Title page

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Title: Low-disturbance farming regenerates healthy critical zone towards sustainable agriculture

Running title: Low-disturbance farming, sustainable agriculture

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Abstract

Intensive conventional farming has degraded soil quality in farmlands and other ecosystems globally. Although low-disturbance practices have been widely adapted to restore soil health and save energy, the underlying mechanisms associated with farm sustainability are still unclear. Here, we compared soil microbiome, physiochemical parameters along 3-m deep soil profiles, and crop yield in Northeast China subjected to ten years of farming practices at 3 levels of disturbance, including conventional tillage (CT), no-tillage without stover mulching (NTNS), and no-tillage with stover mulching (NTSM). We found that low-disturbance practices (NTNS and NTSM) promoted the ability of the soil to retain water and nitrogen, regenerated whole-soil microbial diversity and function, and significantly improved corn yield at the drought year. This study implies that the low-disturbance practice could substantially reduce energy consumption and cut greenhouse gas emissions, thus contributing to sustainable farming.

Introduction

Since the Industrial Revolution, the rate of soil carbon loss has increased dramatically, resulting in a global carbon debt due to agriculture of 116 Pg carbon for the top 2 m of soil(Sanderman *et al.* 2017). The loss of carbon in farmlands has not only changed global climate but also produced catastrophic cascade impacts on global food security, as soil carbon is the cornerstone for healthy and productive soil that will be needed to feed 10 billion people in 2050 (United Nations, World Population Prospects 2019). It is well known that intensive conventional farms with high energy inputs and disturbance (e.g. tillage/compaction, burn/remove stover) have caused soil carbon loss with a series of environmental issues(Congreves *et al.* 2015). Even worse, increasing the amount of chemical fertilizer is unlikely to continue the increase in quantity and quality of food products worldwide(Vitousek *et al.* 2009). Moreover, tillage particularly prevents root growth into deeper soil(Kemper *et al.* 2011), thus affecting mineral weathering in deep soil(Billings *et al.* 2018) and reducing crop resilience to drought.

Since the 1970s, low-disturbance conservative practices (e.g. reduced tillage, no-tillage and stover mulching) have been gradually applied to restore soil health and reduce non-point source pollution(Salem). Growing evidence shows that no-tillage and stover mulching boosted top-soil organic carbon (SOC)(Blanco-Canqui & Lal 2008; Lu *et al.* 2009; Liu *et al.* 2014), increased soil aggregate(Song *et al.* 2019) and reduced soil erosion and surface runoff(Prosdocimi *et al.* 2016). All these benefits from low-disturbance practices are tied with complex microbial processes that interact with crops and drive soil carbon transformation and stabilization(Schimel & Schaeffer 2012; Liang *et al.* 2017). However, most studies only focused on topsoil or soils within 1-m depth(Zhang *et al.* 2017; Nevins *et al.* 2018; Schmidt *et al.* 2018). Soil

below 1 meter, which belongs to Earth's Critical zone, was often overlooked despite that some crops have roots over 1 meter deep and microbes in the deep soils (> 1 m) may substantially impact long-term carbon sequestration, mineral weathering and crop production(Eilers *et al.* 2012; Sagova-Mareckova *et al.* 2016; Pries *et al.* 2017). Furthermore, deep roots influence material cycles in surficial soil and microbes inhabiting in the deep soils, which plays important roles in bridging aboveground vegetation with parent soils and even acts as an essential buffer protecting underground water(Chorover *et al.* 2007). To completely evaluate the impact of low-disturbance practices on agro-ecosystem, an urgent need is to test the changes and functions of microbial communities in deep soil(Richter & Yaalon 2012). Since microbial activities in deep soil are generally limited by the availability of labile carbon, we hypothesized that low-disturbance practices are conducive to deeper root growth, which could provide labile carbon and nutrients(Kemper *et al.* 2011) and accelerate mineral weathering(Billings *et al.* 2018), thus substantially influencing the microbial composition in the deep soils and in turn the sustainability of whole ecosystem.

Recent research shows that corn belts in the U.S.A., western Europe, and China have experienced the most soil carbon loss globally(Sanderman *et al.* 2017). The corn belt in Northeast China is considered as the "breadbasket" of the country, having the largest grain production and overlapping with the most fertile Mollisol region that sustains 3% of population in the world(Liu *et al.* 2010), accounting for over 30% of corn production of China(Liu *et al.* 2012). Here, a 10-year manipulative experiment was conducted at a temperate corn farm in Northeast China, investigating farming practices with three levels of disturbance: high-disturbance—conventional tillage (CT), low disturbance—no-tillage without stover mulching (NTNS) and no-tillage

with 100% stover mulching (NTSM). We compared corn yield, soil properties and microbial communities of the 3-m soil profiles at the end of 10 years. We aimed at testing our main hypothesis that the lowest disturbance practice—no-tillage with 100% stover mulching, similar to undisturbed natural ecosystem, would regenerate microbial diversity and function toward a high-resilient natural ecosystem.

Materials and methods

Site description and soil sampling. The field experiment was established in 2007 at the Lishu Conservation Tillage Research and Development Station of the Chinese Academy of Sciences in Jilin province, Northeast China (43.19° N, 124.14° E). The region has a humid continental climate with a mean annual temperature of 6.9 °C and the mean annual precipitation of 614 mm. The soils are classified in the Mollisol order (Black Soil in Chinese Soil Classification) with a clay loam texture(IUSS Working Group 2006). The site has been continuously planted with maize since 2007. We set up an experiment by a randomized complete block design with four replicates and five treatments. Each plot area was 261m^2 (8.7×30m). The five treatments included conventional tillage (moldboard plowing to a depth around 30 cm and removed the stover), no-tillage (no soil disturbance and direct seeding), and no-tillage with three-level stover mulching (33%, 67% and 100% newly produced maize stover were evenly spread over the soil surface each fall). For each treatment, slow-release fertilizer was applied at one time when sowing, which was equal to 240 kg/ha N; 47 kg/ha P; 90 kg/ha K. The rainfall data were obtained from local meteorological admistration. The grain yield was estimated by manually harvesting 20 m^2 area, randomly taken from each plot.

In this experiment, in order to reduce the damage to the plots and reduce costs, 3 plots were randomly taken from each treatment including conventional tillage (CT),

no-tillage without stover mulching (NTNS), no-tillage with 100% stover coverage (NTSM) as three comparative practices. In April 2017, triplicate soil cores (0-300 cm) were collected from each plot at the dormant season. After removing surface stover, we took soil cores by a stainless-steel hand auger and sliced each into ten layers: 0-10 cm, 10-20 cm, 20-40 cm, 40-60 cm, 60-90 cm, 90-120 cm, 120-150 cm, 150-200 cm, 200-250 cm, 250-300 cm. In total, 90 soil samples were collected and transported to the laboratory within 3 hours, then passed through a 2-mm sieve. All visible roots, crop residues and stones were removed. Each soil sample was divided into three subsamples: one subsample for DNA extraction and soil salt-extractable organic carbon (SEOC) measurement that was immediately placed into a polyethylene plastic bag and stored at -80 °C, one for chemical measurements including ammonium nitrogen (NH_4^+-N) and nitrate nitrogen (NO_3^--N) (within one day), and the remaining one was air dried for other soil physicochemical properties.

Soil properties. Soil total nitrogen (TN) content was measured by an Element analyzer Vario EL III (Elementar Analysensysteme GmbH, Hanau, Germany). Soil organic carbon (SOC) was converted from soil organic matter (SOM) that was measured by potassium dichromate oxidation(Nelson & Sommers 1982). Soil pH was measured in deionized free-CO_2 water (1:2.5 w/v). Gravimetric soil moisture was determined by oven-drying fresh soil to a constant weight at 105 °C. Soil NH_4^+-N and NO_3^--N were extracted from fresh soil by 2 M KCl and measured by a continuous flow analytical system (AA3, SEAI, Germany). To reflect soil soluble, exchangeable, mineral-bound OC, soil salt-extractable organic carbon (SEOC) was extracted from the frozen soil samples with 0.5 M K_2SO_4 (1:5 w/v)(Canadell *et al.* 1996b; Rousk & Baath 2007; Kemper *et al.* 2011).

DNA extraction, PCR amplification and pyrosequencing. Soil DNA was extracted

from the frozen soil samples (0.5 g wet weight) by using MoBio PowerSoil DNA isolation kit (MoBio Laboratories, Carlsbad, CA, USA) following the instructions of the manufacturer. The quality of DNA was determined by 1% agarose gel electrophoresis. The V3–V4 region of the bacterial 16S rRNA gene was amplified by PCR using the primers 338F and 806R with barcode for Illumina MiSeq sequencing. PCR was performed in a total volume of 50 μl containing 30 ng DNA as a template, 20 mol of each primer, 10mM dNTPs, 5μl 10× Pyrobest buffer and 0.3 U of Pyrobest polymerase (Takara Code: DR005A). The PCR cycle conditions were as follows: initial denaturation at 95°C for 5 min followed by 26 cycles of denaturation at 95°C for 45s, annealing at 50°C for the 30s, and extension at 72°C for 45s, with a final extension at 72°C for 10 min. Each sample was amplified for three replicates. The PCR products from the same sample were pooled, checked by 2% agarose gel electrophoresis and were then purified using AxyPrepDNA agarose purification kit (AXYGEN). Finally, purified PCR products were sequenced on an Illumina MiSeq platform PE300 sequencer (Illumina, USA).

The raw sequence data were further analyzed by the following protocol. Low-quality sequences with an average quality score of less than 20 were filtered by employing Trimmomatic(Bolger *et al.* 2014). The FLASH software was used to merge overlapping ends and treat them as single-end reads(Derakhshani *et al.* 2016). The non-amplified region sequences, chimeras and shorter tags were also removed using Usearch and Mothur(Kozich *et al.* 2013; Mysara *et al.* 2016). The resulting high-quality sequences were clustered into Operational Taxonomic Units (OTUs) at 97% sequence similarity using Usearch (Version 8.1.1861 http://www.drive5.com/usearch/) (Edgar, 2013). OTUs were then classified against the Silva (Release119 http://www.arb-silva.de) database and the taxonomic

information of each OTU representative sequence was annotated using the RDP Classifier(Wang *et al.* 2007; Quast *et al.* 2012; Werner *et al.* 2012). A total of 3,255,693 high-quality reads were obtained from all soil samples, which were clustered into 9,573 unique OTUs at a 97% sequence similarity. The Good's coverage of all the samples ranged from 0.93 to 0.98, which indicates an adequate level of sequencing to identify the majority of diversity in the samples.

Statistical analyses. Soil properties were analyzed and plotted using Sigmaplot 12.5 software. Alpha diversity indices were calculated in Qiime (version v.1.8) and used to reflect the diversity and richness of the microbial community in different samples. The relative abundances of individual phyla in different samples were computed by R packages. The indicator analysis based on genera-specific to each soil depth was conducted using indicspecies package of R with 9999 permutations, and the P-values were corrected for multiple testing using qvalue package of R(Jiménez-Bueno *et al.* 2016; Zhang *et al.* 2017). Functional profiles of the microbial community were predicted by Tax4fun (an open-source package in R)(Aßhauer *et al.* 2015) and further statistical analysis was conducted by STAMP using Welch's t-test(Parks *et al.* 2014). Non-metric multidimensional scaling (MDS) was performed by "vegan" package of R to describe differences in microbial community structure among samples. Permutational multivariate analysis of variance (PERMANOVA) was employed on Bray-Curtis distances to test the differences in soil microbial communities among various sample groups. The Redundancy analysis (RDA, Canoco 5 software) were conducted to identify the correlations between microbial community composition and environmental variables. One-way and two-way ANOVA tests were conducted by SPSS Version 22. Percentage data were transformed using arcsine square root

function before ANOVA test. All statistical tests were significant at $p \leq 0.05$.

Results

Soil properties and corn yield. Soil properties varied significantly among disturbance practices and at different soil depths (Fig. 1 and Table S1). The SOC, TN and C/N ratio substantially decreased from the soil surface to around 150 cm depths and then remained unchanged within 150-300 cm (Fig. 1). The NTSM slightly increased SOC, TN and C/N ratio at 0-20 cm soil layers compared with the NTNS and the CT (Fig. 1 and Table S1). The no-tillage practices of NTSM and NTNS reduced soil pH in surface and deeper layers (Fig. 1d) and increased soil moisture at surface layers (0-60 cm) (Fig. 1e). In the CT plots, soil NO_3^--N concentration first decreased and then increased remarkably, ranged from 4.19 to 23.32 mg kg^{-1} (Fig. 1i). However, under the NTNS and NTSM treatments, soil NO_3^--N decreased significantly at 0-40 cm then increased to the maximum at 120-150 cm depth. Interestingly, above 120-150 cm layer, NO_3^--N was significantly higher with low-disturbance practices than conventional tillage, while the soil below 150 cm under low-disturbance practices had much lower NO_3^--N compared to conventional tillage (Fig. 1i). The NTNS plots contained much higher amounts of ammonium than the CT and the NTSM plots (Fig. 1h). Soil salt-extractable organic carbon (SEOC) declined from the surface to 40-60 cm and then increase to its peak at 60-90 cm under CT, at 90-120 cm under NTNS and at 120-150 cm under NTSM (Fig. 1b). As large part of root-derived C contribute to dissolved organic C(Liang *et al.* 2002), SEOC as an organic acid proxy, positively associated with root density, can be an indicator of root depth in deep soil(Billings *et al.* 2018). Hence, we estimate that corn roots reached up to 60-90 cm, 90-120 cm and 120-150 cm under the CT, the NTNS and the NTSM, respectively, which is in line with reported corn root depths (~150 cm) (Canadell *et al.* 1996a; Kemper *et al.* 2011).

The NTSM increased the SEOC concentration at almost all soil layers compared with the CT and the NTNS (Fig. 1b), in which at the surface and 120-150 cm depth the contents of SEOC with NTSM were twice higher than CT. The increased SEOC in deep soils under NTSM reduced soil pH as shown by a significant negative relationship between SEOC and pH ($r=0.678$, $p<0.05$). The relative contributions of SEOC to SOC (SEOC/SOC) in the NTSM were also always higher than in the CT and the NTNS (Fig. 1c). Based on the estimated root depths, total soil inorganic nitrogen available for the coming growing season in the NTSM and the NTNS was 427.34 and 352.34 kg ha^{-1}, respectively, while only 179.63 kg ha^{-1} in conventional tillage.

The mean annual corn yield (2013-2016) in the NTSM is 13416.8 kg/ha, which is much higher than the CT and NTNS (Fig. 2), particularly during the drought year of 2015, with only 409.6 mm of rainfall during the growing season (about 100 mm lower than the mean rainfall), while the corn yield in NTSM is 36.4% and 22.3% higher than the CT and NTNS, respectively (Fig. 2).

Microbial diversity, composition, and structure. The microbial richness (Chao1), observed number of species (Observed-species) and diversity (Shannon-Index) first increased within 0-20 cm and decreased from 20 to 90 cm, then increased hereafter (Fig. 3). The low-disturbance practices significantly increased Chao1, Observed-species and Shannon-Index, particularly in 0-40 cm soil depths (Fig. 3). There were 54 microbial phyla across all soil samples. The dominant phyla (relative abundance > 1% across all soil samples) were Proteobacteria, Actinobacteria, Chloroflexi, Acidobacteria, Nitrospirae, Gemmatimonadetes, Planctomycetes, and these phyla accounted for 60-91% of the total microbial abundances in the whole soil profile (Fig. S1a). Bacteroidetes, Verrucomicrobia, Latescibacteria, Parcubacteria, Firmicutes, Microgenomates and Saccharibacteria were less dominant (relative

abundance > 0.1% across all soil samples) but were still found across all soil samples (Fig. S1a). Although no difference in the composition of dominant phyla among treatments were found, there are more non-dominant phyla with higher relative abundance in low disturbance practices than conventional tillage practice (Fig. S1b).

Indicator analysis identified 16 and 51 clearly classified genera (relative abundances > 0.005%) in the NTNS and the NTSM plots, respectively, while no indicator genera were found in the conventional tillage plots (Fig. 4 and Table S2). The indicator genera in the NTNS plots belonged to Proteobacteria, Actinobacteria, Chloroflexi, Gemmatimonadetes and Planctomycetes, and most of them appeared in the surface soil (0-20 cm) with only 1 genus below 150 cm. Importantly, more extra indicator genera — including Bacteroidetes, Acidobacteria, Deferribacteres, Firmicutes, Verrucomicrobia, Chlorobi and Spirochaetae — existed in the NTSM plots, in which under 150 cm we observed 7 genera (Fig. 4 and Table S2).

Microbial community structures were visualized by Non-metric multidimensional scaling (MDS) and tested by Permutational multivariate analysis of variance (PERMANOVA) based on Bray–Curtis. The microbial communities among treatments in the root zones were marginally different (PERMANOVA p=0.08); however, below the root zone they differed distinctively (PERMANOVA p=0.02). The disturbance practices influenced the vertical distribution dissimilarity in microbial community structure (Fig. 5). Three clusters — 0-10 cm and 10-20 cm, 20-150 cm and 150-300 cm — were observed in the CT plots (PERMANOVA-F=9.57, p=0.0001) (Fig. 5). In the NTNS plots, 0-10 cm formed an independent cluster, while other soil depths showed some separation (e.g. 20-120 cm were separated from 150-300 cm soil depths by axis 1); however, Bray-Curtis distances between adjacent depths were too close to be separated (PERMANOVA-F=8.18, p=0.0001) (Fig. 5). The NTSM

treatment clustered 0-10 cm and 10-20 cm together, 120-150 cm, 150-200 cm, 200-250 cm and 250-300 cm separately, and the other depths show some separations as well (PERMANOVA-F=11.32, p=0.0001) (Fig. 5).

Predicted Ecological functions of microbial communities. According to the results of microbial diversity, composition and structure, the metabolic capabilities of microbial community in the whole 3-m soil profiles were predicted using Tax4Fun (Fig. S2). Results showed that low-disturbance practices significantly increased the abundance of predicted functions related to carbohydrate metabolism, nucleotide metabolism, glycan biosynthesis and metabolism, lipid metabolism and metabolism related to cofactors and vitamins (Fig. S2a). Moreover, the relative abundances of genes encoding for assimilatory nitrate reduction in low-disturbance practices were higher than that in conventional tillage practice (Fig. S3). The results suggested that in low disturbance practices, microbial community prefer to convert the nitrate/nitrite to ammonia. We then further assessed the impact of stover mulching on functional profiles (Fig. S2b). The extended error bar plot shows that the NTNS enriched the abundance of amino acid metabolism and lipid metabolism, while the NTSM enriched the functions associated to energy metabolism, carbohydrate metabolism, biosynthesis of secondary metabolites, glycan biosynthesis and metabolism as well as metabolism of cofactors and vitamins (Fig. S2b).

Relationships between microbial communities and soil properties. Forward selection in Redundancy analysis (RDA) revealed that soil depth (pseudo-F=48, p= 0.002), SOC (pseudo-F=11.5, p= 0.002), SM (pseudo-F=3.4, p= 0.012), soil pH (pseudo-F=2.3, p=0.018) and soil NH_4^+-N (pseudo-F=2.7, p= 0.026) significantly affected the vertical distribution of microbial communities (Fig. S4). Furthermore, the soil properties that regulated the distribution of soil microbes were different under

different disturbance practices. Under the CT treatment, soil microbial community was mainly affected by soil NH_4^+-N (pseudo-F=4, p= 0.002) and soil NO_3^--N (pseudo-F=2.3, p= 0.012) that mainly came from applied fertilizer (Fig. 6). The microbial community positively correlated to soil NH_4^+-N in the 0-20 cm soil, to soil NO_3^--N negatively within 20-150 cm, while to soil NO_3^--N positively after 150 cm (Fig. 6). Under the NTNS treatment, soil pH (pseudo-F=3.7, p=0.004) constrained the distribution of the microbial community, in which strong negative correlations occurred in 0-10 cm soil and a positive correlation in 90-150 cm (Fig. 6). Under the NTSM treatment, soil TN (pseudo-F=11, p=0.002), SM (pseudo-F=2.6, p=0.004) and C/N ratio (pseudo-F=1.8, p=0.016) significantly influenced the soil microbial community separation (Fig. 6). In general, the microbes positively correlated with the soil TN and C/N ratio in the surface soil layers (0-40 cm) and with SM in the middle layers (40-150 cm), while they were mainly influenced by depth in the deeper soil (150-300 cm) (Fig. 6).

Discussion

No-tillage practices promote soil health and corn yield. No-tillage promotes root growth into deep soil, up to 150 cm in the NTSM. The root exudates with various organic acid and dead roots likely contributed to the lower soil pH and higher SEOC in the NTNS and the NTSM, which in turn increased mineral weathering(Billings *et al.* 2018) and diversified the microbial communities with multi-ecological functions. The increased fine roots in deeper soil retained more nutrients including nutrients in dead roots and converting nitrate to more stable ammonium (Fig. S3) and also provided labile carbon (Fig. 1b) to remove leaked nitrate through denitrification in deeper soil (below 1.5 m), as higher relative abundance of the denitrification bacteria (*Pseudomonas* and *Caldithrix*)(Koike & Hattori 1975; Miroshnichenko *et al.* 2003)

(Fig. 4 and Table. S2) and denitrification genes (Fig. S3) were detected in low disturbance practices — particularly in no-tillage with stover mulching. However, shallower roots in the CT treatment can't provide enough labile carbon to remove extra soil NO_3^--N in deep soil, thus causing nitrite accumulation and leaching into deeper soil layers. The amount of inorganic nitrogen accumulated in the root zones under NTSM (427.34 kg ha^{-1}) likely could provide plenty of nitrogen for corn growth in the coming growing season (Fig. 2), based on the removed nitrogen in the grain (~200 kg ha^{-1}). Additionally, in line with many studies that show stover mulching reduces water evaporation and surface runoff and increase soil moisture in top soils(De Vita *et al.* 2007; Prosdocimi *et al.* 2016), we found that the soil moisture was significantly higher in the NTSM than in the CT plots. Therefore, no-tillage with stover mulching not only restores soil health by increasing the holding capacities for nutrients and water, thus reducing energy input to farm, but also tended to reduce the risk of nitrate leaching to groundwater. And more importantly, the healthy soil in turn raises corn production and promote the crop resistance to drought (Fig. 2). All these are critical to the development of sustainable agriculture and the associated ecosystems.

No-tillage with stover mulching promotes microbial diversity, richness, and ecological function contributing to sustainable farming. Under the CT treatment, tillage heavily disturbed the topsoil and liberated occluded organic materials. Microbes tended to rapidly use available nutrients in the plowed layer (e.g. NH_4^+-N)(Ramirez-Villanueva *et al.* 2015), thereby causing the reduction of microbial metabolic diversity (Fig. S2a). Then, the resistance of the soil to stress or disturbance may also decrease(Kremen 2005). In deeper soil layers, due to shallower roots, NO_3^--N could quickly move downward and accumulate in deeper soil (Fig. 1i), which

not only contaminated the underground water but also limited the activity of non-dominant microbes with important ecological functions, as no indicator genera were identified for each soil depth in CT treatment (Fig. 4 and Table S2). Because the microbial communities were closely associated with inorganic nitrogen, the microbes under CT were mainly influenced by added chemical fertilizer. Although the dominant microbial communities in CT were similar to those in the NTNS and NTSM, the loss of function resulted from the difference of non-dominant microbes, indicating that the soil under CT had degraded.

Under the NTNS treatment, soil pH was the major edaphic factor affecting the microbial community and the indicator genera (Fig. 6 and Table S2). The lower soil pH possibly was caused by deeper roots as shown by higher SEOC that is generally positively related to root density(Billings *et al.* 2018). Soil pH is often observed as a major factor determining the microbial composition and structure in natural ecosystems(Lauber *et al.* 2009; Zhalnina *et al.* 2015), as microbes often show a narrow tolerance to soil pH. In addition, soil pH regulates the availability of nutrient and mitigate ion toxicity(Lauber *et al.* 2009; Rousk *et al.* 2010; Zhalnina *et al.* 2015). Under NTNS, soil pH and depth only explained 35% distribution of the microbial community (Fig. 6). We speculated that other edaphic factors (e.g. salinity and iron) directly or indirectly related to soil pH and SEOC also influenced the changes in the microbial community.

Under NTSM treatment, TN and C/N significantly correlated with soil microbial community due to the high C/N ratio of stover and roots (Fig. 6). Prior studies have reported that, following maize stover mulching, more organic N, amino acid N, and amino sugar N were observed in soil(Liu *et al.* 2016; Lu *et al.* 2018), which increased the retention time of nitrogen, hence meeting the nutrient requirement of corn growth

and reducing nitrate loss to underground water. The increased available nitrogen, labile carbon and water in deep soil under NTSM can increase the resilience and resistance of maize to disturbances with higher grain production (Fig. 2). Zhang et al.(Zhang *et al.* 2013a) also observed litter-covered soil showed greater resistance to heating and copper addition due to the changes in soil properties and microbial community structure. Resistance to disturbance or stresses is the nature of a healthy soil and is essential for maintaining ecosystem functions, such as decomposing organic matter (Kibblewhite *et al.* 2008; Zhang *et al.* 2013a). Under the NTSM treatment, the microorganisms associated with the degradation of relatively stable carbon compounds, such as Planctomycetes and Verrucomicrobia (Table S3)(Herlemann *et al.* 2013; Erbilgin *et al.* 2014) as well as the indicator *Cellulomonas* and *Azospirillum* (Fig. 4 and Table S2) with the function of cellulose decomposition(Pathma *et al.* ; Halsall & Goodchild 1986) were increased. The predicted functional profiles related to energy metabolism (Carbon fixation pathways in prokaryotes), carbohydrate metabolism (TCA cycle, amino sugar, nucleotide sugar, galactose, fructose), biosynthesis of secondary metabolites (Carotenoid and Betalain) and glycan biosynthesis were increased, suggesting a higher metabolic activity and a change in substrate quality (Fig. S2). In addition, stover mulching also increased the ecological filter function of soil depth for selecting microbial communities as more indicator genera of each soil depths were identified under NTSM compared to NTNS and CT practices (Fig. 4 and Table S2). And these indicators residing at different soil depths might enhance the anti-disturbance ability of NTSM. For example, denitrification bacteria *Caldithrix* and *Pseudomonas*(Koike & Hattori 1975; Miroshnichenko *et al.* 2003) were the indicator genera of 150-200 cm and 250-300 cm, respectively (Fig. 4 and Table S2), which might explain the low nitrate in the

deep soil in NTSM. *Ignavibacteria* and *Spirochaeta*, the indicator genera of deep soil, have the ability to grow under the conditions of strictly anaerobic(Iino *et al.* 2010) and severely limited nutrients(Terracciano & Canale-Parola 1984), respectively. Surface indicator genera belonging to Bacteroidetes might have the ability to degrade organic matter that is difficult to decompose(Thomas *et al*. 2011).

Implications for climate change. It was observed that about 179.63, 352.34 and 427.34 kg ha^{-1} inorganic N were kept in the root-zone soil in the CT, NTNS and NTSM, respectively. Generally, corn roots reach their maximum depth at the silking stage(Archontoulis & Licht 2017), which is also the time when the heaviest rainfall occurs in northeastern China. We therefore expect that the available N kept in the root zone would be utilized by crops in the coming growing season, which means that fertilizer N could be cut to meet crop growth in, at least, Northeast China and also prevent reactive N losses. Since the nitrogen use efficiency (NUE) of maize system under the conventional management is 51% in northeast China (NUE is defined as the efficiency of fertilizer N transferring to harvested crop N)(Zhang *et al.* 2019). Then, we conservatively calculate the required fertilizer N in the next year based on two assumptions: 1) the NUE of soil available N in root zone is equal to that NUE of applied fertilizer N, both of them are 50%; 2) the mineralized N during the coming growing season is neglected. Thus, N supply requirement = Fertilizer N×NUE + N in root zone ×NUE + Stover-N, where Stover-N for NTSM is 60 kg ha^{-1}. We estimated the N requirement for each disturbance practice by multiplying grain yield by grain N concentration (1.4%)(Zhang *et al.* 2019) plus multiplying stover yield by stover N concentration (0.8%)(Izewska & Woloszyk 2015). For CT, NTNS and NTSM, the mean annual corn yields were 10946.74, 12487.81 and 13416.81 kg ha^{-1}, and the stover

yields were 966.67, 10083.33 and 10833.33 kg ha^{-1}, respectively. Thus, the N requirements were 230.6, 255.5 and 274.5 kg ha^{-1} for CT, NTNS and NTSM, respectively. Therefore, the theoretically conservative amounts of fertilizer N in the coming growing season are 281.6, 158.7 and 1.7 kg ha^{-1} for CT, NTNS and NTSM, respectively. No fertilizer-N is needed to apply without reducing corn yield in the NTSM plot. Compared to CT, the NTNS and NTSM could at least save respectively about 122.9 and 281.6 kg ha^{-1} N-fertilizer. For every kilogram of fertilizer-N produced and used on cropland, up to 87.9 MJ of energy is consumed(Kennedy 2000) and 13.5 kg of CO_2-equivalent (eq) (CO_2-eq) is emitted(Zhang *et al.* 2013b). Hence, totally 24,752.6 MJ of energy consumption could be reduced and 3,801.6 kg CO_2-eq emission could be cut per hectare cornland in Northeast China at least by using NTSM tillage practice. If this could be applied to all maize farmland in China (42,000,000 ha, Source: China Statistics Yearbook 2018), 1.0 EJ of energy could be saved and 159.7 Mt of CO_2-eq could be reduced. Based on the average annual energy consumption for households of China in 2017 (15 EJ, China Statistics Yearbook 2018) and CO_2 emissions (9,839 Mt, Global Carbon Atlas), the NTSM practice in corn farming has the potential to save 6.7% of household energy and to reduce 1.6% of CO_2 emissions each year in China. While the saved fertilizer-N and energy were estimated based on a series of fair simplifications with compromising rigorous complexity and deviate existed with the real situation, further long-term and large-scale experiments are needed.

Taken together, we provide new evidence that low-disturbance practice promotes deep-soil stability to cope with environmental stress through increasing water and nutrient holding capacity, microbial richness, microbial diversity and ecological

functions. According to ecological theory(Stegen *et al.* 2012; Goss-Souza *et al.* 2017), microbial community assembly in the CT treatment was mainly based on deterministic processes and significantly influenced by environmental stress and fertilizer nitrogen. Stover mulching might alter these processes through deeper roots affecting the vertical heterogeneity in resource availability(Kemper *et al.* 2011). When energy resources are richer in the soil, environmental stress tend to alleviate(Feng *et al.* 2017), and higher biodiversity was caused due to more stochastic processes introduced in community assembly(Chase 2010). Moreover, low disturbance practice also showed the potential to increase the maize yield (Fig. 2), save energy, and decrease the risk of groundwater leaching and greenhouse gas emissions. In view of the importance of microbial community assembly in predicting ecosystem service functions(Ferrenberg *et al.* 2013; García-Orenes *et al.* 2013), our results demonstrated that the lowest disturbance-practice — no-tillage with stover mulching increases the sustainability of agro-ecosystems.

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References

Archontoulis, S. & Licht, M.A. (2017). How Fast and Deep do Corn Roots Grow in Iowa? *Integrated Crop Management News*, 2442.

Aßhauer, K.P., Wemheuer, B., Daniel, R. & Meinicke, P. (2015). Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data. *Bioinformatics*, 31, 2882-2884.

Billings, S.A., Hirmas, D., Sullivan, P.L., Lehmeier, C.A., Bagchi, S., Min, K. *et al.* (2018). Loss of deep roots limits biogenic agents of soil development that are only partially restored by decades of forest regeneration. *Elem Sci Anth*, 6, 34.

Blanco-Canqui, H. & Lal, R. (2008). No-tillage and soil-profile carbon sequestration: An on-farm assessment. *Soil Sci. Soc. Am. J.*, 72, 693-701.

Bolger, A.M., Lohse, M. & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*, 30, 2114-2120.

Canadell, J., Jackson, R., Ehleringer, J., Mooney, H., Sala, O. & Schulze, E.-D. (1996a). Maximum rooting depth of vegetation types at the global scale. *Oecologia*, 108, 583-595.

483 Canadell, J., Jackson, R.B., Ehleringer, J.B., Mooney, H.A., Sala, O.E. & Schulze, E.-D.
484 (1996b). Maximum rooting depth of vegetation types at the global scale. *Oecologia*,
485 108, 583-595.
486 Chase, J.M. (2010). Stochastic community assembly causes higher biodiversity in more
487 productive environments. *Science*, 328, 1388-1391.
488 Chorover, J., Kretzschmar, R., Garcia-Pichel, F. & Sparks, D.L. (2007). Soil biogeochemical
489 processes within the critical zone. *Elements*, 3, 321-326.
490 Congreves, K., Hayes, A., Verhallen, E. & Van Eerd, L. (2015). Long-term impact of tillage and
491 crop rotation on soil health at four temperate agroecosystems. *Soil Tillage Res.*, 152,
492 17-28.
493 De Vita, P., Di Paolo, E., Fecondo, G., Di Fonzo, N. & Pisante, M. (2007). No-tillage and
494 conventional tillage effects on durum wheat yield, grain quality and soil moisture
495 content in southern Italy. *Soil Tillage Res.*, 92, 69-78.
496 Derakhshani, H., Tun, H.M. & Khafipour, E. (2016). An extended single-index multiplexed 16S
497 rRNA sequencing for microbial community analysis on MiSeq illumina platforms. *J.*
498 *Basic Microbiol.*, 56, 321-326.
499 Eilers, K.G., Debenport, S., Anderson, S. & Fierer, N. (2012). Digging deeper to find unique
500 microbial communities: the strong effect of depth on the structure of bacterial and
501 archaeal communities in soil. *Soil Biol. Biochem.*, 50, 58-65.
502 Erbilgin, O., McDonald, K.L. & Kerfeld, C.A. (2014). Characterization of a planctomycetal
503 organelle: a novel bacterial microcompartment for the aerobic degradation of plant
504 saccharides. *Appl. Environ. Microbiol.*, 80, 2193-2205.

505 Feng, Y., Guo, Z., Zhong, L., Zhao, F., Zhang, J. & Lin, X. (2017). Balanced fertilization
506 decreases environmental filtering on soil bacterial community assemblage in north
507 China. *Front. Microbiol.*, 8, 2376.
508 Ferrenberg, S., O'neill, S.P., Knelman, J.E., Todd, B., Duggan, S., Bradley, D. *et al.* (2013).
509 Changes in assembly processes in soil bacterial communities following a wildfire
510 disturbance. *ISME J.*, 7, 1102.
511 García-Orenes, F., Morugán-Coronado, A., Zornoza, R. & Scow, K. (2013). Changes in soil
512 microbial community structure influenced by agricultural management practices in a
513 Mediterranean agro-ecosystem. *PloS ONE*, 8, e80522.
514 Goss-Souza, D., Mendes, L.W., Borges, C.D., Baretta, D., Tsai, S.M. & Rodrigues, J.L. (2017).
515 Soil microbial community dynamics and assembly under long-term land use change.
516 *FEMS Microbiol. Ecol.*, 93, fix109.
517 Halsall, D.M. & Goodchild, D.J. (1986). Nitrogen fixation associated with development and
518 localization of mixed populations of Cellulomonas sp. and Azospirillum brasilense
519 grown on cellulose or wheat straw. *Appl. Environ. Microbiol.*, 51, 849-854.
520 Herlemann, D.P., Lundin, D., Labrenz, M., Jürgens, K., Zheng, Z., Aspeborg, H. *et al.* (2013).
521 Metagenomic de novo assembly of an aquatic representative of the verrucomicrobial
522 class Spartobacteria. *MBio*, 4, e00569-00512.
523 Iino, T., Mori, K., Uchino, Y., Nakagawa, T., Harayama, S. & Suzuki, K.-i. (2010).
524 Ignavibacterium album gen. nov., sp. nov., a moderately thermophilic anaerobic
525 bacterium isolated from microbial mats at a terrestrial hot spring and proposal of
526 Ignavibacteria classis nov., for a novel lineage at the periphery of green sulfur bacteria.

527 *Int. J. Syst. Evol. Microbiol.*, 60, 1376-1382.

528 IUSS Working Group, W. (2006). World reference base for soil resources. *World Soil*
529 *Resources Report*, 103, FAO, Rome.

530 Izewska, A. & Woloszyk, C. (2015). Yields of grain and straw, their content and ionic
531 proportions of macroelements in maize fertilized with ash from municipal sewage
532 sludge combustion. *J Elementology*, 20, 319-329.

533 Jiménez-Bueno, N., Valenzuela-Encinas, C., Marsch, R., Ortiz-Gutiérrez, D., Verhulst, N.,
534 Govaerts, B. *et al.* (2016). Bacterial indicator taxa in soils under different long-term
535 agricultural management. *J. Appl. Microbiol.*, 120, 921-933.

536 Kemper, W.D., Schneider, N.N. & Sinclair, T.R. (2011). No-till can increase earthworm
537 populations and rooting depths. *J. Soil Water Conserv.*, 66, 13A-17A.

538 Kennedy, S. (2000). Energy use in American agriculture. *Sustainable energy term paper*, 5,
539 1-26.

540 Kibblewhite, M., Ritz, K. & Swift, M. (2008). Soil health in agricultural systems. *Philos Trans R*
541 *Soc Lond B Biol Sci*, 363, 685-701.

542 Koike, I. & Hattori, A. (1975). Growth yield of a denitrifying bacterium, Pseudomonas
543 denitrificans, under aerobic and denitrifying conditions. *Microbiology*, 88, 1-10.

544 Kozich, J.J., Westcott, S.L., Baxter, N.T., Highlander, S.K. & Schloss, P.D. (2013).
545 Development of a dual-index sequencing strategy and curation pipeline for analyzing
546 amplicon sequence data on the MiSeq Illumina sequencing platform. *Appl. Environ.*
547 *Microbiol.*, 79, 5112-5120.

548 Kremen, C. (2005). Managing ecosystem services: what do we need to know about their

549 ecology? *Ecol. Lett.*, 8, 468-479.

550 Lauber, C.L., Hamady, M., Knight, R. & Fierer, N. (2009). Pyrosequencing-based assessment
551 of soil pH as a predictor of soil bacterial community structure at the continental scale.
552 *Appl. Environ. Microbiol.*, 75, 5111-5120.

553 Liang, B., Wang, X. & Ma, B. (2002). Maize root-induced change in soil organic carbon pools.
554 *Soil Sci. Soc. Am. J.*, 66, 845-847.

555 Liang, C., Schimel, J.P. & Jastrow, J.D. (2017). The importance of anabolism in microbial
556 control over soil carbon storage. *Nat. Microbiol.*, 2, 17105.

557 Liu, C., Lu, M., Cui, J., Li, B. & Fang, C. (2014). Effects of straw carbon input on carbon
558 dynamics in agricultural soils: a meta-analysis. *Glob. Chang. Biol.*, 20, 1366-1381.

559 Liu, X., Hu, G., He, H., Liang, C., Zhang, W., Bai, Z. *et al.* (2016). Linking microbial
560 immobilization of fertilizer nitrogen to in situ turnover of soil microbial residues in an
561 agro-ecosystem. *Agric., Ecosyst. Environ.*, 229, 40-47.

562 Liu, X., Zhang, X., Wang, Y., Sui, Y., Zhang, S., Herbert, S. *et al.* (2010). Soil degradation: a
563 problem threatening the sustainable development of agriculture in Northeast China.
564 *Plant Soil Environ.*, 56, 87-97.

565 Liu, Z., Yang, X., Hubbard, K.G. & Lin, X. (2012). Maize potential yields and yield gaps in the
566 changing climate of northeast China. *Glob. Chang. Biol.*, 18, 3441-3454.

567 Lu, C., Chen, H., Teng, Z., Yuan, L., Ma, J., He, H. *et al.* (2018). Effects of N fertilization and
568 maize straw on the dynamics of soil organic N and amino acid N derived from fertilizer
569 N as indicated by 15 N labeling. *Geoderma*, 321, 118-126.

570 Lu, F.E.I., Wang, X., Han, B., Ouyang, Z., Duan, X., Zheng, H.U.A. *et al.* (2009). Soil carbon

571 sequestrations by nitrogen fertilizer application, straw return and no-tillage in China's
572 cropland. *Glob. Chang. Biol.*, 15, 281-305.
573 Miroshnichenko, M.L., Kostrikina, N.A., Chernyh, N.A., Pimenov, N.V., Tourova, T.P., Antipov,
574 A.N. *et al.* (2003). Caldithrix abyssi gen. nov., sp. nov., a nitrate-reducing, thermophilic,
575 anaerobic bacterium isolated from a Mid-Atlantic Ridge hydrothermal vent, represents
576 a novel bacterial lineage. *Int. J. Syst. Evol. Microbiol.*, 53, 323-329.
577 Mysara, M., Leys, N., Raes, J. & Monsieurs, P. (2016). IPED: a highly efficient denoising tool
578 for Illumina MiSeq Paired-end 16S rRNA gene amplicon sequencing data. *BMC*
579 *Bioinformatics*, 17, 192.
580 Nelson, D. & Sommers, L.E. (1982). Total carbon, organic carbon, and organic matter. In:
581 *Methods of soil analysis,Part 2 (2nd).* (eds. Page, A, Miller, R & Keeney, D). American
582 Society of Agronomy and Soil Science Society of America Madison, WI, pp. 539-579.
583 Nevins, C.J., Nakatsu, C. & Armstrong, S. (2018). Characterization of microbial community
584 response to cover crop residue decomposition. *Soil Biol. Biochem.*, 127, 39-49.
585 Parks, D.H., Tyson, G.W., Hugenholtz, P. & Beiko, R.G. (2014). STAMP: statistical analysis of
586 taxonomic and functional profiles. *Bioinformatics*, 30, 3123-3124.
587 Pathma, J., Raman, G. & Sakthivel, N. Microbiome of Rhizospheric Soil and Vermicompost
588 and Their Applications in Soil Fertility, Pest and Pathogen Management for
589 Sustainable Agriculture. *189-210 (Springer, Singapore, 2019).*
590 Pries, C.E.H., Castanha, C., Porras, R. & Torn, M. (2017). The whole-soil carbon flux in
591 response to warming. *Science*, 355, 1420-1423.
592 Prosdocimi, M., Jordán, A., Tarolli, P., Keesstra, S., Novara, A. & Cerdà, A. (2016). The

593 immediate effectiveness of barley straw mulch in reducing soil erodibility and surface
594 runoff generation in Mediterranean vineyards. *Sci. Total Environ.*, 547, 323-330.
595 Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P. *et al.* (2012). The SILVA
596 ribosomal RNA gene database project: improved data processing and web-based
597 tools. *Nucleic Acids Res.*, 41, D590-D596.
598 Ramirez-Villanueva, D.A., Bello-López, J.M., Navarro-Noya, Y.E., Luna-Guido, M., Verhulst,
599 N., Govaerts, B. *et al.* (2015). Bacterial community structure in maize residue
600 amended soil with contrasting management practices. *Appl. Soil Ecol.*, 90, 49-59.
601 Richter, D.d.B. & Yaalon, D.H. (2012). " The Changing Model of Soil" revisited. *Soil Sci. Soc.*
602 *Am. J.*, 76, 766-778.
603 Rousk, J. & Baath, E. (2007). Fungal and bacterial growth in soil with plant materials of
604 different C/N ratios. *FEMS Microbiol. Ecol.*, 62, 258-267.
605 Rousk, J., Bååth, E., Brookes, P.C., Lauber, C.L., Lozupone, C., Caporaso, J.G. *et al.* (2010).
606 Soil bacterial and fungal communities across a pH gradient in an arable soil. *ISME J.*,
607 4, 1340.
608 Sagova-Mareckova, M., Zadorova, T., Penizek, V., Omelka, M., Tejnecky, V., Pruchova, P. *et*
609 *al.* (2016). The structure of bacterial communities along two vertical profiles of a deep
610 colluvial soil. *Soil Biol. Biochem.*, 101, 65-73.
611 Salem, M.A. Economics of reduced tillage technology on soil conservation and risk analysis for
612 Eastern Oklahoma farmers. *(Oklahoma State University, 1983).*
613 Sanderman, J., Hengl, T. & Fiske, G.J. (2017). Soil carbon debt of 12,000 years of human land
614 use. *Proc. Natl. Acad. Sci. U.S.A.*, 114, 9575-9580.

615 Schimel, J. & Schaeffer, S.M. (2012). Microbial control over carbon cycling in soil. *Front.*
616 *Microbiol.*, 3, 348.
617 Schmidt, R., Gravuer, K., Bossange, A.V., Mitchell, J. & Scow, K. (2018). Long-term use of
618 cover crops and no-till shift soil microbial community life strategies in agricultural soil.
619 *PloS ONE*, 13, e0192953.
620 Song, K., Zheng, X., Lv, W., Qin, Q., Sun, L., Zhang, H. *et al.* (2019). Effects of tillage and
621 straw return on water-stable aggregates, carbon stabilization and crop yield in an
622 estuarine alluvial soil. *Sci. Rep.*, 9, 4586.
623 Stegen, J.C., Lin, X., Konopka, A.E. & Fredrickson, J.K. (2012). Stochastic and deterministic
624 assembly processes in subsurface microbial communities. *ISME J.*, 6, 1653.
625 Terracciano, J. & Canale-Parola, E. (1984). Enhancement of chemotaxis in Spirochaeta
626 aurantia grown under conditions of nutrient limitation. *J. Bacteriol.*, 159, 173-178.
627 Thomas, F., Hehemann, J.-H., Rebuffet, E., Czjzek, M. & Michel, G. (2011). Environmental
628 and gut bacteroidetes: the food connection. *Front. Microbiol.*, 2, 93.
629 Vitousek, P.M., Naylor, R., Crews, T., David, M.B., Drinkwater, L., Holland, E. *et al.* (2009).
630 Nutrient imbalances in agricultural development. *Science*, 324, 1519-1520.
631 Wang, Q., Garrity, G.M., Tiedje, J.M. & Cole, J.R. (2007). Naive Bayesian classifier for rapid
632 assignment of rRNA sequences into the new bacterial taxonomy. *Appl. Environ.*
633 *Microbiol.*, 73, 5261-5267.
634 Werner, J.J., Koren, O., Hugenholtz, P., DeSantis, T.Z., Walters, W.A., Caporaso, J.G. *et al.*
635 (2012). Impact of training sets on classification of high-throughput bacterial 16s rRNA
636 gene surveys. *ISME J.*, 6, 94.

Zhalnina, K., Dias, R., de Quadros, P.D., Davis-Richardson, A., Camargo, F.A., Clark, I.M. *et al.* (2015). Soil pH determines microbial diversity and composition in the park grass experiment. *Microb. Ecol.*, 69, 395-406.

Zhang, B., Penton, C.R., Xue, C., Quensen, J.F., Roley, S.S., Guo, J. *et al.* (2017). Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems. *Soil Biol. Biochem.*, 112, 140-152.

Zhang, B., Wang, H., Yao, S. & Bi, L. (2013a). Litter quantity confers soil functional resilience through mediating soil biophysical habitat and microbial community structure on an eroded bare land restored with mono Pinus massoniana. *Soil Biol. Biochem.*, 57, 556-567.

Zhang, C., Ju, X., Powlson, D.S., Oenema, O. & Smith, P. (2019). Nitrogen surplus benchmarks for controlling N pollution in the main cropping systems of China. *Environ. Sci. Technol.*, 53, 6678-6687.

Zhang, W.-f., Dou, Z.-x., He, P., Ju, X.-T., Powlson, D., Chadwick, D. *et al.* (2013b). New technologies reduce greenhouse gas emissions from nitrogenous fertilizer in China. *Proc. Natl. Acad. Sci. U.S.A.*, 110, 8375-8380.

Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure Legends

Figure 1. Soil properties (mean±SE, n = 3) along soil depth under different practices. SOC = soil organic carbon, SEOC = salt-extractable organic carbon, SEOC/SOC = ratio of SEOC to SOC, SM = soil moisture, TN = total nitrogen content, C/N = ratio of SOC to TN, NH_4^+-N = ammonium nitrogen, NO_3^--N = nitrate nitrogen, Inorganic N = NH_4^+-N + NO_3^--N.

Figure 2. Corn yield (line+symbol) and annual rainfall during growing and dormant seasons (bar) under different disturbance practices during 2013-2016. Error bars indicate standard errors (n = 3 or 4), different letters indicate significant differences at $P < 0.05$.

Figure 3. Microbial richness (Chao1), observed number of species (Observed_species) and diversity (Shannon_Index) in the CT (conventional tillage), NTNS (no-tillage without stover mulching) and NTSM (no-tillage with stover mulching) plots. Error bars indicate standard deviation (n = 3).

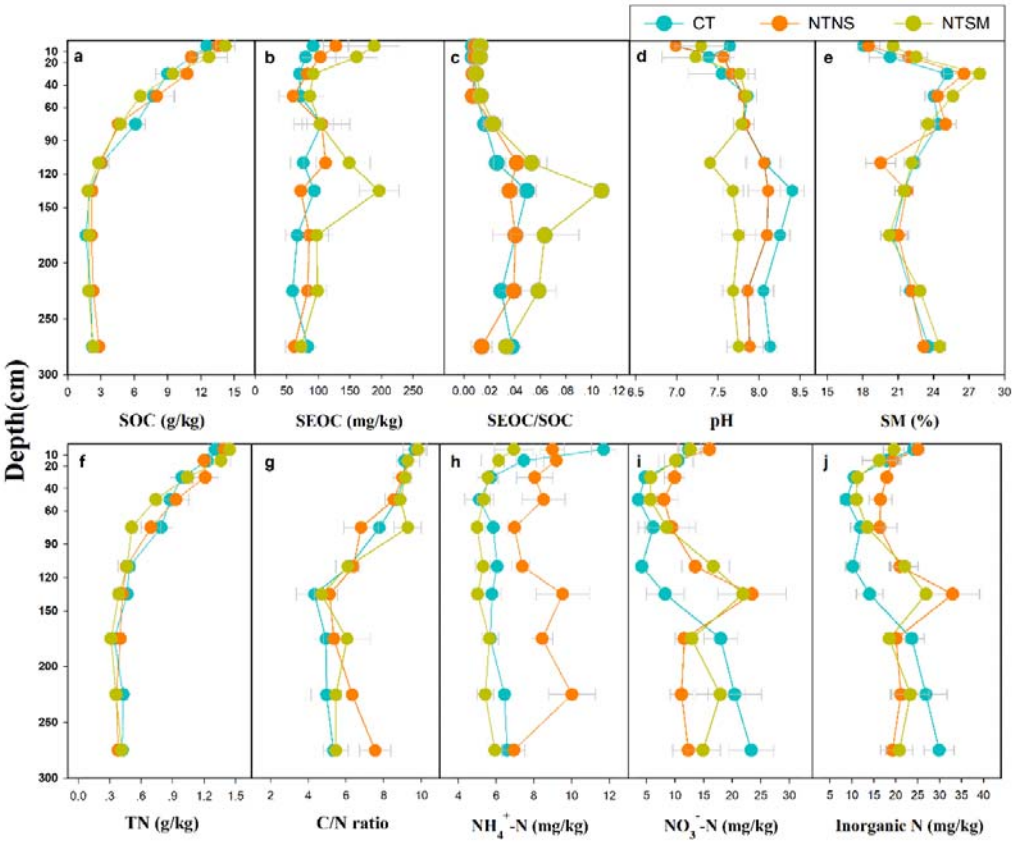
Figure 4. Indicator genera significantly ($q < 0.1$) associated with tillage practices. The size of each circle represents the indicator value of a specific genus in the different soil depths. The color indicates the relative abundance of each indicator genus. Taxonomic information, indicator values, P-values, and q-values of all indicator genera are given in Table S2. Zero indicator genera were identified in CT treatment.

Figure 5. Non-metric multidimensional scaling (MDS) ordination of soil microbial community structures based on Bray-Curtis distances among soil depths at different agricultural disturbance practices. Permutational multivariate analysis of variance (PERMANOVA) revealed that the overall microbial community structures among soil depth were significantly different at each disturbance practice. Circles, triangles and

squares represent CT (conventional tillage), NTNS (no-tillage without stover mulching) and NTSM (no-tillage with stover mulching), respectively.

Figure 6. Redundancy analysis (RDA) of the soil microbial community originating from microbial phyla constrained by soil properties under different agricultural practices. Only soil variables that significantly explained variability in microbial community structure in the forward selection procedure were selected to the ordination (arrows). TN, total nitrogen content; C/N, a ratio of carbon to nitrogen content; NH_4^+-N, ammonium nitrogen; NO_3^--N, nitrate nitrogen ; SM, soil moisture. Circles, triangles and squares represent CT (conventional tillage), NTNS (no-tillage without stover mulching) and NTSM (no-tillage with stover mulching), respectively.

Figures



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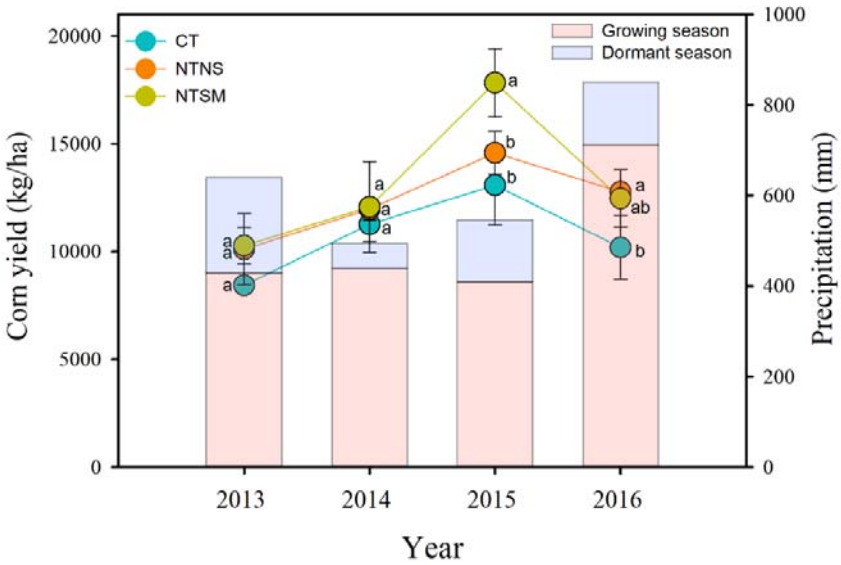

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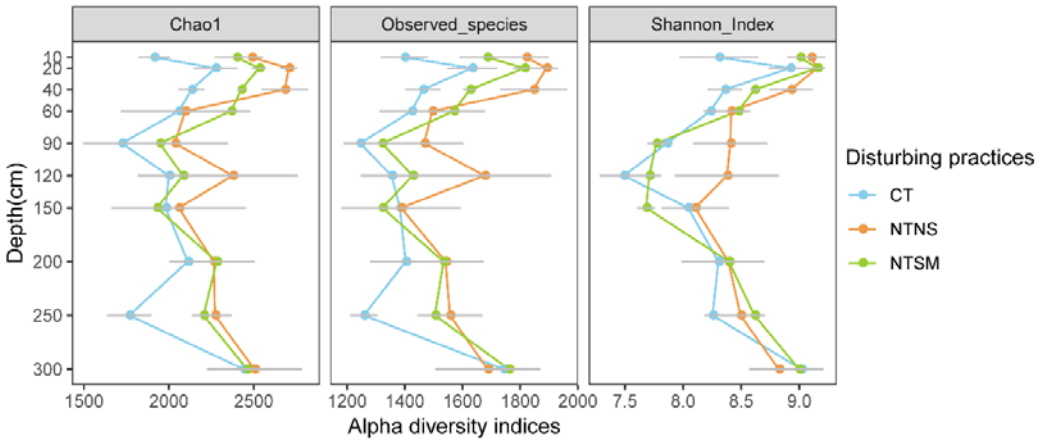

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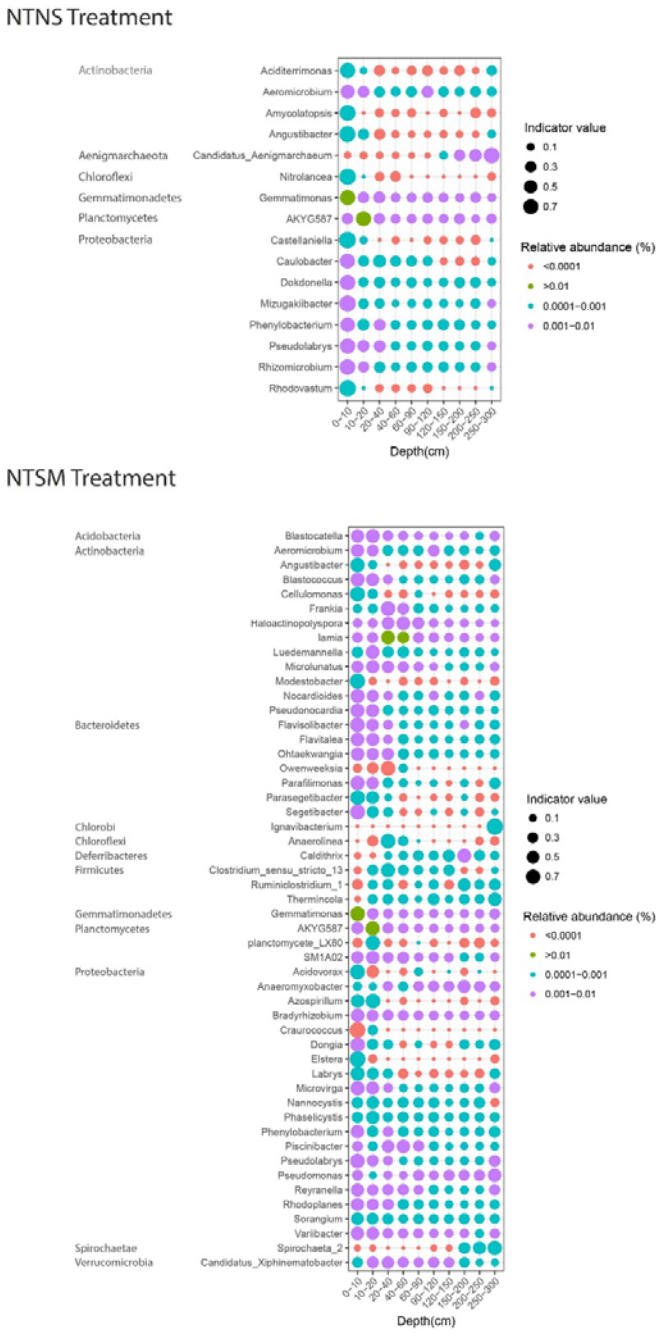

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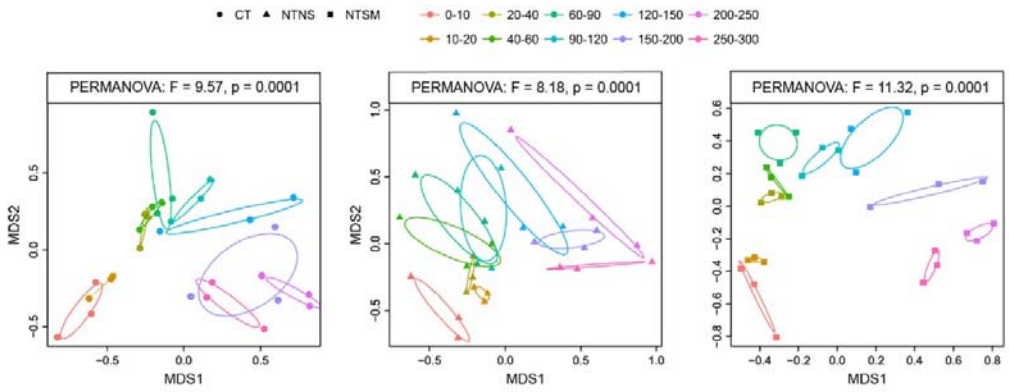

Figure 5. Non-metric multidimensional scaling (MDS) ordination of soil microbial community structures based on Bray-Curtis distances among soil depths at different agricultural disturbance practices. Permutational multivariate analysis of variance (PERMANOVA) revealed that the overall microbial community structures among soil depth were significantly different at each disturbance practice. Circles, triangles and squares represent CT (conventional tillage), NTNS (no-tillage without stover mulching) and NTSM (no-tillage with stover mulching), respectively.

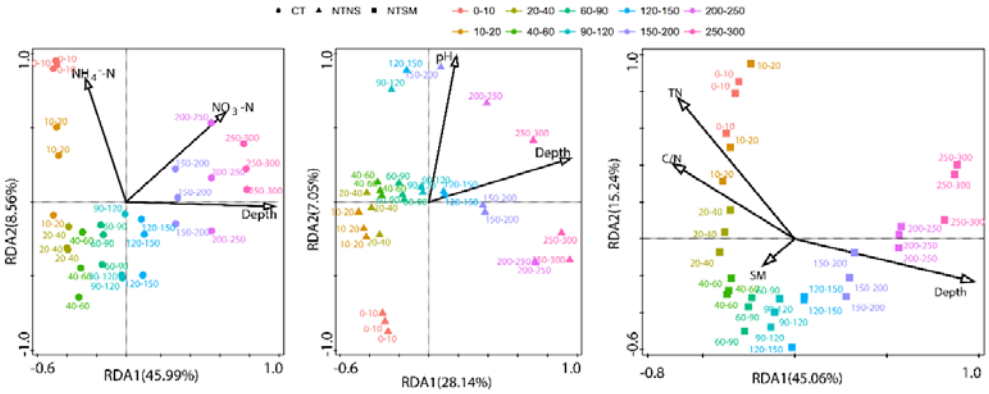

Figure 6. Redundancy analysis (RDA) of the soil microbial community originating from microbial phyla constrained by soil properties under different agricultural practices. Only soil variables that significantly explained variability in microbial community structure in the forward selection procedure were selected to the ordination (arrows). TN, total nitrogen content; C/N, a ratio of carbon to nitrogen content; NH_4^+-N, ammonium nitrogen; NO_3^--N, nitrate nitrogen ; SM, soil moisture. Circles, triangles and squares represent CT (conventional tillage), NTNS (no-tillage without stover mulching) and NTSM (no-tillage with stover mulching), respectively.