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Host functionality as a driver in the modularisation of fungi-roots association

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Abstract

Tropical rainforests are the most diverse biome on our planet, composed of a mosaic of micro-habitats highly associated with a heterogeneous distribution of organisms. This includes the rhizosphere as a host for thousands of biological organisms, such as plant-associated microbial communities. The plant-microbiome interaction modulates plant health through the recruitment of specific microbial communities that act as suppressing antagonists (such as predators, and parasites) and inhibit pathogenic activities. Host-fungi associations are likely to be modulated by plant functional groups, instead of reflecting individual species interactions. Host characteristics have proved to be deciding factors for the selective distribution and composition of the fungal community, and therefore, decisive in the structuring of co-occurrence networks. Our main interest lies in non-random associations between root-associated fungi and host plants. We hypothesise that network compartmentalisation of rhizosphere fungal community composition and plant species host community will be explained by host functionality. We employed amplicon sequences of roots and fungal communities from 31 samples obtained from five soil cores (15 cm depth, 4 cm diameter) extracted from 5 × 5 m subplots evenly sampled within the established research plots (50 × 50 m) located in four land-use types (lowland rainforests, jungle rubber, rubber, and oil palm plantations) in Jambi, Indonesia. Our preliminary results based on the reconstructed modules uncovered an association between specific plant functional groups and particular fungal guilds, i.e. herbaceous or shrub alien taxa (*Clidemia*, *Asystasia*, and *Centotheca*) grouped together with the monoculture crop *Elaeis guineensis* and appear to be correlated with pathotrophic fungi. *Hevea brasiliensis* clustered together with another cash crop *Dioscorea persimilis* and other species such as *Uvaria leichhardtii* and *Spatholobus pulcher* and showed only a few associations with AM and saprotroph fungi. Root traits such as specific root length and root diameter, together with the phylogenetic distance of host species are expected to explain non-random associations between roots-fungi.

Keywords: Co-occurrence network, fungi, Indonesia, roots

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