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"Resilience of agricultural systems against crises"

## Organic Management Practices Enhance AM Biodiversity in Tropical Agricultural Soils

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## Abstract

Arbuscular mycorrhizal fungi (AMF) have been recognised as an important component of organic agriculture. Modern agricultural practices, such as chemical fertilisation, pest control, continuous monoculture and tillage impact AMF and plant interactions. To study the impact of these practices, investigation was undertaken to compare the AMF diversity in trap cultures raised on conventially managed as well as on organically managed fields. Spores of AMF were collected from trap cultures of both fields (northern India) and based on their morphology were grouped into morphotypes. Partial sequence analysis of rDNA from single spore of each morphotype was undertaken using either a small-subunit internal transcribed spacer (SSU-ITS) or a large subunit (LSU) region and fatty acid methyl ester profiles (FAME) of similar morphotypes were compared.

Organic managed sites contributed 18 AM species belonging to genera *Rhizophagus* and *Funneliformis* and 7 AM fungi of *Acaulospora*, *Gigaspora* and *Scutellospora*. In contrast, conventional managed sites selectively favour only smaller size AM species belonging to genera *Rhizophagus* and *Funneliformis* species. We observed that organically managed farmland showed the largest AMF species richness and colonisation potential, which suggests that factors contributing to the diversity of AMF are indeed complex: for example, chemically managed farmland not only causes loss of fungal biodiversity but also selectively favours smaller spores (*Rhizophagus* sp.), thereby affecting ecosystem functioning adversely. The present study showed that both abundance and diversity of AMF is favoured by low-input agriculture incorporating planting on raised beds (RB) and organic practices such as zero tillage that do not disturb the physical properties of the soil.

**Keywords:** Arbuscular mycorrhizal fungi, fatty acid methyl ester profiles, large subunit, raised beds, Ribosomal DNA

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