. Conversely, *Fusarium* is pathogenic fungi that were highly dominant in CK-amended soils instead of organically-amended soils at both time points. Several studies have shown that the amendment of organic materials has a significant impact on controlling the plant diseases, which were caused by *Fusarium sp.* [49,50]. Concerning the beneficial fungi, *Mortierella* was highly abundant in CK instead of the organically-amended soil at the first time point. *Mortierella* has been known as a potential biological control agent for various plant pathogens [37], as well as a biological control agent for insects and pests [38]. Additionally, the *Mortierella* genus is also known as a phosphate-solubilizing fungi; they could support arbuscular mycorrhizal fungi (AMF) colonization and mitigate the damaging effects of salt on plant growth, including soil enzyme activity [36]. Members affiliated to the *Podospora* genus are considered to be the most abundant members of healthy soil [51], and can suppress *Verticillium* wilt on tomato [52]. These were highly abundant in M and MS-amended soils at both time points. Furthermore, the *Zopfiella* genus was enhanced in S-amended soil at the first time point than a second time point. *Zopfiella ssp.* survives in healthy soils and produces antifungal compounds that control the disease of various crops caused by soil-borne pathogens [51–53]. These results demonstrated that fungal communities and functions render differently to the short-term amendment of different organic materials in soils at two different time points. These results are useful in providing a novel understanding in order to manage soil-borne pathogens by organic amendments for the sustainable production of short-term crops.

5. Conclusions

Overall, our short-term observations exposed that M and MS amendments increased soil pH and nutrient availability, especially C, N, and P as compared to CK and S amendments at both time points, which in turn reduced species' richness and affected the proliferation of some genera that are plant pathogenic or beneficial. These changes induced by organic amendment may affect the stability and productivity of the agroecosystem. Soil fungi respond differently to the inputs of organic fertilizers under short-term experiments, which offers novel insights into the potential of managing soil-borne and soil-beneficial fungi for sustainable agricultural productivity. More research on field levels is needed in order to study the quick response of soil pathogenic and beneficial fungi to different organic amendments in the short-term cropping system.

Supplementary Materials: The following are available online at http://www.mdpi.com/2071-1050/11/1/198/s1, Figure S1: Venn diagram for soil samples at two time points. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days, Figure S2: Top 10 Fungi with high relative abundance at genus level in the soil samples. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days, Figure S3: Variation in fungal function at different time points. CK1: control soil at 50 days; M1: goat manure-amended soil at 50 days; MS1: goat manure plus sugarcane straw-amended soil at 50 days; S1: sugarcane straw-amended soil at 50 days. CK2: control soil at 100 days; M2: goat manure-amended soil at 100 days; MS2: goat manure plus sugarcane straw-amended soil at 100 days; S2: sugarcane straw-amended soil at 100 days, Table S1: Effective tags from the soil samples derived after organic amendment in both time points, Table S2: Composition of different fungal phyla in soil samples derived after different organic amendments at both time points, Table S3: Top fungi with high relative abundance at genus level in the soil samples, Table S4: Variation in fungal function under organic-amended soils at different time points, Table S5: Shift in structure of fungal functional groups (guilds) inferred by FUNGuild at two different time points, Table S6: Physiochemical characteristics of the soil.

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analyzed the data. M.T. wrote the manuscript. C.G.L., H.Z., W.L., and S.L. reviewed the manuscript. W.L. and H.Z. supervised the work and approved the manuscript for publication.

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