



Inconsistent Changes in Microbial Community Structure and Abundance with Biochar Amendment in Rice Paddy Soils from South China

J. Chen, J. Qu, X. Liu, J. Zheng, L. Li, and G. Pan

Institute of Resource, Ecosystem and Environment of Agriculture, Nanjing Agricultural University, Nanjing 210095, China
(junhui5@126.com)

Abstract: Effects of biochar amendment on soil microbiota had not yet been well understood. We conducted a cross site field study on biochar amendment to rice paddies from south China in 2010. The experiment was performed with four treatments including N fertilization only (CON), N fertilization plus biochar at 20t/ha (C1N) and at 40t/ha (C2N) as well as a control without N fertilization and biochar (CON0) consistently with three sites. Biochar was spread at soil surface and incorporated into soil and thoroughly mixed to depth of about 12cm before padding for rice seedling transplantation. Rice production was conducted with conventional water and nutrient management practices adapting to local climate and cultivar conditions. Topsoil samples were collected from each treatment plot across sites for chemical properties and molecular analysis after rice harvest in autumn of 2010. Contents of organic carbon, total N as well as soil microbial biomass carbon were determined with recommended methods. Quantitative real-time PCR coupled with 16S rRNA gene and 18S rRNA gene denaturing gradient gel electrophoresis (DGGE) were respectively employed to trace changes in abundance and structure of bacteria and fungi community with biochar amendment. Increase in microbial biomass carbon (SMBC) was not observed in one site but by 10-20% in other two sites while SOC contents were increased by 25-45% in all sites under biochar treatments. Copy numbers of bacterial genes were different between the sites but no changes with biochar treatment in a single site. However, cluster analysis revealed a more or less decreased similarity of bacterial community to the control (ranging from 75% to 85%) by biochar treatment in a single site. Nevertheless, a number of special bands appeared both in bacterial and fungal DGGE patterns under biochar treatments, though varying with site also. While the fungi copy numbers markedly varied both with sites and with biochar treatments, lower similarity and greater number of special bands than bacterial were found in fungal DGGE patterns. This may indicate a higher sensitivity of fungi in rice paddies to biochar, a high stable carbon source. This study suggests a long term monitoring protocol for assessing the potential biological risk of biochar amendment in rice paddy soils from China.

Keywords: Biochar, microbial biomass carbon, microbial community structure, DGGE, Quantitative real-time PCR, rice paddy soils