Reintroduction of Decomposed Straw To Maize Fields Resulted In Soil Microbial Community Change And Increased Corn Production

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Abstract

Purpose Returning decomposed straw to crop fields could address many agricultural shortcomings. In this study, the soil microbial community, soil nutrients, soil enzyme activities and maize yield were investigated after returning decomposed straw to the field.

Methods To investigate the effects of returning decomposed straw to field on soil microorganisms and maize growth, field experiments were carried out to measure soil nutrient content, soil enzyme activity and maize yield, and the soil microbial community structure was measured by 16SRNA and ITS amplicon sequencing technology.

Results The results showed that the contents of total nitrogen (TN), nitrate nitrogen (NN), total phosphorus (TP), available phosphorus (AP) and pH were significantly increased, and the contents of ammonium nitrogen (AN) and available kalium were decreased in both the rotary tillage (SR) and mulching (SM) treatments. The bacterial and fungal community structures in bulk and rhizosphere soils were clearly changed under SR and SM. The relative abundances of bacterial genera related to soil denitrification, such as *Skermanella*, *Blastococcus*, *Geodermatophilus* and *Asanoa*, were significantly increased. The relative abundances of *Conexibacter*, *Streptomyces* and *Trichoderma*, which bacteria that has shown to inhibit plant diseases, were increased. In addition, the relative abundances of growth-promoting bacteria, such as *Arthrobacter* and *Mesorhizobium*, were also significantly increased. Moreover, adding decomposed straw back to the field promoted the absorption of nutrients by maize, and resulted in higher yield of maize.

Conclusions Our findings suggest positive responses of soil microbial community structure and maize growth to decomposition straw returning.

Introduction

Maize is one of the three major food crops in the world and is one of the most economically important crops in China (He et al. 2020). Ensuring the production of corn is critical to the agricultural development of China. The soil microbial community, physical and chemical properties, and soil extracellular enzyme activity are the key factors affecting crop growth and production (Liu et al. 2021b).

Straw contains a large amount of nitrogen, phosphorus, potassium and other nutrients (Liu et al. 2021a). The total amount of straw in China is significant, with the annual production of crop straw has exceeded 900 million tons (Shi et al. 2017). The burning of straw produces a large amount of PM 2.5 (Chen et al. 2016) and can cause serious environmental pollution (Xiao 2012). Straw reincorporation has become a prevailing agricultural practice for improving soil fertility and reducing air pollution induced by crop straw burning (Cui et al. 2021). It is well established that straw applied directly to the soil increases soil fertility and nutrient substrates for microbial attachment (Zhou et al. 2016), stimulates the activity of soil heterotrophic microorganisms (Cai et al. 2003), promotes the absorption of nutrients by the root system, and increases maize yield (Qin et al. 2015; Zhang et al. 2014). However, excessive amounts of returned straw provide favorable environments for the growth and reproduction of pests due to its slow rate of decomposition, promoted the occurrence and damage from subsurface pests (Hu et al. 2011), and increased the incidence of soilborne diseases (Khaliq et al. 2011; Prasad et al. 2016). Moreover, straw returned directly to the field was suitable for the growth, propagation and accumulation of pathogens (Su et al. 2020b; Zhen et al. 2009). Composting straw can accelerate the maturity of straw, and the high temperature generated by composting can kill pathogenic bacteria. Returning straw to the field after composting can prevent the abovementioned problems caused by the direct application to the field. Decomposed straw applied could release more available nutrients to soils and lower the relative abundance of pathogenic fungi (Su et al. 2020a) and plant pathogens (Boulter-Bitzer et al. 2006). Compost can increase the content of humic acid and soil fertility (Ndzelu et al. 2020), incapacitate pathogenic bacteria (Klein et al. 2011), and maintain or enhance the levels of colonization of arbuscular mycorrhizal fungi in roots (Cavagnaro 2015). The addition of decomposed straw increased the contents of soil humus and organic carbon and stimulated a potential beneficial microbial population (Liu et al. 2021a).

Returning decomposed straw to crop fields could avoid a series of harmful effects (Siedt et al. 2021). Therefore, the objectives of the study were (1) to explore the changes in soil chemical properties, enzyme activities and soil microbial community structure after the application of decomposed straw. (2) To explore whether straw compost affected the growth and development of corn crops. These results provide a theoretical basis for maintaining soil quality and long-term productivity.

Materials And Methods

Site description and sampling

The maize variety selected in the experiment was Fujitai 519 (Henan Fujitai Seed Industry Co., LTD). The experiment had a randomized design with three replicates. Each treatment had three plots, and each plot was 10 m long and 3.3 m wide. The experiment included three groups of treatment. The three plot treatments were no returned straw (S0), decomposed straw spread evenly over the field and was rotated by a rototiller to 0.2 m depth (SR), and decomposed straw was evenly mulched on the plot (SM). The three treatments were planted in the same experimental area, which has the same soil properties, climate conditions and field management (Fig. S1). Decomposed maize straw was applied to the soil at 7.5 t/ha-1 dry weight. The basic properties of the soil (0–20 cm depth) are shown in Table S1.

For the treatment of decomposed straw, the straw was collected by the harvester and then composted in October 2019. Straw decomposing inoculants (Heilongjiang Heiwotu Biological Technology Co., Ltd.) were evenly sprayed on the straw by a sprinkler, and the added content was 1 kg/m³. The straw was covered with plastic film after adding water to prevent water volatilization. The straw compost was completed over 40 days. the straw compost was turned over twice to achieve a more even fermentation of the material. After composting, the degradation rate of decomposed straw was 28%. The decomposed straw was returned to the field in April 2020. The chemical properties of the decomposed straw are shown in Table S2.

Soil samples were taken at the Research Station of Qiqihar University of Meilise district, Qiqihar (123°74'90.67E, 47°40'43.17N). The soil type was characterized as chernozem. Bulk soil and rhizosphere soil samples were collected separately during the jointing and flowering period. The bulk soil was collected from the top layer (0–20 cm) of soil around the plant. Five randomly located soil samples were taken from each plot and combined into one composite sample. Then, the composite sample was air-dried, sieved (< 2 mm), and mixed to achieve a high degree of homogeneity and to reduce the variability among replicates. Fine roots and visible plant residues were carefully removed prior to use. The bulk soil samples were divided into two subsamples: one was air-dried and then stored at 25°C to determine the physical and chemical properties, and the other was stored at -80°C. Rhizosphere soil was collected by shaking the roots vigorously to obtain soil attached to the roots. Rhizosphere soil samples was stored at -80°C. There were three duplicates for bulk soil samples and rhizosphere soil for each plot. Bulk soil and rhizosphere soil stored at -80° were subjected to high-throughput sequencing (Majorbio Technology Co., Ltd.)

Determination of the soil chemical properties

Soil pH values were measured using potentiometry with a pH meter. Total organic carbon (TOC) was measured by the K₂Cr₂O₇ titrimetric method, and total nitrogen (TN) was determined using the Kjeldahl method (Opdyke and Loehr 1999). Soil hydrolytic nitrogen (HN) was measured using the alkaline hydrolysis diffusion method (Bronner and Bachler 1980). Ammonium nitrogen (AN) was determined by 2 mol/L KCl extraction and indophenol blue colorimetry. Nitrate nitrogen (NN) was determined by dual wavelength ultraviolet spectrophotometry. Total phosphorus (TP) and available phosphorus (AP) were determined using the NaHCO₃ leaching molybdenum antimony colorimetric technique (Pu et al. 2014). Available kalium (AK) was analyzed based on the ammonium acetate extraction-flame photometric method.

Determination of the soil enzymatic activities

Urease activity was assayed by the colorimetric sodium phenate-sodium hypochlorite method (Kandeler and Gerber 1988). The activities of amylase and invertase were determined by salicylic acid colorimetry. Sucrose was used as an invertase substrate using sucrose as the substrate, and maltose was used as an amylase substrate. Anthracene colorimetry was used to measure cellulase activity (Dunn et al. 2014).

DNA extraction, PCR amplification, and MiSeq sequencing

DNA was extracted from 0.5 g fresh soil of each sample using the DNeasy® PowerSoil® Pro Kit (Qiagen Inc., Carlsbad, CA, USA) following the manufacturer's instructions. We used the primer sets 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') to amplify the V3– V4 hypervariable region of the 16S rRNA gene (Bates et al. 2011).

The primer pair ITS1- F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and ITS2-R (5'- GCTGCGTTCTTCATCGATGC- 3') were used to amplify the fungal ITS region (Adams et al. 2013). To permit multiplexing of samples, a 10-bp barcode unique to each sample was attached to the 5' end of the primers. PCR products were pooled in equimolar concentrations and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA) following to the manufacturer's instructions. Purified amplicons were pooled in equimolar amounts and paired-end sequenced on an Illumina MiSeq PE300 platform/NovaSeq PE250 platform (Illumina, San Diego, USA) according to standard protocols by Majorbio Technology Co. Ltd. (Shanghai, China).

Processing of the sequencing data

Briefly, the raw gene sequencing reads were demultiplexed, quality-filtered with FASTP version 0.20.0 (Gu et al. 2013) and merged by FLASH version 1.2.7 (Mago and Salzberg 2011). Then, samples with low quality (containing < 20 low-quality bases), undetermined nucleotides (N) and inappropriate length were removed. Subsequently, the remaining sequences were clustered into operational taxonomic units (OTUs) at a 97% similarity level using the UPARSE algorithm (Edgar 2013), and chimeras were eliminated during this procedure. Furthermore, "Chloroplast", "Mitochondria", or "unknown" were identified and removed from the dataset. The most abundant sequence in each OTU was selected as the representative sequence. Taxonomic annotations of OTUs were determined using the Ribosomal Database Project classifier tool (Wang et al. 2007) with a confidence threshold of 0.7 against the Silva 138 database (Quast et al. 2012) for bacteria and UNITE 8.0 database (Nilsson et al. 2019; Tedersoo et al. 2018) for fungi. OTUs that were not classified into bacteria and fungi were removed before subsequent analyses. To standardize sampling effort, we rarefied all samples to the smallest number of sequences per sample (19791 sequences for bacteria and 31819 sequences for fungi).

All PCR and sequencing processes were performed by Majorbio Bio-Pharm Technology Co. LTD., Shanghai, China. The raw data of the bacterial and fungal communities have been submitted to the NCBI sequence Read Archive (SRA) under the accession numbers SRP339548 and SRP339534, respectively.

Determination of the maize yield

Five plants were randomly selected from each plot, and plant height and root fresh weight were measured at the jointing stage. Ear height, fresh kernel weight, dry kernel weight, early weight, and thousand grain weight were measured at the ripening stage. 10 uniform ears of corn were taken, and the yield was measured after air-drying (Cao et al. 2009).

Statistical analysis

Sequenced data analysis was performed using R packages (v4.1.0) and an open, web-based platform, Galaxy (<https://cloud.majorbio.com>), which was provided by Majorbio Technology Co. LTD. Soil physical and chemical properties, soil enzyme activity, maize yield and other data were analyzed using GraphPad Prism 8.0 software. RDA was used to evaluate the correlation of environmental factors and microbial community structure. Statistical analyses were performed using SPSS 22 software (IBM Corporation, New York, NY, USA). One-way ANOVA was used to test for differences between treatments.

Results

Response of soil chemical properties to decomposed straw

The soil chemical properties were measured, and some properties were found to be different among the different ways that decomposed straw was returned to the field. Compared with no straw fertilizer (S0), at the jointing stage, the contents of TOC, TN, NN and TP in the decomposed straw treatments were remarkably higher ($p < 0.05$, Fig. 1a, b, c, d), and the content of AN in

the decomposed straw treatments was remarkably lower ($p < 0.05$, Fig. 1e). At the ripening stage, the contents of TOC, TP, NN, and AN recovered to the S0 level (Fig. 1j, n, o, l), and the content of TN was significantly lower ($p < 0.05$) in both the SR and SM treatments (Fig. 1k). The AP content and pH were significantly higher ($p < 0.05$) in the decomposed straw treatments at the two growth stages (Fig. 1g, p, i, r). The contents of HN and AK were significantly lower ($p < 0.05$) in the decomposed straw treatments at the two growth stages (Fig. 1d, m, h, q). Soil enzymatic activities were changed and are shown in Fig. S2. Correlation analysis showed that α -amylase activity was positively correlated with the contents of TN, NN, and AP but was negatively correlated with the contents of AN and AK. Cellulase activity was positively correlated with the contents of HN, AN, and AK but was negatively correlated with the contents of pH, NN, TP, and AP. (Table S3).

Bacterial community responses to decomposed straw treatment

A total of 10235952 valid chimera sequences from bacteria. Change of shannon index is shown in Table S4. The Shannon index was calculated to reflect the α diversity of bacterial and fungal communities. Among the rhizosphere samples, the α diversity of bacteria was the highest ($p < 0.05$) in SR during the jointing stage and lowest ($p < 0.05$) in SM during the ripening stage. In addition, there was no significant difference in the α diversity of bacteria among bulk samples.

The bacterial community compositions at the phylum level in the rhizosphere and bulk samples under different growth stages and decomposed straw treatments are shown in Fig. S3. The community composition between rhizosphere and bulk samples was similar. The dominant phyla were Actinobacteriota, Proteobacteria, Chloroflexi, Acidobacteriota, Firmicutes, Gemmatimonadota, Myxococcota, and Bacteroidota in rhizosphere and bulk samples, which together accounted for approximately 85% of each sample (Fig. S3a, b). Among the rhizosphere samples, there was no difference between each treatment at the jointing stage. The contents of Actinobacteriota and Chloroflexi treated with decomposed straw (two methods of returning to the field) were significantly increased (ANOVA, $p < 0.05$), and the contents of Proteobacteria, Gemmatimonadota, Myxococcota, Bacteroidota, and Nitrospirota treated with decomposed straw (two methods of returning to the field) were significantly decreased (ANOVA, $p < 0.05$) at the ripening stage. Among the bulk soil samples, there was no difference between each treatment at the jointing stage. However, the content of Actinobacteriota was significantly increased in the decomposed straw treatment (ANOVA, $p < 0.05$) at the ripening stage (Fig. S3).

Principal coordinate analysis (PCoA) was performed at the operational taxonomic unit OTU level. The OTUs from both the rhizosphere (Fig. 2c) and the bulk samples (Fig. 2e) were clearly separated at the plant ripening stage, whereas no separation was observed at the jointing stage.

The bacterial community composition at the genus level was also similar among rhizosphere and bulk samples. Except for the norank and unclassified genera, the dominant genera were *Arthrobacter*, *Rubrobacter*, *Microvirga*, *Blastococcus*, *Sphingomonas*, *RB41*, *Nocardioideis*, *Bacillus*, *Skermanella*, *Microlunatus*, and *Solirubrobacter*, which together accounted for approximately 30% of each sample (Fig. 2a, b). In rhizosphere samples (Fig. 2a), compared with S0, the relative abundance of *Nocardioideis* was decreased by SR, and *Streptomyces* was significantly increased by SM during the jointing stage. Relative abundance of *Sphingomonas*, *Microlunatus*, *Skermanella* were significantly decreased by decomposed straw, and the relative abundance of *Rubrobacter* was significantly increased, with the relative abundance of *Pseudonocardia* significantly decreased by SR; also the relative abundance of *Arthrobacter*, *Nocardioideis*, *Solirubrobacter* were higher and *Microvirga*, *Bacillus*, *Bryobacter* were lower in treatment SM during the ripening stage. In the bulk soil samples (Fig. 2b), the relative abundances of *Skermanella* and *Streptomyces* were higher in treatment SM than in treatments S0 and SR at the jointing stage. During the ripening stage, the relative abundances of *Blastococcus* and *Solirubrobacter* were significantly increased by the decomposed straw, the relative abundance of *Skermanella* was lower in the SR treatment, and the relative abundance of *Rubrobacter* was significantly decreased by SM.

The analysis of different bacterial genera other than the dominant bacterial genera is shown in Fig. 2d, f. In the rhizosphere samples, the abundance of *Mesorhizobium* was significantly increased by SR, and the abundance of *Ellin6055* was significantly increased by SM at the jointing stage. The abundance of *Conexibacter* was significantly increased by decomposed straw, and the abundances of *Ellin6055*, *Lysobacter* and *Acidibacter* were significantly decreased by decomposed straw at the

ripening stage. The abundance of *Paenibacillus* was significantly increased by SR at the ripening stage. The abundances of *Iamia*, *Geodermatophilus*, *Asanoa*, *Marmoricola* and *Knoellia* were significantly increased by SM, and the abundances of *Nitrospira* and *Bradyrhizobium* were significantly decreased by SM at the ripening stage. In the bulk soil samples (Fig. 2f), the abundance of *Paenisporosarcina* was significantly decreased by decomposed straw at the jointing stage. The abundances of *Knoellia* and *Ellin6067* were significantly increased by SR at the jointing stage. The abundance of *Pedomicrobium* was significantly increased by SM at the jointing stage. The abundances of *Knoellia*, *Geodermatophilus*, *Asanoa* and *Iamia* were significantly increased by decomposed straw at the ripening stage. The abundances of *Conexibacter* and *Gaiella* were significantly increased by SR at the ripening stage. The abundance of *Lysobacter* was significantly increased by SM at the ripening stage.

Fungi community responses to the decomposed straw treatment

A total of 9835338 valid chimera sequences from fungi were conducted. Among the rhizosphere samples, the α diversity of SR was significantly higher ($p < 0.05$) than that of the other two groups in the jointing stage; however, there was no significant difference at the ripening stage. In bulk soil samples, compared with the S0 group, the α diversity was significantly increased by the SR treatment at the two growth stages (Table S4).

As shown in Fig. S4, the rhizosphere fungal community composition was the same as that of the bulk soil sample, but the fungal community composition was different among each treatment at the phylum level. The dominant fungal phyla of rhizosphere and bulk samples were Ascomycota, Basidiomycota and Mortierellomycota, which together accounted for approximately 95% of each sample (Fig. S4a, b). In the rhizosphere samples (Fig. S4a), compared to S0, the content of Basidiomycota was clearly increased (ANOVA, $p < 0.05$) by SM and decreased by SR during the jointing stage. The content of Mortierellomycota was clearly increased by SR during the ripening stage. In the bulk soil samples (Fig. S4b), the content of Ascomycota was clearly decreased, and the contents of Basidiomycota and Mortierellomycota were clearly increased by the decomposed straw treatment during the jointing stage. The contents of Ascomycota and Mortierellomycota were clearly increased, and the content of Basidiomycota was clearly decreased by SR during the ripening stage. The content of Ascomycota was clearly decreased and the content of Basidiomycota was obviously increased by SM during the ripening stage.

The PCoA of three treatments for fungal communities based on the relative abundance of OTUs was clearly separated in the rhizosphere and bulk samples at two stages of plant growth (Fig. 3c, e).

For fungi, except for the norank genus, the dominant genera were *Tausonia*, *Schizothecium*, *Talaromyces*, *Monodictys*, *Gibberella*, *Thelebolus*, *Pseudombrophila*, *Chaetomium*, and *Mortierella*, which together accounted for more than 85% of each sample in both rhizosphere and bulk samples (Fig. 3a, b). For rhizosphere samples (Fig. 3a), the relative abundance of *Talaromyces* was evidently decreased by decomposed straw during the jointing stage. The relative abundances of *Cercophora* and *Microdochium* were clearly increased, and the relative abundance of *Tausonia* was decreased by SR during the jointing stage. The relative abundance of *Gibellulopsis* was increased and the relative abundance of *Schizothecium* was decreased by SM during the jointing stage. During the ripening stage, the relative abundance of *Mortierella* was increased and the relative abundance of *Talaromyces* was decreased by SR, the relative abundance of *Gibellulopsis* was increased and the relative abundances of *Schizothecium*, *Thelebolus*, *Mortierella*, *Pyrenochaetopsis* and *Neocosmospora* were decreased by SM. In bulk soil samples (Fig. 3b), the relative abundances of *Schizothecium*, *Chaetomium*, *Mortierella*, *Thelebolus* and *Fusicolla* were clearly increased, and the relative abundance of *Talaromyces* was evidently decreased by decomposed straw during the jointing stage. The relative abundances of *Monodicty*, *Pseudombrophila*, *Thermomyces* and *Solicoccozyma* were obviously increased by SR during the jointing stage. The relative abundances of *Gibberella*, *Gibellulopsis*, *Clonostachys*, *Pyrenochaetopsis* and *Preussia* were evidently increased by SM during the jointing stage. During the ripening stage, the relative abundances of *Mortierella*, *Leptosphaeria* and *Thermomyces* were obviously increased, and the relative abundance of *Tausonia* was obviously decreased by SR. During the ripening stage the relative abundances of *Gibellulopsis*, *Metarhizium* and *Preussia* were obviously increased, and the relative abundances of *Schizothecium*, *Pyrenochaetopsis* and *Sporormia* were obviously decreased by SM.

In addition, the analysis of different fungal genera other than the dominant fungal genera is shown in Fig. 3d, e. In rhizosphere samples (Fig. 3d), the abundance of *Microdochium* and *Thermomyces* was obviously increased by SR, and the abundance of *Preussia* was obviously decreased by SR at the jointing stage. During the ripening stage, the abundance of *Pithoascus* was clearly increased by decomposed straw treatment, the abundance of *Leptosphaeria* was obviously decreased by SR, the abundance of *Preussia* was obviously increased by SM, and the abundance of *Trichoderma* and *Striatibotrys* was obviously decreased by SM. In bulk soil samples (Fig. 3f), the abundance of *Neocosmospora* was obviously increased by decomposed straw, and the abundances of *Cladosporium*, *Leptosphaeria*, *Sporormia*, *Pseudogymnoascus* and *Pithoascus* were clearly increased by SR during the jointing stage. The abundances of *Pithoascus* and *Cylindrocarpon* were obviously decreased by SM, and the abundance of *Trichoderma* was obviously increased by decomposed straw at the ripening stage.

Bacterial and fungal correlation with environmental factors

Changes in soil chemistry played an important role in shaping the composition of microbial communities. For bacteria, the relative abundances of *Pseudonocardia*, *Nocardioides*, *Geodermatophilus*, *Asanoa*, *Knoellia*, *Gaiella*, and *Blastococcus* were negatively correlated with the nitrogen nutrient content to varying degrees (Fig. 4a). The relative abundances of *Bacillus*, *Bryobacter*, *Ellin6055*, *Paenibacillus*, *Acidibacter*, *Nitrospira*, *Bradyrhizobium*, *MND1*, and *Ellin6067* were positively correlated with nitrogen nutrients and pH to varying degrees. The relative abundances of *Bryobacter*, *Streptomyces*, *Ellin6055*, *Paenibacillus*, *Lysobacter*, *Acidibacter*, *Nitrospira*, *Iamia*, *MND1*, and *Ellin6067* were positively correlated with AP, and the relative abundances of *Sphingomonas*, *Pseudonocardia*, *Asanoa*, and *Gaiella* were negatively correlated with AP. The relative abundances of *Microlunatus*, *Bryobacter*, *Lysobacter*, and *Nitrospira* were positively correlated with AK, and the relative abundances of *Nocardioides*, *Asanoa*, *Marmoricola*, *Knoellia*, and *Blastococcus* were negatively correlated with AK.

For fungi, the relative abundances of *Striatibotrys*, *Thelebolus*, *Neocosmospora*, *Cladosporium*, *Fusarium*, and *Solicoccozyma* were negatively correlated with pH, nitrogen nutrient content and AP (Fig. 4b). The relative abundances of *Talaromyces*, *Cercophora*, and *Pseudogymnoascus* were positively correlated with the nitrogen nutrient content. The relative abundances of *Preussia*, *Thermomyces*, *Gibellulopsis*, *Chaetomium*, and *Metarhizium* were positively correlated with TP and AP. Relative abundances of *Microdochium*, *Thermomyces*, *Pithoascus*, *Trichoderma*, *Mortierella*, *Pyrenochaetopsis*, *Gibellulopsis*, *Cylindrocarpon*, *Chaetomium*, *Pseudombrophila*, *Gibberella*, and *Clonostachys* with AK.

Response of maize yield to the decomposed straw treatment

As shown in Table 5, maize plant height and root weight were significantly increased ($p < 0.001$) by SM, while maize plant height was significantly decreased ($p < 0.05$) by SR at the jointing stage. Furthermore, maize yield was significantly higher ($p < 0.05$) in both SR and SM at the ripening stage. In addition, the coefficients of variation of the three groups were SR (1.49%) < S0 (1.53%) < SM (2.37%).

Therefore, the maize yield under the SM treatment was more stable.

Discussion

Straw is rich in organic matter and nutrients, which could improve soil quality (Delcher et al. 2007). Straw that is returned to soil increases soil organic carbon and other nutrients (Benbi and Senapati 2009), biodiversity, and diversifies nutrient supply (Song et al. 2019). Returned straw also provides abundant carbon for soil microorganisms, thus promoting their growth and activity (Song et al. 2020). However, this reintroduction of straw to fields also has many disadvantages. Excessive amounts of straw slows the rate of decomposition, which results in poor germination, poor seedling growth, and increased incidence of soil-borne diseases (Prasad et al. 2016). This leads to greatly reduced agricultural production efficiency. In the current study, we aimed to explore the rational application of straw compost in soil and to explore the response of crop growth and the soil microbial community to straw compost.

Our results indicate that both the SR and SM treatments highly increased the pH and the contents of TN, NN, TP, and AP. This result shows that decomposed straw can improve soil nutrients, especially available nutrients. Soil enzyme activities are used

as the most important soil quality and fertility indicators. In our study, α -amylase activity (Fig. S2) was significantly increased by SR, and cellulase activity was significantly decreased by SM. Correlation analysis (Table S3) showed that α -amylase activity was positively correlated with the contents of TN, NN, and AP but was negatively correlated with the contents of AN and AK. Cellulase activity was positively correlated with the contents of HN, AN, and AK but was negatively correlated with the contents of pH, NN, TP, and AP. This is consistent with the findings of previous studies (Dong et al. 2017; Rousk et al. 2010; Zheng et al. 2019). The diversity of the soil microbial community is closely related to changes in ecosystem functions. Higher soil microbial diversity means higher complexity of the relationship between microorganisms and the soil environment and a higher degree of stability within the ecosystem (Kong et al. 2020). In our study, the α diversity of bacteria and fungi in rhizosphere and bulk samples was notably higher ($p < 0.05$) in SR during the jointing stage. The α diversity of bacteria in rhizosphere samples in SM was notably higher ($p < 0.05$) at the ripening stage. This may mean that for the two methods of reintroduction of decomposed straw to the field, the SR treatment had a greater impact on the function of maize rhizosphere and bulk soil microbes during the jointing stage, while the SM treatment may have a greater impact on the functional complexity of the rhizosphere soil at the maturity stage.

The bacterial community structures in the rhizosphere and bulk samples were clearly separated by the decomposed straw (Fig. 2c). This indicates that the two methods have affected the composition of soil microorganisms. In this study, bacterial differences at the genus level at the jointing stage were small, and bacteria were quite different at the genus level at the ripening stage. The relative abundances of *Blastococcus*, *Asanoa* and *Geodermatophilus* in the bulk samples were higher in the decomposed straw treatments at the ripening stage. *Blastococcus*, *Asanoa* and *Geodermatophilus* are bacteria that are heavily involved in the nitrogen cycle (Jin et al. 2013; Lebedinsky et al. 2007). Spearman correlation analysis showed that these genera correlated negatively with nitrogen nutrient content (Fig. 4a). In addition, the relative abundances of *Iamia* also increased significantly. Research has shown that *Iamia* can degrade antibiotics (Zhang et al. 2021). The spearman correlation analysis showed that *Iamia* have been positively correlated with pH. In rhizosphere samples, the relative abundance of *Sphingomonas* was significantly lower ($p < 0.05$) in the fields with the decomposed straw treatment at the ripening stage. *Sphingomonas* have been demonstrated to be capable of causing human diseases (Ryan and Adley 2010). The relative abundances of *Mesorhizobium* at the jointing stage and *Paenibacillus* at the ripening stages in rhizosphere samples were higher in the SR treatment. They were described as plant growth-promoting rhizobacteria (Barnawal et al. 2017; Grady et al. 2016). In addition, the relative abundances of the degrading bacteria *Ellin6067* at the jointing stage and *Gaiella* at the ripening stages were higher in the SR treatment in bulk samples, and they have been demonstrated to be able to degrade complex organic compounds and pollutants (Lezcano et al. 2017; Ruan et al. 2020). The relative abundance of the beneficial bacterium, *Conexibacter*, was also significantly increased by SR. *Conexibacter* has been shown to be mostly beneficial microorganisms, with functions such as bioremediation, alleviation of adversity, promotion of soil nutrient availability and suppression of soil-borne plant pathogenic bacteria (Akinola and Babalola 2020; Deng et al. 2021; Zhao et al. 2019). The relative abundances of *Streptomyces* at the jointing stage and *Arthrobacter*, *Nocardioide*, *Iamia*, and *Marmoricola* at the ripening stage in rhizosphere samples were higher in SM. *Streptomyces* can control pathogenic bacteria and participate in soil nutrient cycling (Kinkel et al. 2012). *Arthrobacter* can promote plant growth (Li et al. 2018), and the degrading bacteria *Nocardioide* and *Marmoricola* can degrade organic pollutants (Ruan et al. 2020), degrade antibiotics (Zhang et al. 2021) and bioremediate (Li et al. 2020), respectively. Moreover, the relative abundance of the bacterial genera *Geodermatophilus* and *Asanoa* involved in the nitrogen cycle in rhizosphere samples also increased significantly in SM. SM had a greater impact on nitrogen nutrient cycling in rhizosphere soil than SR. Both SR and SM treatments increased the relative abundance of growth-promoting bacteria in rhizosphere soil, thereby promoting corn growth.

The fungal community structure was significantly altered by all three treatments. (Gomes et al. 2003). In this study, most of the fungi with significant differences were saprophytes. The relative abundances of *Leptosphaeria* in rhizosphere samples in SR and *Pyrenochaetopsis* in rhizosphere samples and *Cylindrocarpon* in bulk samples in SM were significantly lower ($p < 0.05$) at the ripening stage (Fig. 3d), and these genera have been shown to be plant pathogens (Massimo et al. 2015; Song et al. 2014; Tedersoo et al. 2014). The abundance of *Trichoderma* was significantly higher ($p < 0.05$) in decomposed straw in the bulk sample at the ripening stage (Fig. 3d). *Trichoderma* was shown to be able to control pathogens, improve plant health, stimulate root growth, and control disease (Harman et al. 2004; Hugoni et al. 2018). The abundance of *Trichoderma* may have increased,

and the return of straw may have reduced the incidence of soil disease. However, the abundance of *Trichoderma* has a positive correlation with the content of nitrate nitrogen, the content of nitrate nitrogen has been increased, and maize absorption of nitrogen nutrients is promoted, leading to an increase in production (Liu et al. 2021a; Vishwakarma et al. 2020).

Our results show that decomposed straw returned to the field increased the maize yield. Correlation analysis showed that maize plant height was positively related to the contents of TOC and NN (Table S5). Maize yield was positively related to the NN content and negatively related to the TP content. These correlations are consistent with the results of previous studies (Ning et al. 2021). Both root and rhizosphere fungi are closely related to the edaphic factors of the surrounding soil (Chen et al. 2019). However, correlation analysis also showed that the abundance of most bacteria and fungi had positive or negative correlations with TOC and NN contents, which affects the nutrient cycling of carbon and nitrogen in the soil (Trivedi et al. 2020). A straightforward explanation is that the application of straw fertilizer leads to changes in soil nutrient content. Plants adjust the quantity and composition of root exudates to recruit different rhizosphere microorganisms to cope with changes in nutrients (Chen et al. 2019). In addition, the coefficient of variation indicates that the yield of maize in the mulched field was more stable, while the maize yield stability of rotary tillage with decomposed straw was lowest. The reason for this variation may be that the soil microbial community structure under the two return modes is different, so the utilization of nutrients in the growth stage of maize is also different, which leads to changes in plant height and yield. The long-term effects of decomposed straw on soil properties and maize production need to be studied.

Conclusions

The chemical properties of the soil were improved, and the available nutrient content was changed by the return of decomposed straw corn fields. The diversity of bacteria and fungi in the rhizosphere and bulk soil was altered by returned rotary tillage with decomposed straw. The microbial community structures of bacteria and fungi were all changed by the two return modes. The nutrient cycle in the soil was promoted, and the composition of bacteria and fungi was changed by two ways of returning to the field, which had a greater impact at the ripening stage. The yield of corn was increased by decomposed straw, and cover return to the field was more stable.

Declarations

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Tables

Table 1 Growth index and yield of maize under different straw compost reduction field methods

Sample	Jointing		Ripening				
	Height (cm)	Root weight (g)	Ear high (cm)	Ear weight (g)	Grain weight (g)	Yield (kg/ha ⁻¹)	Coefficient of variation (%)
S0	126.11 ± 11.94	41.69 ± 10.82	257.97±8.68	285.05±22.54	154.84±11.92	7536.13±140.76	1.53
SR	117.84 ± 9.05**	45.59±12.88	256.13±9.72	297.62±27.30	159.09±13.87	7935.27±144.99*	1.49
SM	138.36 ± 13.14***	66.82±19.74***	261.43±10.20	299.57±28.53	166.93±15.98	7988.37±231.66*	2.37

Significance levels of one-way ANOVA: ***, $p < 0.001$; **, $p < 0.01$; *, $p < 0.05$

Figures

Figure 1

Soil chemical properties in the jointing and ripening stages. Total organic carbon (a), total nitrogen (b), total phosphorus (c), hydrolytic nitrogen (d), ammonium nitrogen (e), nitrate nitrogen (f), available phosphorus (g), available kalium (h), pH (i) at the jointing stage; total organic carbon (j), total nitrogen (k), total phosphorus (l), hydrolytic nitrogen (m), ammonium nitrogen (n), nitrate nitrogen (o), available phosphorus (p), available kalium (q), pH (r) at the ripening stage. Significance level: $p < 0.05$, *; $p < 0.01$, **; $p < 0.001$, ***

Figure 2

Bacterial community composition of the rhizosphere (a) and bulk (b) samples at the genus level. Columns of different colors represent different species; the length of the columns represent the proportion of the species. Principal coordinate analysis (PcoA) of the bacterial communities in the rhizosphere (c) and bulk (e) samples. Abundance heatmap of different bacteria other than the dominant bacteria at the genus level in rhizosphere (d) and bulk (f) samples

Figure 3

Fungal community composition of the rhizosphere (a) and bulk (b) samples at the genus level. Principal coordinate analysis (PcoA) of the fungal communities in the rhizosphere (c) and bulk (e) samples. Abundance heatmap of different fungi other than the dominant fungi at the genus level in rhizosphere (d) and bulk (f) samples

Figure 4

(a) Spearman correlation analysis between the different bacterial genera and soil chemistry properties in the rhizosphere. (b) Spearman correlation analysis between the different fungal genera and soil chemistry properties in the rhizosphere.

Significance level: $p < 0.05$, *; $p < 0.01$, **; $p < 0.001$, ***

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