

Microbial Diversity and Bioactive Substances in Disease Suppressive Composts from India

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Abstract

© 2016 Taylor and Francis Group, LLC. The present study aimed to investigate microbial communities in seven Indian composts and their potential for biocontrol of *Fusarium oxysporum* f. sp. *lycopersici*. In addition, identification of bioactive substances in disease suppressive composts was also attempted. Composts were chosen based on disease suppressiveness and subjected to molecular microbial analyses. Total genomic DNA from the composts was extracted and amplified with polymerase chain reaction using primers targeting the 18S rRNA and 16S rRNA genes of fungi and bacteria, respectively. Denaturing gradient gel electrophoresis (DGGE) fingerprinting and DNA sequencing were used to identify the fungal and bacterial targets. Phylogenetic analysis of the fungal 18S rRNA ITS gene sequences showed that phylum Ascomycota was dominant in all composts, while in the bacterial 16S rRNA gene sequences, the phylum Proteobacteria was dominant. Some fungi in disease suppressive composts grouped phylogenetically close to *F. oxysporum*. Bacterial sequences with close similarity (>95% identity) with *Actinobacterium* showed a strong presence only in disease suppressive composts. Disease suppressive composts formed a separate group in the cluster analysis of 18S rRNA ITS and 16S rRNA gene sequences. Gas chromatography-time of flight-mass spectrometry was performed with compost extracts to determine if bioactive substances were present in disease suppressive composts. The analysis of compost organic matter showed a negative association of disease suppressiveness with phloroglucinol, sitosterol, and monoenoic fatty acid, while cholesterol and certain organic acids were positively associated with suppressiveness.

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