



Responses of soil fungi to 5-year conservation tillage treatments in the drylands of northern China



Ziting Wang, Qing Chen, Lu Liu, Xiaoxia Wen, Yuncheng Liao*

College of Agronomy, Northwest A&F University, Taicheng Road 3, Yangling, Shaanxi, China

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ABSTRACT

Soil fungi have many important ecological functions such as decomposition of soil organic matter and facilitation of nutrient turnover and availability in agricultural soils, which can be influenced by tillage treatments. Conservation tillage is widely used in the dryland regions of northern China. However, insights into the effect of conservation tillage on soil fungal community compositions and structures are considerably limited. This study aimed to investigate the effect of 5-year conservation tillage treatments, including chisel plow tillage (CPT), zero tillage (ZT), and plow tillage (PT) as convention tillage treatment, on soil fungal communities by using high-throughput sequencing technology and quantitative polymerase chain reaction. Conservation tillage significantly influenced soil fungal diversity and phylogenetic composition by altering soil organic carbon content and texture. The fungal diversity and composition structure were similar for treatments causing higher soil perturbation, i.e., CPT and PT; ZT, a less disruptive agriculture practice, preserved soil biological integrity. The most abundant phyla across all samples were Ascomycota and Basidiomycota, which are considered to be the main classical fungal decomposers in soils. These results suggested that conservation tillage can affect crop residue decomposition and the soil organic carbon content, leading to changes in soil fungal community distribution patterns. Our findings might form the basis for the application of conservation tillage to produce more stable and sustainable soil ecosystems in the drylands of northern China.

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1. Introduction

Soil fungi play a major role in terrestrial ecosystems. They are important decomposers that recycle soil organic matter and mineral components, including cellulose, lignin, carbon, and nitrogen (Hollister et al., 2010; Joergensen and Wichern, 2008). The functional diversity of soil fungi is related to taxonomic community structures, and greater functional diversity improves plant nutrient acquisition, protects plants against pathogens, and directly affects plant productivity (Deacon et al., 2006; van der Heijden et al., 2008). Soil fungal community structures are significantly influenced by the physical and chemical properties of the soil, which are determined by agricultural practices (Jirout et al., 2011; Wu et al., 2007). Tillage is a major agricultural practice that can affect soil quality, since physical disturbance of the soil leads to alterations in soil water content, causes changes in the structural composition of the soil particles, and affects the degree

of crop residue incorporation into the soil matrix (Kladivko, 2001). Hence, analysis of soil fungal communities as a powerful tool for monitoring changes in environmental conditions and responses to conservation tillage treatments has attracted considerable attention (Arenz and Blanchette, 2011; Nie et al., 2012).

Many studies have focused on the effects of conservation tillage treatments on fungal abundance and structure; most of these studies were based on indirect techniques used to measure the physiological and biochemical properties of the microorganisms (Wang et al., 2010). However, because of the limited sensitivity and scope of these classical measurement techniques, an attainment of an accurate overview of the quantitative and qualitative changes occurring in soil microbial communities cannot be obtained (Maron et al., 2011). Thus far, only a few studies have applied high-throughput sequencing technology, which enables metagenomic analysis of the vast soil microbial diversity and elucidation of the effects of tillage practices on soil microbial communities (Maron et al., 2011; Terrat et al., 2012).

The dryland regions in northern China account for approximately 56% of the nation's total land area and 46% of the agricultural industrial production. Crop production in these regions is constrained by adverse weather, topography, and water resource conditions; exacerbation of soil erosion; and water and

* Corresponding author.

E-mail addresses: zitingwang@nwsuaf.edu.cn (Z. Wang), 498875835@qq.com (Q. Chen), 1164284760@qq.com (L. Liu), 335438819@qq.com (X. Wen), yuchengliao@163.com, yuchengliao@sina.cn (Y. Liao).

nutrient losses under conventional tillage treatments. Many studies have indicated that conservation tillage, including zero tillage (ZT) and chisel plough tillage (CPT), can improve soil structure, conserve soil water, enhance soil nutrient levels, promote efficient crop water usage, and increase crop yields (Chen et al., 2011; Hu et al., 2007; Huang et al., 2008; Jin et al., 2007; Li et al., 2007; Su et al., 2007; Zhang et al., 2012). Because of these advantages, conservation tillage has been extensively applied in the dryland regions of northern China. However, only a few studies have investigated the effects of conservation tillage on the microbial biomass in these regions (Chen et al., 2009; Wang et al., 2008). Therefore, a preliminary understanding of the correlations between soil physico-chemical properties of the soil and fungal community compositions is important.

This study aimed to analyze the effect of tillage treatments on the enumeration, taxonomic distribution, and phylogenetic composition of soil fungal communities, and to determine the correlations between soil properties and changes in the abundance, diversity, and composition of soil fungal community under conservation and conventional tillage treatments. We collected soil samples from plots that were subjected to three types of 5-year tillage treatments, namely, CPT, ZT, and plow tillage (PT), and compared their fungal communities in the samples by using high-throughput sequencing and quantitative polymerase chain reaction (qPCR). We hypothesized that tillage treatments would lead to the selection of distinct soil fungi, based on the different soil physico-chemical properties resulting from each tillage treatment. The findings of this study might facilitate the application of conservation tillage in the drylands of northern China.

2. Materials and methods

2.1. Experiment site and tillage treatments

This study was performed at Northwest A & F University, Yanglin, Shaanxi, China (34°17' N, 108°04' E at an elevation of 521 m

above sea level; Fig. 1A); the study site has Eum-Orthosols (Chinese soil taxonomy) soil with a mean bulk density of approximately 1.29 g cm^{-3} . The experimental area was located in the Guanzhong Plain (Fig. 1B), which belongs to zone 5 (semi-humid) of the drylands of northern China (Wang et al., 2007). The mean annual precipitation in the region is 633 mm, with an average yearly temperature of 13.2°C .

Soil samples were collected from a site of a long-term trial that began in 2009. Before 2009, the experimental area ($32 \text{ m} \times 75 \text{ m}$) was managed using rotary cultivation. The experimental treatments combined three tillage methods and residue retention in the croplands, with wheat–maize rotation. We used the same tillage management as in previous years for both wheat and maize. An area of $32 \text{ m} \times 75 \text{ m}$ was divided into 12 plots of $8 \text{ m} \times 25 \text{ m}$ each, and treatments were assigned to randomized block (Fig. 1C). Each plot was tilled using the CPT, ZT, or PT treatment (Fig. 1C). For the CPT treatment, a 30–35-cm deep chisel plough with a 40-cm distance between the tines was used once following the application of fertilizers. For the ZT treatment, soil disturbance was limited; thus, to ensure germination, we used 0–5-cm rotary tillage. For PT, the soil was plowed to a depth of 20–30 cm by using a moldboard plow, followed by the application of a rotavator for the final seedbed preparation.

Winter wheat (cv. Shaanmai 139) was sown over the residues of maize (cv. Shaandan 609) on October 17, 2013, by using wheat drills. Crop details from 2009 to 2013 are shown in Table S1. Urea fertilizer with nitrogen (N) content of >46% and calcium phosphate [$\text{Ca}_2(\text{PO}_4)_3$] fertilizer with 16% phosphorous (P) were applied for all treatments at a rate of 750 kg ha^{-1} at the time of soil preparation.

2.2. Soil sampling and physico-chemical analysis

Soil samples were obtained from depths of 5–20 cm on May 6, 2014 (210 days after wheat sowing). Five subsamples were collected from each sampling site. Samples were collected away from the plant roots by using a standard soil corer and sieved

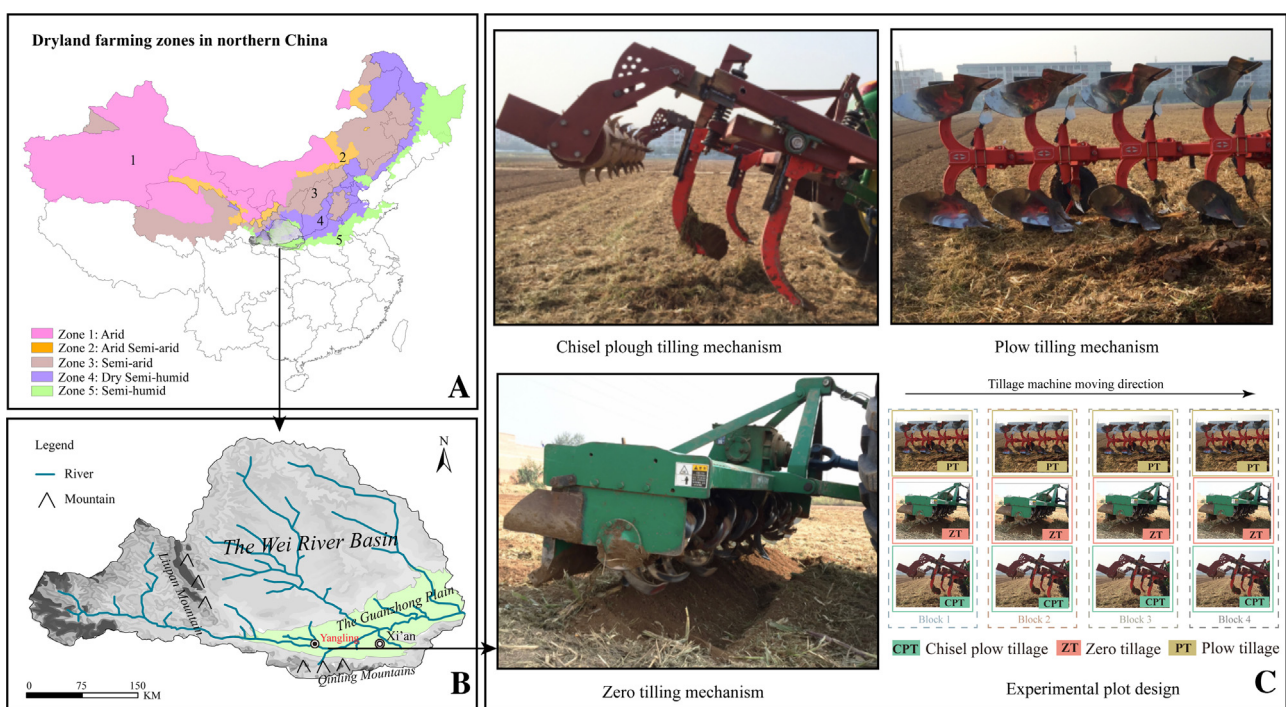


Fig. 1. Map of the dryland agricultural zones in North China (A). Sampling point in Guanzhong Plain (B). Different conservation tillage treatments applied to the experimental field (C).

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