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Influences of different tillage and residue management systems on soil nematode community composition and diversity in the tropics

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ABSTRACT

Soil nematode and microbial community composition in different tillage and residue systems were investigated in a 12-year old field experiment in Hainan Island. The experiment was based on a split-plot design with tillage system (conventional tillage, conv. till; reduced tillage, reduced till; no-tillage, no till) as main plots and residue management (0% residue input, 0% res.; 50% residue input, 50% res.; 100% residue input, 100% res.) as subplots. Soil samples were taken at depth of 0–40 cm in 2015–2016. A total of 56 nematode genera with relative abundance over 0.1% were identified. *Rotylenchulus* and *Meloidogyne* in 0% res. conv. till were the dominant genera. In comparison with conv. till, reduced till and no till increased the number of protozoa, bacterivores and omnivore–carnivores. In case of microflora, similar patterns were observed with greater abundance of bacteria and arbuscular mycorrhizal fungi in reduced till and no till than in conv. till. The residue addition soils favored bacterivores, fungivores and high colonizer-persister (c-p) value omnivores and carnivores, but less plant parasites. Soil food web in 50% res. no till, 100% res. reduced till and 100% res. no till treatments were highly structured, mature and moderately enriched as indicated by Structure (SI), Maturity (MI) and Enrichment (EI) indices, respectively. Higher number of bacterivores and lower values of Channel index (CI) suggested bacterial-dominated decomposition in no-tillage soil. Nematode community analysis indicated that no-tillage with residue addition increased nematode abundance and their functional metabolic footprint, and favored a more diverse residue resource entry into soil food webs.

1. Introduction

Nematodes are one of the most abundant groups of soil invertebrates. More than four out of five metazoan individuals on earth are nematodes, often reaching several millions per square meter (Li et al., 2016). Although the contribution of soil nematodes to total soil respiration is very low, soil nematodes are believed to have profound effects on soil processes through their influence on the composition and activity of soil microflora (Scharroba et al., 2016). Several microcosm studies have shown that the presence of soil animals (e.g. protozoa, collembolans and nematodes) can directly affect the biomass and activity of the microbial community through feeding on fungi and bacteria (Grabau and Chen, 2016). Soil nematodes are significant regulators of residue decomposition and nutrient release in natural ecosystems through their high turnover rates and their interactions with microflora (Lu et al., 2016). Based on model calculations, approximately 35–45% of the annual C and N mineralization in agricultural soil was due to the contribution of bacterivores and fungivores (Zhang et al., 2013).

The Hainan Island of China has been intensively cropped for centuries. Problems related to soil erosion from declining soil fertility threaten the sustainability of agriculture throughout this agroecological zone (Zhong et al., 2015). It is well documented that many agronomic practices such as stubble retention and tillage exert a great influence on important soil quality attributes such as soil structure, organic matter content and moisture retention capacity of soils (Golabi et al., 2014). At the same time, there is accumulating evidence suggesting that the abundance and composition of different trophic groups of nematodes are affected by these agronomic practices. For example, Löbmann et al. (2016) demonstrated that the abundance and population levels of

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fungivores and omnivores-predators were significantly higher in unploughed perennial apple orchard than in ploughed annual cropping of rape. Forge et al. (2015) showed that in comparison with conventional tillage, no-tillage or minimum tillage significantly decreased *Pratylenchus neglectus* population. Soil nematode community structures and functions were also influenced by the application of residues. Coudrain et al. (2016) reported that bacterivores were 40–50% lower in the zero residue input treatment than the high input or low input treatments. Therefore, abundance and population structure of nematodes were considered potential bio-indicators of soil quality (Sithole et al., 2016). However, more information is needed, particularly over a range of cropping systems and environments, to demonstrate the effects of tillage and stubble practices on the abundance and diversity of nematodes in cultivated soils.

In this paper, we report results of an investigation into the effects of different tillage/residue management on the abundance and diversity of nematodes in a long-term experiment that commenced in 2003. The objectives of this preliminary investigation were to determine the interactive effect of tillage and residue management on soil nematode community composition.

2. Materials and methods

2.1. Site descriptions

The experiment was carried out on Wanzhong Farm in the city of Ledong (18° 36′ –18° 38′ N, 108° 47′ –108° 49′ E), Hainan Province, China. The region has a tropical monsoon climate with a mean annual temperature of 25.8 °C and a mean annual precipitation of 2065 mm. The test soil was classified as sandy loam according to the USDA texture classification system with 13.6% clay, 23.3% silt and 63.1% sand. The soil has initial properties of 7.12 g kg^{-1} total organic C, 0.76 g kg^{-1} total N, 0.59 g kg^{-1} total P, 1.21 g kg^{-1}, total K and pH 6.53. The rotation of banana (*Musa acuminata*) and passion fruit (*Passiflora edulis*) was chosen for the experiment.

The experiment was a split-plot design with four replicates, initiated in 2003 with tillage management as the main plot and residue system as the sub-plot. The field experiment was divided into nine plots and the size of each individual plot was 170 m^2. Tillage systems included a no-tillage (no till), a reduced tillage (reduced till) and a conventional tillage (conv. till) treatment. The soil was stubble cultivated with a tine cultivator to 15 cm in the reduced till plots and mouldboard ploughed to a depth of 30 cm in the conv. till plots. Both reduced till and conv. till plots were ploughed once a year at the end of May and the crops of all treatments were re-sown at the end of June. Chopped banana or passion fruit residues were incorporated into soil in the conv. till plots and covered the soil surface in the reduced till and no till plots after crops harvest in the middle of May. Three residue treatments were 0% res. (0%, no residues incorporation or coverage), 50% res. (50%, 7.5 t ha^{-1} residues incorporation or coverage). and 100% res. (100%, 15 t ha^{-1} residues incorporation or coverage). The chemical N fertilizer (urea), P fertilizer (superphosphate) and K fertilizer (sulphate) were applied at the rates of 129 kg N ha^{-1}, 68 kg P ha^{-1} and 292 kg K ha^{-1} to a depth of 0–30 cm after transplanting every year. The manure used was cow manure compost (14.4 t ha^{-1}), with 53.3% water content, containing 145 g C kg^{-1}, 3.2 g N kg^{-1}, 2.5 g P_2O_5 kg^{-1}, 1.6 g K_2O kg^{-1} on a dry weight basis, which was basally applied before transplanting (June 25th) to a depth of 0–30 cm every year. Lime was used (125 kg ha^{-1}) together with cow manure compost to increase soil pH.

2.2. Soil sampling

All soil samples were collected at the same time in the last growing season (2015–2016). After the removal of above-ground plant debris, soil samples were collected using a soil corer (3.0 cm diameter) at a depth of 0–40 cm below the soil surface at the seedling stage (September 16, 2015), jointing stage (December 10, 2015), booting stage (March 7, 2016) and ripening stage (May 19, 2016) within the plant rows of banana plants, 50 cm from the base of the banana plant. For each sample, five random cores were combined to form one composite sample. The fresh soil samples were stored in individual plastic bags and then immediately stored in a 4 °C cold room.

A subsample of 100 g soil (fresh weight) was used for nematode extraction. Subsamples were first elutriated and sieved (mesh size 250 and 38 μm) with water. Nematodes from the suspensions were then extracted using a modified cotton-wool filter method (Zhong et al., 2015). The abundance of nematodes was expressed per 100 g dry weight soil. Nematodes were counted using a dissecting microscope and identified using an inverted compound microscope. An average of 150 nematodes (100 nematodes at minimum) per sample were identified at 400 × to 1000 × to genus or family level within one week of extraction or fixed in 4% formalin until identification. Following identification, the length (μm) and width of each specimen were determined using an ocular micrometer. Nematodes were classified into the following trophic groups (Bongers, 1988): bacterivores (BF), fungivores (FF), plant parasites (PP) and omnivores-predators (OP).

Phospholipid fatty acids (PLFA) were used as indicators of total, bacterial, fungal and actinomycete biomass in the soil. Lipids were extracted from 8 g of freeze-dried soil using a chloroform–methanol–citrate buffer mixture (1:2:0.8). The polar lipids were separated from neutral lipids and glycolipids on a solid phase extraction columns (Supelco Inc., Bellefonte, PA). The phospholipids were *trans*-esterified to a mild-alkali methanolysis and the resulting fatty acid methyl esters were extracted in hexane and dried under N_2. Samples were then dissolved in hexane and analyzed in an Agilent 6850 series Gas Chromatograph with MIDI peak identification software (Version 4.5; MIDI Inc., Newark, DE). The following biomarkers were used: total PLFAs (TP, sum of all identified PLFAs; from C14 to C20); bacterial PLFA (BP, *iso* 15:0, *anteiso* 15:0, 15:0, *iso* 16:0, 16:1ω5c, i*so* 17:0, *anteiso* 17:0, 17:0cy, 17:0 and 19:0cy); fungal PLFA (FP, 18:2ω, 6 and 9c); actinomycete PLFA (AP, 10Me16:0, 10Me17:0, and 10Me18:0); gram-negative bacteria (16:1v7c, cy17:0, 16:1v9c, 17:1v8c, 18:1v7c, cy19:0, 16:1 2OH); gram-positive bacteria (i14:0, i15:1, i15:0, a15:0, i16:0, i17:0, a17:0); saprophytic fungi (SF, 18:1v9c and 18:2v6c); arbuscular mycorrhizal fungi (AMF, 16:1v5c) (Guckert et al., 1985).

The most-probable-number method was used to determine flagellate populations (Rodriguez-Zaragoza et al., 2005). The assays were performed in 24-well cell culture plates and the growth medium in each well was 0.9 ml autoclaved and filtered soil extract (1:5, soil:water). The first well of each dilution series was inoculated with a 0.1 ml aliquot of 1:10 soil suspension shaken in a vortex for five 15-s pulses. Four replicates 10-fold dilutions to 10^{-7} were prepared for each soil sample. The plates were incubated at 28 °C for 7–10 days and reviewed with an inverted microscope for the presence of flagellates. Abundance of flagellates was expressed as the number of individuals or taxa per 100 g of dry soil.

2.3. Statistical analysis

Nematode ecological indices were analyzed by the following approaches: Maturity index (MI) was calculated as $\sum P(i) \cdot C(i)$, where C(i) is the colonizer-persister (c-p) rating of taxon i