Long-term tillage effects on bacterial biomass and community structure distribution within water stable aggregates

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Abstract

This study addresses the tillage effect on the distribution of bacterial biomass and their community structure in a subtropical purple rice soil ecosystem. Similar distribution patterns of soil bacterial biomass within water-stable aggregates (WSA) were observed under different tillage managements. Although the distribution pattern of soil microbial biomass was not changed by tillage practice, soil microbial biomass increased significantly in all size fractions of WSA under combined ridge with no-till (RNT) treatment. While tillage management did not change the distribution patterns of soil microbial biomass, it did change their community structure. Results indicated that the distribution pattern of microbial biomass in WSA was governed by aggregate size, whereas bacterial community structure was significantly affected by tillage management.

Key Words

Soil structure, no-tillage, microbial community.

Introduction

Agricultural land management is one of the most significant anthropogenic activities that greatly alter soil characteristics, including physical, chemical, and biological properties and processes. Thus, while agriculture is expected to affect the diversity and structure of soil microbial communities, the specific responses of various bacterial groups to the changing environment in agricultural soils are not well understood (Buckley and Schmidt 2001). The aim of the present study was to evaluate how soil bacterial biomass and their diversity varies with soil aggregation under different tillage management in a sub-tropical purple rice soil.

Material and methods

Experimental site

The Sichuan Basin is located in southwestern China (latitude 28-32° N, longitude 103-108° E) with an annual mean temperature of 14-19 °C, and rainfall of 1000-1400 mm. Field experiment has been carried out at Southwest University since 1990. The soil was Gleyi-stagnic Anthrosols. Crops: Rape (*Brassica napus L.*) in winter and rice (*Oryza sativa* L.) in summer.

Tillage treatments and soil sample

Combines Ridge with no-tillage (RNT): No-till treatment was imposed on the soil that was ridge tilled before the experiment, and the ridges were kept intact from 1989. Crops: Rice + Rape rotation in a year. Conventional Tillage (CT): Rice + Rape rotation in a year. Flooded Paddy Field (FPF)**:** Rice was planted in a flooded field in summer and land remains fallow in winter. Water was kept flooded in the field all year. Surface soil samples (0-15 cm) were collected in April, 2008. Samples were stored at 4°C for analysis. Fractionation of soil aggregates was achieved using a wet-sieving procedure (Elliott and Cambardella 1991; Cambardella and Elliott 1994).

Microbial biomass assay

Soil bacterial biomass content was calculated from muramic acid content according to Appuhn *et al.* (2004). A direct and an indirect method were used (Tsaiand Olsen, 1991) followed by purification steps (Smalla*et al.* 1993) with slight modifications. The 16S rRNA genes from soil microbial communities were amplified by PCR by using the primer pair F984CC/R1378 described by Heuer *et al.* (1999).

Data analysis

All analyses were carried out on the four replicates. Data (measured or calculated) were subjected to ANOVA.

Result

Distribution pattern of bacterial biomass within soil WSA under different tillage managements

The distribution pattern of bacterial biomass under CT, RNT, and FPF had a similar trend. Except for the macro-aggregates bigger than 4.76mm, in which bacterial biomass under CT was significantly higher than for RNT and FPF.

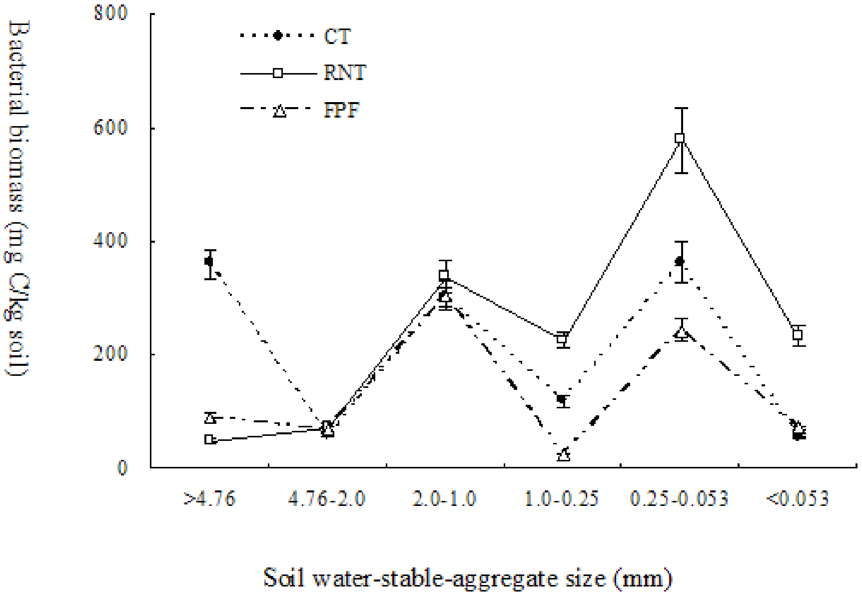

Figure 1. Distribution of bacterial biomass within soil aggregates under different tillage managements. Error bars represent standard error.

Bacterial DNA fingerprint within soil WSA under different tillage managements

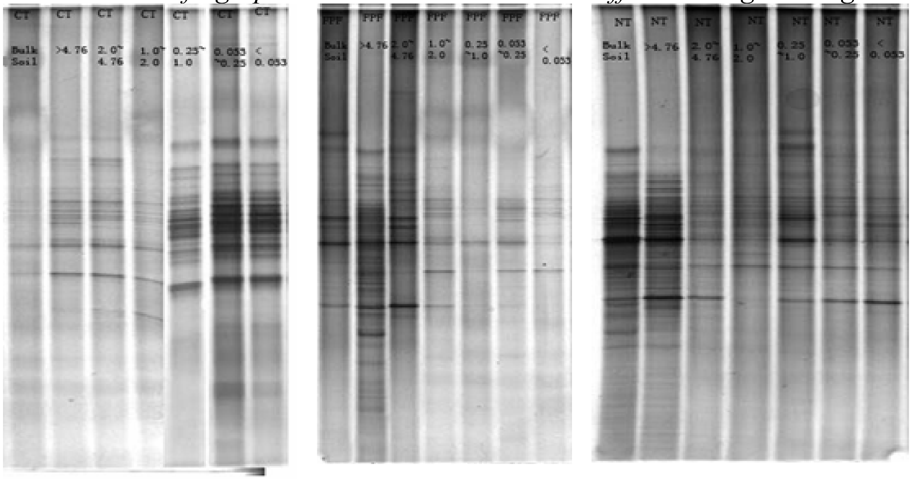

Figure 2. Distribution of bacterial DGGE banding patterns within soil aggregates under different tillage managements (CT, conventional tillage; RNT, combines ridge with no tillage; PFP, flooded paddy field).

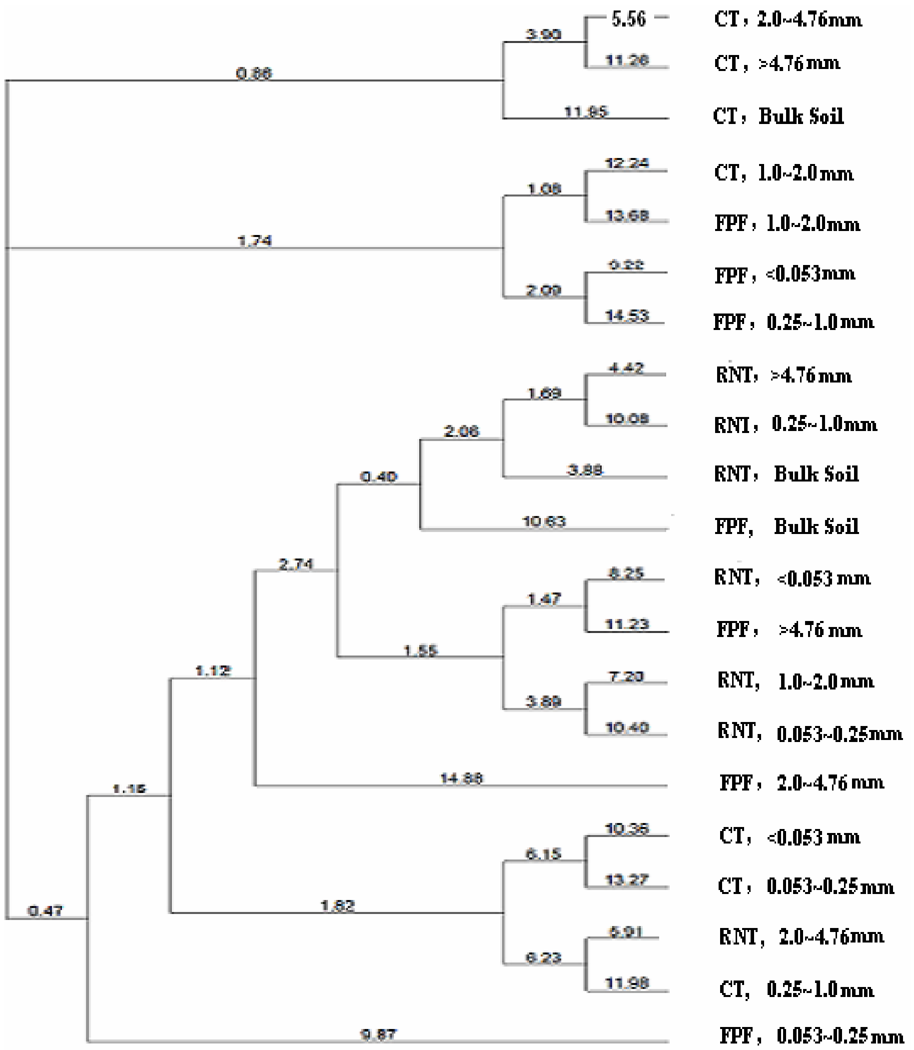

Figure 3.Cluster analysis of bacterial structure using 16S rDNA-DGGE within soil aggregates under different tillage managements (CT, conventional tillage; RNT, combines ridge with no tillage; PFP, flooded paddy field).

Discussion

It was found that the trend of soil total microbial biomass distribution in WSA size fractions were similar under all of the three tillage treatments. All three had their lowest contents in the <0.053 mm (silt + clay) fraction, while their peak concentrations were expressed in the 0.25-0.053 mm WSA size. The soil microbial biomass changes can sensitively reflect the difference of land use and management. This paper firstly points out that in the sub-tropical purple paddy soil, the distribution mode of microbial biomass had no significant differences between tillage managements which had synchronized and similar distributing properties, and it indicated that the forms of tillage had no significant effects on the distribution of bacterial biomass in aggregates. The diversity of soil bacteria is important for sustainable agriculture because different species of bacteria perform diverse ecological services in agricultural systems. In the present study, bacterial profiles strictly linked together at a lower linkage distance under the same tillage management compared to other managements. Results indicate that bacterial community structure was significantly affected by tillage management.

Conclusions

1. The distribution pattern of soil bacterial biomass was governed by aggregate size, whereas the tillage effect was not significant;
2. Bacterial community structure was significantly affected by tillage management.

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