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 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 were 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°C 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. Anthracone 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 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 \( (p < 0.05, \text{Fig. 1a, b, c, d}) \), and the content of AN in
the decomposed straw treatments was remarkably lower \( (p < 0.05, \text{Fig. 1e}) \). 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 \( \alpha \)-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 \( \alpha \) diversity of bacterial and fungal communities. Among the rhizosphere samples, the \( \alpha \) 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 \( \alpha \) 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 \( (\text{ANOVA}, p < 0.05) \), and the contents of Proteobacteria, Gemmatimonadota, Myxococcota, Bacteroidota, and Nitrospira treated with decomposed straw (two methods of returning to the field) were significantly decreased \( (\text{ANOVA}, p < 0.05) \) 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 \( (\text{ANOVA}, p < 0.05) \) 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 genes were Arthrobacter, Rubrobacter, Microvirga, Blastococcus, Sphingomonas, RB41, Nocardioides, 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 Nocardioides 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, Nocardioides, 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
The abundance of *Paenibacillus* was significantly increased by SR at the ripening stage. The abundances of *lamia, Geodermatophilus, Asanoa, Marmorica* 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 *Paenisororarcina* 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 *Pedomicrobiium* was significantly increased by SM at the jointing stage. The abundances of *Knoellia, Geodermatophilus, Asanoa and lamia* 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 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 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. 3a), the content of Basidiomycota was 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 genes were *Tausonia, Schizothecium, Talaromyces, Monodictys, Gibberella, Thelebolus, Pseudomorphina, 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 *Fusicola* were clearly increased, and the relative abundance of *Talaromyces* was evidently decreased by decomposed straw during the jointing stage. The relative abundances of *Monodictys, Pseudomorphina, Thermomyces* and *Solicoocozyma* 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*, *Pseudogymnoascu* 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*, *Marmorica*, *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 *Pseudogymnoascu* 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 slow 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 lamia also increased significantly. Research has shown that lamia can degrade antibiotics (Zhang et al. 2021). The spearman correlation analysis showed that lamia 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 (Bamawal 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, lamia, 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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**References**

1. Adams RI, Miletto M, Taylor JW, Bruns TD (2013) Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances. ISME J 7:1262–1273. doi: https://doi.org/10.1038/ismej.2013.28
2. Akinola SA, Babalola OO (2020) The importance of adverse soil microbiomes in the light of omics: Implications for food safety. Plant Soil Environ 66:421–430. doi: https://doi.org/10.17221/118/2020-pse
3. Barnawal D, Pandey SS, Bharti N, Pandey A, Ray T, Singh S, Chanotiya CS, Kalra A (2017) ACC deaminase-containing plant growth-promoting rhizobacteria protect Papaver somniferum from downy mildew. J Appl Microbiol 122:1286–1298. doi: https://doi.org/10.1111/jam.13417
4. Bates ST, Berg-Lyons D, Caporaso JG, Walters WA, Knight R, Fierer N (2011) Examining the global distribution of dominant archaeal populations in soil. ISME J 5:908–917. doi: https://doi.org/10.1038/ismej.2010.171
5. Benbi DK, Senapati N (2009) Soil aggregation and carbon and nitrogen stabilization in relation to residue and manure application in rice–wheat systems in northwest India. Nutr Cycl Agrosyst 87:233–247. doi: https://doi.org/10.1007/s10705-009-9331-2

6. Boulter-Bitzer JI, Trevors JT, Boland GJ (2006) A polyphasic approach for assessing maturity and stability in compost intended for suppression of plant pathogens. Appl Soil Ecol 34:65–81. doi: https://doi.org/10.1016/j.apsoil.2005.12.007

7. Bronner H, Bachler W (1980) Evaluating the nitrogen requirement of sugarbeet from hydrolyzable soil nitrogen. Soil Sci 130:303–306. doi: https://doi.org/10.1097/00010694-198012000-00002

8. Cai XB, Qian C, Zhang YQ, Xue HY, Chen ZL, Qiong PU (2003) Effect of straw returning on the environment of degenerated soil in central Tibet. Plant Nutrition and Fertilizing ence 9:411–415. doi: https://doi.org/10.11674/zwyf.2003.0406

9. Cao Q, W H, Z M, J. C (2009) Effect of plant density on spring corn yield under high rate fertilizer. Journal (Academy of Hospital Administration (India)) 17:113–115. doi: https://doi.org/10.13597/j.cnki.maize.science.2009.03.029

10. Cavagnaro TR (2015) Biologically regulated nutrientsupply systems. Adv Agron 129:293–321. doi: https://doi.org/10.1016/bs.agron.2014.09.005

11. Chen J, Li C, Ristovski Z, Milic A, Gu Y, Islam MS, Wang S, Hao J, Zhang H, He C (2016) A review of biomass burning: emissions and impacts on air quality, health and climate in China. Sci Total Environ 579:1000–1034. doi: https://doi.org/10.1016/j.scitotenv.2016.11.025

12. Chen S, Waghmode TR, Sun R, Kuramae EE, Hu C, Liu B (2019) Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. Microbiome 7:136113. doi: https://doi.org/10.1186/s40168-019-0750-2

13. Cui SY, Cao GQ, Zhu XK (2021) Evaluation of ecosystem service of straw return to soil in a wheat field of China. Int J Agr Biol Eng 14:192–198. doi: https://doi.org/10.25165/j.ijabe.20211401.5698

14. Delcher AL, Bratke KA, Powers EC, Salzberg SL (2007) Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics 23:673–679. doi: https://doi.org/10.1093/bioinformatics/btm009

15. Deng Q, Zhang T, Xie D, Yang Y (2021) Rhizosphere microbial communities are significantly affected by optimized phosphorus management in a slope farming system. Front Microbiol 12:739844. doi: https://doi.org/10.3389/fmicb.2021.739844

16. Dong L, Xu J, Zhang L, Yang J, Liao B, Li X, Chen S (2017) High-throughput sequencing technology reveals that continuous cropping of American ginseng results in changes in the microbial community in arable soil. Chin Med 12:11. doi: https://doi.org/10.1186/s13020-017-0139-8

17. Dunn C, Jones TG, Girard A, Freeman C (2014) Methodologies for extracellular enzyme assays from wetland soils. Wetlands 34:9–17. doi: https://doi.org/10.1007/s13157-013-0475-0

18. Edgar RC (2013) Uparse: highly accurate OTU sequences from microbial amplicon reads. Nat Methods 10:996–998. doi: https://doi.org/10.1038/nmeth.2604

19. Gomes NC, Fagbola O, Costa R, Rumjanek NG, Buchner A, Mendona-Hagler L, Smalla K (2003) Dynamics of fungal communities in bulk and maize rhizosphere soil in the tropics. Appl Environ Microbiol 69:3758–3766. doi: https://doi.org/10.1128/AEM.69.7.3758-3766.2003

20. Grady EN, MacDonald J, Liu L, Richman A, Yuan ZC (2016) Current knowledge and perspectives of paenibacillus: a review. Microb Cell Fact 15:203218. doi: https://doi.org/10.1186/s13020-016-0603-7

21. Gu J, Chen S, Zhou Y, Chen Y (2013) Fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:884–890. doi: https://doi.org/10.1093/bioinformatics/bt356

22. Harman GE, Howell CR, Viterbo A, Chet I, Lorito M (2004) Trichoderma species-opportunistic, avirulent plant symbionts. Nat Rev Microbiol 2:43–56. doi: https://doi.org/10.1038/nrmicro797

23. He HY, Q H, Li R, Pan XB, Huang BX, He QJ (2020) Regional gap in maize production, climate and resource utilization in China. Field Crops Research 254:107830:107838. doi: https://doi.org/10.1016/j.fcr.2020.107830
24. Hu R, Xing CY, Yuan-Jie LI, Liu ZZ, Cong-Ling SU (2011) Analyses and control of increased damage of wire worm in Zhengzhou. Journal of Henan Agricultural Sciences 40:103–106. doi: https://doi.org/10.15933/j.cnki.1004-3268.2011.02.015

25. Hugoni M, Luis P, Guyonnet J, Haichar FEZ (2018) Plant host habitat and root exudates shape fungal diversity. Mycorrhiza 28:451–463. doi: https://doi.org/10.1007/s00572-018-0857-5

26. Jin L, Lee HG, Kim HS, Ahn CY, Oh HM (2013) Geodermatophilus soli sp. nov. and geodermatophilus terrae sp. nov., two actinobacteria isolated from grass soil. Int J Syst Evol Microbiol 63:2625–2629. doi: https://doi.org/10.1099/ijs.0.048892-0

27. Kandeler E, Gerber H (1988) Short-term assay of soil urease activity using colorimetric determination of ammonium. Biol Fertil Soils 6:68–72. doi: https://doi.org/10.1007/BF00257924

28. Khaliq A, Matloob A, Farooq M, Mushtaq MN, Khan MB (2011) Effect of crop residues applied isolated or in combination on the germination and seedling growth of horse purslane (Trianthema portulacastrum). Planta Daninha 29:121–128. doi: https://doi.org/10.1590/S0100-83582011000100014

29. Kinkel LL, Schlatter DC, Bakker MG, Arenz BE (2012) Streptomyces competition and co-evolution in relation to plant disease suppression. Res Microbiol 163:490–499. doi: https://doi.org/10.1016/j.resmic.2012.07.005

30. Klein M, Brown L, Ashbolt NJ, Stuetz RM, Roser DJ (2011) Inactivation of indicators and pathogens in cattle feedlot manures and compost as determined by molecular and culture assays. FEMS Microbiol Ecol 77:200–210. doi: https://doi.org/10.1111/j.1574-6941.2011.01098.x

31. Kong X, Han Z, Tai X, Jin D, Al S, Zheng X, Bai Z (2020) Maize (zea mays L. sp.) varieties significantly influence bacterial and fungal community in bulk soil, rhizosphere soil and phyllosphere. FEMS Microbiol Ecol 96. doi: https://doi.org/10.1093/femsec/aa020. aa020:011

32. Lebedinsky AV, Chernyh NA, Bonch-Osmolovskaya EA (2007) Phylogenetic systematics of microorganisms inhabiting thermal environments. Biochemistry-Moscow 72:1299–1312. doi: https://doi.org/10.1134/s0006297907120048

33. Lezcano MA, Velazquez D, Quesada A, El-Shehawy R (2017) Diversity and temporal shifts of the bacterial community associated with a toxic cyanobacterial bloom: an interplay between microcystin producers and degraders. Water Res 125:52–61. doi: https://doi.org/10.1016/j.watres.2017.08.025

34. Li J, Peng K, Zhang D, Luo C, Cai X, Wang Y, Zhang G (2020) Autochthonous bioaugmentation with non-direct degraders: a new strategy to enhance wastewater bioremediation performance. Environ Int 136:105473. :105478. doi: https://doi.org/10.1016/j.envint.2020.105473

35. Li M, Guo R, Yu F, Chen X, Zhao H, Li H, Wu J (2018) Indole-3-acetic acid biosynthesis pathways in the plant-beneficial bacterium arthrobacter pascens ZZ21. Int J Mol Sci 19:443415. doi: https://doi.org/10.3390/ijms19020443

36. Liu L, Ding MJ, Zhou LK, Chen Y, Li HP, Zhang FM, Li G, Zhou ZF, Zhang Y, Zhou XX (2021a) Effects of different rice straw on soil microbial community structure. Agron J 113:794–805. doi: https://doi.org/10.1002/agj2.20509

37. Liu S, Wang Z, Niu J, Dang K, Zhang S, Wang S, Wang Z (2021b) Changes in physicochemical properties, enzymatic activities, and the microbial community of soil significantly influence the continuous cropping of Panax quinquefolius L. (American ginseng). Plant Soil 463:427–446. doi: https://doi.org/10.1007/s11104-021-04911-2

38. Mago T, Salzberg SL (2011) Flash: fast length adjustment of short reads to improve genome assemblies. Bioinformatics 27:2957–2963. doi: https://doi.org/10.1093/bioinformatics/btr507

39. Massimo NC, Devan MMN, Arendt KR, Wilch MH, Arnold AE (2015) Fungal endophytes in aboveground tissues of desert plants: infrequent in culture, but highly diverse and distinctive symbionts. Microb Ecol 70:61–76. doi: https://doi.org/10.1007/s00248-014-0563-6

40. Ndzelu BS, Dou S, Zhang XW (2020) Changes in soil humus composition and humic acid structural characteristics under different corn straw retuming modes. Soil Res 58:452–460. doi: https://doi.org/10.1071/sr20025

41. Nilsson RH, Larsson KH, Taylor AFS, Bengtsson-Palme J, Jeppesen TS, Schigel D, Kennedy P, Picard K, Glockner FO (2019) etc The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research 47: D259-D264. doi: https://doi.org/10.1093/nar/gky1022
42. Ning XL, Wang XH, Guan ZY, Gu Y, Wu CS, Hu WH (2021) Effects of different patterns of maize-straw application on soil microorganisms, enzyme activities, and grain yield. Bioengineered 12:3684–3698. doi: https://doi.org/10.1080/21655979.2021.1931639

43. Opdyke DR, Loehr RC (1999) Statistical analysis of chemical release rates from soils. Journal of Soil Contamination 8:541–558. doi: http://dx.doi.org/10.1080/1058839991339469

44. Prasad JVNS, Rao CS, Srinivas K, Jyothiswarlu B, Ramachandrappa BK, Dhanapal GN, Ravichandra K, Mishra PK (2016) Effect of ten years of reduced tillage and recycling of organic matter on crop yields, soil organic carbon and its fractions in alfisols of semi arid tropics of southern India. Soil Tillage Res 156:131–139. doi: https://doi.org/10.1016/j.still.2015.10.013

45. Pu P, Zhang M, Zhang LN (2014) A study on temperature and time conditions of colorimetric method in measuring moil available phosphorus. Advanced Materials Research 838-841: 2047-2051. doi: https://doi.org/10.4028/www.scientific.net/AMR.838-841.2047

46. Qin W, Hu C, Oenema O (2015) Soil mulching significantly enhances yields and water and nitrogen use efficiencies of maize and wheat: a meta-analysis. Sci Rep-Uk 5:16210. :16213. doi: https://doi.org/10.1038/srep16210

47. Quast C, Pruesse E, Yilmaz P, Gerken J, Glöckner FO (2012) The silva ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Res 41:D590–D596. doi: https://doi.org/10.1093/nar/gks1219

48. Rousk J, Baath E, Brookes PC, Lauber CL, Caporaso JG, Knight R, Fierer N (2010) Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME J 4:1340–1351. doi: https://doi.org/10.1038/ismej.2010.58

49. Ruan M, Zhang Y, Chai T (2020) Rhizosphere soil microbial properties on tetraena mongolica in the arid and semi-arid regions, China. Int J Environ Res Public Health 17:5142. :5116. doi: https://doi.org/10.3390/ijerph17145142

50. Ryan MP, Adley CC (2010) Sphingomonas paucimobilis: a persistent gram-negative nosocomial infectious organism. J Hosp Infect 75:153–157. doi: https://doi.org/10.1016/j.jhin.2010.03.007

51. Shi Z, Tao J, Wang Y, Wang J, Sun R, Fei W, Xiang L, Bi Y (2017) Comprehensive utilization status of crop straw and estimation of carbon from burning in china. Chinese Journal of Agricultural Resources Regional Planning 38:32–37

52. Siedt M, Schaffer A, Smith KEC, Nabel M, Ross-Nickoll M, van Dongen JT (2021) Comparing straw, compost, and biochar regarding their suitability as agricultural soil amendments to affect soil structure, nutrient leaching, microbial communities, and the fate of pesticides. Sci Total Environ 751:141607141619. doi: https://doi.org/10.1016/j.scitotenv.2020.141607

53. Song JY, Seo MW, Kim SI, Nam MH, Kim HG (2014) Genetic diversity and pathogenicity of cylindrocarpon destructans isolates obtained from Korean panax ginseng. Mycobiology 42:174–180. doi: https://doi.org/10.5941/MYCO.2014.42.2.174

54. Song K, Sun Y, Qin Q, Sun L, Zheng X, Terzaghi W, Lv W, Xue Y (2020) The effects of earthworms on fungal diversity and community structure in farmland soil with returned straw. Front Microbiol 11:594265. doi: https://doi.org/10.3389/fmicb.2020.594265

55. Song K, Zheng X, Lv W, Qin Q, Sun L, Zhang H, Xue Y (2019) Effects of tillage and straw return on water-stable aggregates, carbon stabilization and crop yield in an estuarine alluvial soil. Sci Rep 9:4586. :4511. doi: https://doi.org/10.1038/s41598-019-40908-9

56. Su Y, Lv JL, Yu M, Ma ZH, Xi H, Kou CL, He ZC, Shen AL (2020a) Long-term decomposed straw return positively affects the soil microbial community. J Appl Microbiol 128:138–150. doi: https://doi.org/10.1111/jam.14435

57. Su Y, Yu M, Xi H, Lv J, Ma Z, Kou C, Shen A (2020b) Soil microbial community shifts with long-term of different straw return in wheat-corn rotation system. Sci Rep 10:6360. :6310. doi: https://doi.org/10.1038/s41598-020-63409-6

58. Tedersoo L, Bahram M, Plme S, Kljalg U, Abarenkov K (2014) Fungal biogeography, global diversity and geography of soil fungi. Science 346:1256688:1256612. doi: https://doi.org/10.1126/science.aaa4269

59. Tedersoo L, Sánchez-Ramírez S, Kljalg U, Bahram M, Dring M, Schigel D, May T, Ryberg M, Abarenkov K (2018) High-level classification of the fungi and a tool for evolutionary ecological analyses. Fungal Divers 90:135–159. doi: https://doi.org/10.1007/s13225-018-0401-0
60. Trivedi P, Leach JE, Tringe SG, Sa T, Singh BK (2020) Plant–microbiome interactions: from community assembly to plant health. Nat Rev Microbiol 18:607–621. doi: https://doi.org/10.1038/s41579-020-0412-1
61. Vishwakarma K, Kumar N, Shandilya C, Mohapatra S, Bhayana S, Varma A (2020) Revisiting plant-microbe interactions and microbial consortia application for enhancing sustainable agriculture: a review. Front Microbiol 11:560406. doi: https://doi.org/10.3389/fmicb.2020.560406
62. Wang Q, Garrity GM, Tiedje JM, Cole JR (2007) Naive bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. Appl Environ Microb 73:5261–5267. doi: https://doi.org/10.1128/aem.00062-07
63. Xiao Y (2012) The analysis of straw burning and use. Journal of Green Science and Technology 11:72–74
64. Zhang G, Zhao Z, Yin XA, Zhu Y (2021) Impacts of biochars on bacterial community shifts and antibiotic biodegradation in an agricultural soil during short-term incubation. Sci Total Environ 771:144751. doi: https://doi.org/10.1016/j.scitotenv.2020.144751
65. Zhang P, Wei T, Jia Z, Han Q, Ren X (2014) Soil aggregate and crop yield changes with different rates of straw incorporation in semi-arid areas of northwest China. Geoderma 230–231:41–49. doi: https://doi.org/10.1016/j.geoderma.2014.04.007
66. Zhao R, Feng J, Liu J, Fu W, Li X, Li B (2019) Deciphering of microbial community and antibiotic resistance genes in activated sludge reactors under high selective pressure of different antibiotics. Water Res 151:388–402. doi: https://doi.org/10.1016/j.watres.2018.12.034
67. Zhen W, Wang S, Zhang C, Ma Z (2009) Influence of maize straw amendment on soil-borne diseases of winter wheat. Frontiers of Agriculture in China 3:7–12. doi: https://doi.org/10.1007/s11703-009-0003-4
68. Zheng Q, Hu Y, Zhang S, Noll L, Böckle T (2019) etc. Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. Soil Biology and Biochemistry 136: 107521:107513. doi: https://doi.org/10.1016/j.soilbio.2019.107521
69. Zhou G, Zhang J, Zhang C, Feng Y, Chen L, Yu Z, Xin X, Zhao B (2016) Effects of changes in straw chemical properties and alkaline soils on bacterial communities engaged in straw decomposition at different temperatures. Sci Rep-Uk 6:2218622112. doi: https://doi.org/10.1038/srep22186

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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