



# Development of soil food web of microbes and nematodes under different agricultural practices during the early stage of pedogenesis of a Mollisol



Na Li <sup>a,1</sup>, Feng-juan Pan <sup>a,1</sup>, Xiao-Zeng Han <sup>a,\*\*</sup>, Bin Zhang <sup>b,\*</sup>

<sup>a</sup> National Observation Station of Hailun Agro-ecology System, Key Laboratory of Mollisols Agroecology, Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Harbin, 150081, PR China

<sup>b</sup> National Engineering Laboratory for Improving Fertility of Arable Soils, Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing, 100081, PR China

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## ABSTRACT

Agricultural practices such as tillage and organic amendment influence development of the soil food web. However, such effects are not well understood at the initial stage of soil formation. Using an eight-year field experiment established on exposed parent materials of a Mollisol, the objectives of this study were: (1) to determine the effects of agricultural practices on soil food web structure in comparison to the structures of soil nematode guilds and microbial communities, *per se*; (2) to elucidate the development of the food web of the young soils in relation to parent materials and a mature Mollisol; and (3) to identify the controlling factors of such relationships. The microbial biomass expressed in phospholipid fatty acids and the abundance of nematode guilds increased in the field treatments compared with parent materials by a larger magnitude in Gram positive (G+) bacteria and plant parasite (PP) nematodes under perennials than under cropping. The abundance of bacterivorous (Ba) nematode guilds was significantly correlated with microbial biomass of total bacteria, but not with that of G+ or G- bacteria. The abundance of total Ba, particularly Ba1 nematode guilds was positively correlated with soil organic carbon and its related nutrient contents. Redundancy analysis showed that the structure of food web was similar to nematode guild structure rather than to soil microbial community structure among the soils. The food web structure was separated between the soils under perennials and those under cropping via Axis 1 and between fertilized and not fertilized soils irrespective of land uses via Axis 2. The separations via Axis 1 were mainly driven by PP nematodes in association with high C:N soils, suggesting the determinant effect of land use type, while the separations via Axis 2 were driven by Ba nematodes and bacteria in association with soil physical and chemical properties, indicating the role of soil carbon and nutrients. The food web in the arable soils with more organic amendments was similar to that of mature Mollisol. These findings suggest that soil food web at the early pedogenesis can develop quickly with restoration practices and the development was more affected by land use type than by soil management practices.

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## 1. Introduction

Soil degradation is one of the largest threats to sustainable

development in 21st century (Lal, 2001, 2003). There is a considerable need for large-scale restoration programs to develop strategies for restoration, sustainable use and protection of soils (Cairns, 1999; Hobbs and Harris, 2001; Schulz et al., 2013). Compared with successful restoration of aboveground ecosystems, our understanding of soil development in vegetation restoration contexts is still very poor (Griffiths et al., 2008; Harris, 2009). This is partly because soil formation has been considered a very slow process as happens under natural conditions (Harrison and Strahm, 2008). Agricultural practices can rapidly influence soil properties

\* Corresponding author. Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing, 100081, PR China.

\*\* Corresponding author. Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, 138 Haping Rd, Harbin, 150081, PR China.

E-mail addresses: [xzhan@iga.ac.cn](mailto:xzhan@iga.ac.cn) (X.-Z. Han), [zhangbin01@caas.cn](mailto:zhangbin01@caas.cn) (B. Zhang).

<sup>1</sup> These authors contributed equally to this work.

and fertility in contrast to natural condition (Knops and Tilman, 2000). However, it is still unclear whether and how agricultural practices as restoration techniques *per se* can accelerate soil development.

Soil microorganisms, including soil fauna and flora, play critical roles in soil formation. They drive the essential processes of mineral weathering (Chorover et al., 2007), the formation of soil structure (Feeney et al., 2006; Rillig and Mummey, 2006), organic matter decomposition and nutrient cycling (Paul and Clark, 1989; Schimel, 1995). Soil fauna such as soil nematodes have very close functional and trophic interactions with soil microbial flora, occupying a central position in the soil food web (Yeates et al., 1993; Wardle, 1995). Based on the trophic interactions, soil nematodes are designated as plant-parasites (PP), bacterivores (Ba), fungivores (Fu), and predators-omnivores (Po) (Bongers, 1990; Yeates et al., 1993). Such trophic relations play a central role in delivering soil functions such as decomposition of plant litter and nutrient cycling (Zak et al., 1994; Aneja et al., 2006). However, many studies have only used soil microbial community structure as indicators to assess the effects of land use and soil managements at the same soil development stage (Lenz and Eisenbeis, 2000; Marschner et al., 2003; Zhong and Cai, 2007; Goldfarb et al., 2012). Only recently, soil nematodes and soil microbial communities have been examined together as parts of food web in well-developed soils (Neher, 2010; Sanchez-Moreno et al., 2011; Zhang et al., 2015a,b). Moreover, some pioneering studies demonstrated that soil microbial community structure can recover quickly under the same land use (Deng et al., 2010) or cropping system (Li et al., 2014) for the soils developed from their parent materials. This similarity indicates an inherent microbial resilience, commonly defined as the capacity to recover to a 'normal' status from a disturbed situation (Taylor et al., 2010; Griffiths and Philippot, 2013). It is unclear whether soil nematodes and the soil food web develop and show biological resilience as the soil microbial communities did at the initial stage of soil development. Measurement of soil nematode and microbial communities together can improve our understanding of the development of soil food web and indicate the development status of restored ecosystems in relation to targets and the effectiveness of management intervention (Harris, 2009).

Agricultural practices impact the food web consisting of nematodes and microbes due to different inputs of plant litter quality and quantity (Ferris and Matute, 2003; Ferris et al., 2004; Sánchez-Moreno et al., 2006; Briar et al., 2011), and to changed soil chemical and physical properties under different organic and mineral fertilizations (Li et al., 2010) and soil tillage (Treonis et al., 2010). Plant diversity and plant roots have particular influences on the abundance of plant parasites and rhizosphere microbes (Stirling et al., 2005; Pan et al., 2012). Chemical fertilizers can influence both nematode and microbes due to the secondary effects of the management practice on soil pH (Fiscus and Neher, 2002). Organic amendments can significantly enhance microbial activity and nematode abundance, especially some fast growth r-strategy related bacteria and bacterivores (Ferris et al., 2004, 2010; Brant et al., 2006; Briar et al., 2007; Treonis et al., 2010). The effect of tillage is associated with reduced fungal biomass (Beare et al., 1997; Frey et al., 1999; Simmons and Coleman, 2008) and then the slow growth k-strategy fungal-feeding nematodes (Beare et al., 1992; Treonis et al., 2010). However, most of the knowledge is gained in the context of well-developed soils. We were unable to locate reports about the effects of agricultural practices on development of the interactions between soil nematode and microbial communities at the initial stages of soil development.

In previous studies, we have demonstrated that after 8-yr restoration from the parent material of a Mollisol under different land uses and agricultural practices, soil microbial community

structure was separated in contrasting directions between not-tilled perennial and tilled cropping (Li et al., 2014) and to a larger extent by aggregate size than by agricultural practices (Li et al., 2015). In this study, we aimed: (1) to determine the effects of agricultural practices on soil food web structure in comparison to the structures of soil nematode guilds and microbial communities, *per se*; (2) to elucidate the development of the food web of the young soils in relation to parent materials and a mature surface Mollisol; and (3) to identify the controlling factors of such relationships. We hypothesized that agricultural practices will facilitate the development of the food web consisting of soil nematodes and microbes and the effects of agricultural practices on the food web structure may differ from that on the shift of microbial community structure. Such knowledge may identify factors that allow accelerated restoration and development of critical soil functions that are governed by soil food web.

## 2. Materials and methods

### 2.1. Study site and experimental design

The field experiment was established at the State Key Experimental Station of Agroecology, Chinese Academy of Sciences, Hailun, Heilongjiang Province (47°26'N, 126°38'E) in June 2004 to determine how soil ecosystem and soil functions develop under different agricultural practices. The experimental site is located in the centre region of the Mature Mollisol in Northeast China. The region has a typical temperate continental monsoon climate, with the mean annual temperature of 2.2 °C, the highest monthly temperature (35 °C) in July and lowest in January (−38 °C). The mean annual precipitation is 550 mm, with 65% occurring from June to August. The soils are classified as Pachic Haploborolls according to the USDA Taxonomy (Soil Survey Staff, 2010). The parent materials are clay loess-like materials (Xiong and Li, 1987), containing 42% clay and 35.6% silt and with dominant clay minerals of vermiculate, chlorite and illite.

The basic information of the field experiment was given in Li et al. (2014, 2015). Briefly, parent materials were taken from C horizon (>2 m) from an adjacent field to replace the surface soil down to 0.8 m depth in the field plots of six treatments layout randomly with four replicates. The refilled layer was separated using nylon nets with <75 µm mesh from the below soil. The treatments were natural fallow (NatF) which was dominated with *Poa annua* L., *Equisetum arvense* L. and *Spodiopogon sibiricus* Trin; leguminous alfalfa (*Medicago sativa* L.) (Alfa) and the annual rotation systems between soya bean (*Glycine max* (Merrill.) L.) and maize (*Zea mays* L.) without chemical fertilization (F0) or with chemical fertilization (F1), without the above-ground biomass incorporated (C0) or with the above-ground biomass partially incorporated (C1) or totally incorporated (C2) into soil. The amounts of mineral fertilization and organic C input are presented in Table 1.

### 2.2. Soil sampling and analysis

Soil samples were collected from the surface soil (0–0.20 m) in three replicate plots before sowing in May, 2012. Another plot remained intact for other observations. Parent material collected from C horizon (>2 m deep) and a surface mature Mollisol taken from adjacent fields were used as references. The mature Mollisol was cropped under the same cropping system, with application of mineral N and P fertilizers only and above-ground biomass removed from the field. The soils samples were used for measurement of soil physical, chemical properties and soil microbial communities expressed with phospholipid fatty acids (PLFAs) (Li

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