Biochar influences the succession of microbial communities and the metabolic functions during rice straw composting with pig manure

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Biochar influences the succession of microbial communities and the metabolic functions during rice straw composting with pig manure

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Abstract

The present study determined the dynamic changes of bacterial community structures and its metabolism functions in rice straw composting process with different types of biochar addition. Results showed that both wheat and maize straw biochar addition greatly increased the temperatures and germination index. Biochar addition influenced microbial community structure and metabolic characteristics of the compost. *Firmicutes*, *Actinobacteria* and *Proteobacteria* were the dominant phyla throughout the process, and both biochar addition significantly increased the relative abundance of *Actinobacteria* phylum, especially genus *Saccharomonospora*. The abundance of bacterial genes related to amino acid metabolism, carbohydrate metabolism and energy metabolism were also increased with biochar addition. Moreover, total nitrogen was strongly affected by biochar addition and had the greatest influence on the bacterial community structure. These results indicated that biochar addition improved the maturity and fertility of the compost product as well as significantly regulated the microbial community structure and functions during composting process.

Key words: Pig manure; Bacterial community; Metabolism function; Composting

1. Introduction

The annual production of rice straw in China is reported to be approximately 0.12 billion tonnes (Liu et al., 2008). Rice straw can be used in industrial processing or directly return to fields (Mustafa et al., 2017). However, a large proportion of rice straw is conducted through burning in field in Asian countries. This unreasonable disposal practice leads to a series of environmental