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Impact of no tillage vs. conventional tillage on the soil bacterial community structure in a winter wheat cropping succession in northern China

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ABSTRACT

A comprehensive evaluation of the impacts of different tillage managements on bacterial community structure is fundamental to better understand their roles in maintaining soil health. The objective of this study was to assess the impact of no tillage (NT) vs. conventional tillage (CT) management on soil properties, bacterial community structure in a 22-year experiment established on the Loess Plateau of China, under a winter wheat cropping succession. Our results showed that the long-term application of NT caused a significant increase in bacterial alpha-diversity as indicated by the significantly greater number of unique operational taxonomic units (OTUs), richness (Chao), evenness (ACE), and Shannon index and a lower Simpson index compared to CT. Moreover, the NT treatment changed certain soil physicochemical properties, e.g., soil organic carbon (SOC), total nitrogen (TN), dissolved organic carbon (DOC), microbial biomass C (MBC), microbial biomass N (MBN) and nitrate nitrogen (NO_3-N) were greater under CT. The bacterial communities differed significantly between the different tillage treatments, and NT harboured relatively higher abundances of the dominant genera *Sphingomonas* and *Pseudomonas* and a lower abundance of *Acidobacteria* than CT. A redundancy analysis (RDA) revealed that the bacterial community structure was strongly correlated with variations of SOC, DOC and TN. Thus, based on these findings, it is concluded that NT management is a more sustainable faming practice to improve soil properties and bacterial diversity.

1. Introduction

The Loess Plateau of China is one of the most intense agricultural regions in northern China. Conventional tillage (CT), including mouldboard ploughing, was the dominant management practice in this region during the 20th century. However, this type of intensive cultivation has led to severe land degradation and has threatened sustainable crop production [1]. As an alternative, no-tillage (also referred to as zero tillage, NT) has been recently promoted in these regions, in which seeds are directly sown into untilled soil [2]. Because of concerns about soil quality degradation since 1992, the Australian Centre for International Agricultural Research and the Chinese Ministry of Agriculture have conducted experimental research on the Loess Plateau of Shanxi Province in northern China to monitor soil ecosystem processes and nutrient dynamics under different tillage practices [3].

Microorganisms are the primary active components of soil, mainly due to their high abundance, diversity and multiple metabolic activities [4]. Microbial communities play a vital role in regulating nutrient cycling and affecting plant productivity and the stability of ecosystems [5]. Therefore, quantitative and qualitative changes in the structure of soil microbial communities (e.g., diversity index) may serve as important and sensitive indicators of both short and long-term changes in soil health [6].

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The effects of different tillage practices on physical and chemical soil properties and microbial activity have been investigated in a number of studies [7–9]. Most researches have indicated that NT increases soil carbon stocks and nutrient contents, stabilizes the soil structure [10], and thereby enhances soil microbial activity when compared with CT systems [11,12]. However, NT treatment may also affect soil characteristics and microbial community in another way. Continuous NT treatment may result in problems, such as surface hardening of the soil, leading to a more limited O_2 supply for soil microorganisms [13]. Thus, some debate still remains regarding the effects of different tillage management systems on soil microbial communities.

Among the numerous microorganisms present in soils, bacteria are considered as the most abundant and diverse group [14]. Agricultural practices that impact soil conditions can significantly alter soil microbial community in general and bacterial community in particular [15]. The implementation of NT has been shown to affect soil bacteria in terms of bacterial activity [16] and bacterial diversity [17]. These differences have mainly been attributed to differences in the levels of soil properties among different cropping systems. Tillage management systems are important to characterize bacterial communities and have a strong influence on the main bacterial phyla [18]. The management of tillage favoured the richness and diversity of active soil bacteria in a culture-independent approach [8]. Furthermore, certain bacteria may be differentiated into more ecologically relevant tillage systems based on their substrate preferences and life strategies [19]. From many previous studies, describe bacterial communities and characterize their members was limiting [20]. The implementation of high-throughput sequencing, especially using the recently developed Illumina MiSeq platform, can also detect less abundant members of the bacterial communities and gain information about their ecological importance [21]. However, there is still limited research on the effects of different tillage systems on the taxonomic distributions and phylogenetic compositions of bacterial communities by sequencing, and consequently, the correlation between the physicochemical soil properties and bacterial community structure is still poorly understood. By using Illumina high-throughput sequencing of the 16S rRNA gene, it was demonstrated that the NT system significantly increased soil bacterial diversity in an Acrisol through alterations in the composition and abundance of individual bacterial species [22]. However, further studies on the effects of different tillage systems under varying soil types and environmental conditions are needed to gain a more comprehensive understanding.

A recent study found that 5-year tillage treatments significantly changed the soil texture, moisture, and nutrient levels, and modified the soil bacterial community structure of soil from the drylands of China [23]. Based on this, the objective of this study was to test whether longer-term (22 years) CT and NT created distinctly different ecological habitats for bacteria and whether bacterial composition responded differently to different conditions. Therefore, the diversity and composition (phylum to genus levels) of bacterial communities under two tillage treatments were compared, and the physicochemical properties were analyzed. Moreover, the relationship between bacterial community structure and the physicochemical properties was examined. It was hypothesized that (1) the soil properties would be significantly different in different tillage systems; (2) NT would increase soil bacterial community diversity and alter bacterial composition more than the CT treatment; and (3) significant relationships between soil C and N content, and the composition of the bacterial community would exist in both NT and CT, respectively.

2. Materials and methods

2.1. Study site

The study field was located at Linfen long-term experimental station of Chinese Academy of Agricultural Sciences, in Shanxi Province, China (38°6′N, 113°26′E, 456 m asl). The experimental area was located on Loess Plateau, and was characterized by a semiarid climate. Mean annual precipitation was 555 mm, primarily occurring from July to September. Mean annual temperature was 10.7 °C, with a frost-free period of 180 days. Soil was classified as silt loam using USDA soil taxonomy, and soil type was classified as a Chromic Cambisol according to FAO-UNESCO soil map 25 [24]. Soil texture was mainly composed of 63% sand, 20% silt and 17% clay, respectively. Soil pH was 7.7, and soil organic matter (SOM) content was 13.0 g kg^{-1} with total N content of 0.5 g kg^{-1}, total P of 0.15 g kg^{-1} and total K of 12.0 g kg^{-1} [25].

2.2. Experimental design

A long-term tillage experiment was initiated in 1992 under a winter wheat (Linfen 225) cropping system. In this system, winter wheat was sown at the end of September and harvested in June. Two different treatments were applied: (i) conventional tillage (CT) and (ii) no-tillage (NT). The experiment consisted of six plots (80 m in length and 3 m in width) in a randomized-block design, with three replicates for each treatment. In the CT plot, mouldboard ploughing was conducted to 15–20 cm in depth. The wheat residues were returned to the field as surface mulch (average 3.75 t ha^{-1}). All of the plots were fertilized before sowing with 150 kg $ha^{-1}\cdot yr^{-1}$ of N (as urea ($CO(NH_2)_2$)), 140 kg $ha^{-1}\cdot yr^{-1}$ of P_2O_5 (as diammonium phosphate ($(NH_4)_2HPO_4$)) and 62 kg $ha^{-1}\cdot yr^{-1}$ of K_2O (as Potassium chloride (KCl)). Each plot had the same management regime every year.

2.3. Sampling collection and analysis

2.3.1. Soil sampling

Soil samples were collected from the 6 plots at 10 days after the winter wheat harvest in 2014. In each plot, the soil was sampled from the plough layer (0–20 cm) using an auger with a 5 cm internal diameter at five randomly selected locations and was then mixed into one sample. All of the fresh soil samples were divided into two parts: one stored at 4 °C for chemical analysis and the other one stored at −80 °C for DNA extraction.

2.3.2. Soil chemical property analysis

The soil chemical properties were measured using the methods described by Bao [26]. Soil pH was measured with a glass electrode in a 1:2.5 soil/water suspension. Soil organic carbon (SOC) concentration was measured with a K_2CrO_7-H_2SO_4 oxidation procedure and total nitrogen (TN) was measured with the Kjeldahl method. Soil C/N values were calculated as the ratio of SOC to TN. Dissolved organic carbon (DOC) content of the filtered 0.5 M K_2SO_4 extracts from the fresh soil was measured with a TOC analyser (Liquid TOC Elementar, Vario Max, Germany). Soil microbial biomass C (MBC) and microbial biomass N (MBN) were determined using the chloroform fumigation–extraction technique. Ammonium nitrogen (NH_4-N) and nitrate nitrogen (NO_3-N) concentrations of filtered 2 M KCl extracts from fresh soil were measured with a flow injection autoanalyser (AutoAnalyser 3, Bran + Luebbe, Germany).