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Original article

Tillage and rotation effects on community composition and metabolic footprints of soil nematodes in a black soil

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ABSTRACT

Understanding the response of soil biota to tillage and rotation practices is useful for evaluating the effect of agricultural management. We investigated soil physiochemical properties, nematode community structure and composition and their metabolic footprints in different tillage and crop rotation systems in a 12-year old field experiment in a black soil. The experiment was based on a split-plot design with conventional tillage (CT) and no-tillage (NT) as main plots and corn-soybean rotation (CS) and continuous corn (CC) treatments as subplots. Soil samples were taken at 0–5 cm and 5–15 cm depths. The results showed that in comparison with CT, NT increased total soil organic carbon, soil moisture and microbial biomass carbon at 0–5 cm depth regardless of rotation system. Rotation effect on total nematode abundance was significant. The abundance of fungivores was significantly influenced by the tillage effect, with higher abundance found in CT systems. In total, fifty-eight nematode genera were identified. *Acrobeloides* dominated under CS and *Filenchus* under CC. In NT system, a bacterial-dominated decomposition pathway was dominant under CS, and fungal-based channel under CC at 0–5 cm depth. The interactive effect of tillage and rotation changed the decomposition channel. Under CS system, lower structure index (SI) and higher channel index (CI) were found in CT than in NT at 0–5 cm depth. At both depths, functional metabolic footprint was greater under CS than under CC in both tillage systems. Footprint of fungivores also suggested a greater flow of resources into the food web through fungivorous channels under CC. Redundancy analysis (RDA) showed that tillage and rotation influenced soil nematodes by changing soil physiochemical properties. Nematode community analysis indicated that corn-soybean rotation system increased nematode abundance and their functional metabolic footprint, and favored a more diverse residue resource entry into soil food webs.

1. Introduction

In agroecosystems, agricultural practices such as conservation tillage and crop rotation are beneficial for sustainable crop production due to their positive influences on the soil environment. Furthermore, tillage and crop rotation generally affect soil physicochemical properties and biological activities [1–4]. For example, no-tillage involving surface crop residue application has been adopted as a means to promote soil aggregate stability and fertility, while simultaneously increase the abundance and activity of soil biota [5–8]. In addition, crop rotation can also increase the input of organic C and N into the soil, which enhances soil fertility [9]. When high amounts of crop residues are returned to the soil, crop rotation can influence the soil microbial habitat, improve soil structure, and increase the activity and diversity of soil fauna [10–12].

Among soil fauna, soil nematodes are one of most important metazoa due to their abundance and functional diversity [13]. Plant-parasitic nematodes interact directly with plants and microbiovorous nematodes act as consumers of microflora, and thereby indirectly regulate decomposition and release of nutrients in agroecosystems [14]. Many studies have also documented that soil nematode communities can be used as bioindicators for different ecosystems [15–19]. For example, the relative abundance of fungal-feeding and bacterial-feeding nematodes may be regarded as sensitive indicators of management changes [20]. The decline in diversity of nematode fauna with increasing levels of

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management reflects not only physical disturbance but also the changes in the quantity and quality of organic matter returned to the soil. Considering these indicative functions, many researchers have reported how soil nematodes respond to agricultural practices. Okada and Harada [21], for example, observed that nematode diversity indices, maturity, structure and channel indices were higher in a no-tillage system than in a conventional tillage system. Overstreet et al. [22] showed that in comparison with conventional tillage, soil nematode abundance increased significantly in conservation tillage such as strip tillage, while Zhang et al. [23] showed that the responses of nematode trophic diversity, the enrichment index and the channel index were all sensitive to the tillage effect. Crop rotation sequences including different crop varieties can also influence nematode abundance, diversity and community structure. Rhaman et al. [3], for example, reported that free-living nematodes were more abundant in a wheat-lupin rotation system than in a continuous wheat system, while Postma–Blaauw et al. [24] found that maize monocultures were characterized by plant-parasitic nematodes and a barely-potato rotation system was dominated by bacterivorous and fungivorous nematodes.

Until now, most studies on soil nematode communities have been focused either on the effects of different tillage practices or on the effects of crop rotation. How rotation and tillage interactively affect soil nematode communities is relatively unknown. However, tillage and rotation are two important agricultural practices that are usually applied together in the crop fields of many countries [2,3,25]. Therefore, studies that examine on the interactive effect of tillage and rotation on soil nematode communities are needed. Additionally, from nematode ecology point of view, previous studies have focused on nematode ecological indices to analyze nematode community composition and diversity in different agricultural management systems. These indices of nematode communities do not provide much information on the magnitude or nature of the ecosystem functions these nematode communities provide [26]. To gain insight into the metabolic activity levels of various indicator guilds of nematodes, Ferris [26] proposed the nematode metabolic footprint which provides a quantitative component of ecosystem structure and function based on carbon utilization [27]. Ferris [26] and Zhang et al. [23] showed that the nematode metabolic footprint can provide insight into the structure and function of soil food webs. In this study, we use the nematode metabolic footprint to indicate how crop rotation and tillage influence ecosystem function and service of soil food web.

The objectives of our study were to analyze the interactive effect of tillage and rotation on soil nematode community composition and soil physiochemical properties, to quantify the nematode metabolic footprint in different tillage and rotation practices, and to evaluate which kinds of agricultural management practices are more favorable for agroecosystem stability and sustainability in terms of soil biota in a black soil.

2. Materials and methods

2.1. Site description

The study was conducted at the Experimental Station (44°12′ N, 125°33′ E) of the Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, in Dehui County, Jilin Province, China. The soil at this site is classified as black soil (Typic Hapludoll according to the USDA Soil Taxonomy) with a clay loam texture consisting of 36.0% clay, 24.5% silt and 39.5% sand. Before the establishment of the experiment, the field was used for corn production using a conventional tillage management (see below) for more than 20 years [28].

2.2. Experimental design and management practices

The experiment was a split-plot design with four replicates, initiated in the fall of 2001 with tillage system as the main plot and rotation management as the sub-plot [28]. Tillage systems included a conventional tillage (CT) and a no-tillage (NT) treatment. Rotation management treatments were corn-soybean rotation (CS) (one year corn and one year soybean) and continuous corn (CC).

The practices in CT consisted of mouldboard plowing (20 cm depth) after harvest in October, and disking (7.5–10 cm depth) and harrowing for the secondary seedbed preparation in about May of the next year. All aboveground crop residues in CT were incorporated into the soil. There were minimal human disturbances in NT except for planting using a KINZE-3000 NT planter (Williamsburg, Iowa). After harvest, all the corn straws were collected and cut into pieces of roughly 30 cm leaving a 30–35 cm stubble stand, and the pieces were then returned to the soil surface. Soybean residues were directly returned to the soil surface. The size of each individual subplot was 5.2 m × 20 m. Crops were sown in May and harvested in October. A fallow period (about seven months) was followed after each harvest.

Each year, in the corn field, 100 kg N ha^{-1}, 45.5 kg P ha^{-1} and 78 kg K ha^{-1} were applied as starter fertilizer during the sowing period and 50 kg N ha^{-1} as top dressing at the V-6 stage (6 leaves with collars). During the sowing period of soybean, 40 kg N ha^{-1}, 60 kg P ha^{-1} and 80 kg K ha^{-1} were applied as starter fertilizer [28].

2.3. Soil sampling

Soil samples were collected in April 2012, which was at the end of fallow period following corn harvest in 2011. In each subplot, composite samples of five random sub-samples were collected with a soil auger (2.64 cm diameter). Soil samples were taken at the depths of 0–5 cm and 5–15 cm. In total, 32 soil samples were collected. The fresh samples were placed in the plastic bags and kept at 4 °C until processed and analyzed. Bulk density was determined at 0–5 cm and 5–15 cm depth using a 100 cm^3 cylinder (5 cm height × 5 cm diameter).

2.4. Soil physiochemical properties

Soil organic carbon (SOC) was determined by dichromate oxidation and titration with ferrous ammonium sulfate [29]. Total nitrogen (TN) was determined by Kjeldahl method [30]. Soil NO_3^--N and NH_4^+-N were detected by using a flow injection auto analyzer (FIAstar 5000 Analyzer, Denmark). Microbial biomass carbon (MBC) and microbial biomass nitrogen (MBN) were extracted using the chloroform fumigation and extraction method and measured using a TOC analyzer (Multi C/N 3000, Analytik Jena, Germany) [31]. Soil moisture (SM) was determined gravimetrically by drying samples at 105 °C.

2.5. Soil nematode identification

Nematodes were extracted from 50 g fresh soil by a modified cotton-wool filter method [32]. After counting the total abundance of nematodes in each sample, 100 individuals were randomly selected and identified to genus level using an inverted compound microscope [33]. If the total nematodes did not reach 100 in a sample, all the nematodes in the sample were identified. Nematode abundance was expressed as individuals per 100 g dry soil. Nematodes were assigned to the following the trophic groups according to their feeding habits: bacterivores (BF), fungivores (FF), omnivores-predators (OP) and plant-parasites (PP) [34].