

GUEST EDITORIAL

FUNGAL DIVERSITY: A FOCUS ON ECTOMYCORRHIZAL FUNGI IN TROPICAL FORESTS

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Belowground biological interactions that occur among plant roots, animals and microorganisms are dynamic and substantially influence ecosystem processes. Among belowground biota are the fungi, which are diverse and play a wide range of functions in forest ecosystem processes. In the forest, we can distinguish three main functional groups of fungi according to their carbon acquisition, namely, saprotrophic, pathogenic and symbiotic fungi.

Mycorrhizas are symbiotic fungi and are commonly divided into ectomycorrhizal (ascomycetes such as *Tuber* sp. and basidiomycetes such as *Russula* spp.) and arbuscular fungi (zygomycetes such as *Glomus* spp.). The two main groups are differentiated by the fact that the hyphae of ectomycorrhizal fungi do not penetrate individual cells within the root, while the hyphae of arbuscular fungi penetrate the cell wall and invaginate the cell membrane.

In tropical forests, little is known about the diversity of ectomycorrhizal fungi and their associated host trees. In tropical Africa, ectomycorrhizal trees include Caesalpinioideae, Phyllanthaceae as well as some Dipterocarpaceae, Proteaceae and Sapotaceae. South-East Asian dipterocarp forests, *Nothofagus*-dominated rainforests of Papua New Guinea and Caesalpinioideae rainforests in Guyana and Africa are some notable examples of tropical ecosystems dominated by ectomycorrhizal tree species. In all tropical forests, some ectomycorrhizal tree species tend to aggregate in patches. In the Korup National Park (Cameroon), ectomycorrhizal trees form up to 70% of local patches. Similarly, the ectomycorrhizal tree *Gilbertiodendron dewevrei* represents more than 90% of trees in some stands of the Congo basin. The paleotropical rainforests of South-East Asia are among the most diverse plant communities in the world and are characterised by high abundance of trees in the family Dipterocarpaceae. The

Dipterocarpaceae are known to form associations with ectomycorrhizal fungi, a relationship that likely has ancient Gondwanan origins. It appears that ectomycorrhizal symbiosis can contribute to the success of these monodominant trees. With regard to the diversity of ectomycorrhizal fungi, multiple species are frequently detected (i.e. Russulaceae, Cortinariaceae, Inocybaceae and Thelephoraceae) and these species are mainly associated to different host trees (i.e. *Afzelia africana* and *Uapaca guineensis* in southern Senegal). There is also evidence that common mycorrhizal networks built by ectomycorrhizal fungi between trees may maintain the monodominance of tree species in tropical forests. However, this should be proven as a fact because tropical ectomycorrhizal communities remain poorly characterised relative to temperate counterparts. In this respect, many different methodologies can be applied to tropical forest ecosystems to fill this gap of knowledge.

Traditional mycological identification methods and PCR-based techniques can be used both for taxonomic characterisation and classification. The amplification of the internal transcribed spacer (ITS) region of the ribosomal genes is the most common approach. The generated sequences can be deposited on the molecular database UNITE. These sequences can be used as reference when ectomycorrhizal diversity is assessed by studying ectomycorrhizal root tips or soil extracts. Recently, PlutoF, a web-based workbench for managing data in the UNITE database (<http://unite.ut.ee/workbench.php>) was created to help fungal ecologists in managing their research data starting from planning and fieldwork to analysing molecular data. The morphological and anatomical description of ectomycorrhizal root tips, the traditional description of fruiting bodies and of the habitat, the name of the host tree, the location of the sampling site, and also pictures of both fruiting

bodies and root tips can also be linked to the ITS sequence. So, all selected species have full description and this database will be a compilation of data useful for meta-analysis to draw traits of tropical ectomycorrhizal fungi. For instance, (1) are tropical forest trees dominated by two or three species as in boreal and tropical ecosystems? (2) can one ectomycorrhizal fungal species similar to *Rhizopogon* sp. under Douglas-fir in temperate forest link tropical trees via a common mycorrhizal network?

This fungal database will be very useful for studying ectomycorrhizal fungal diversity by meta-genomics using random shotgun sequencing (pyrosequencing or 454 technology) of DNA extracted from the soil. This rapid and relatively inexpensive sequencing technology used in boreal and temperate ecosystems since a few years ago is now applied to tropical ecosystems. This methodology is a good way of

reducing the gap in knowledge between tropical and temperate–boreal forest ecosystems, and also for comparing tropical and boreal–temperate ecosystems at species, genus or taxa level. The advent of new high-throughput DNA-sequencing technologies will redefine our views on the composition and the place of ectomycorrhizal fungal communities in forest ecosystems.

As a conclusion, methodology applied in boreal and forest ecosystems can be applied to the study of tropical forests. Moreover, the increasing number of collaborations and exchanges allow the description of this fantastic diversity hidden in the under-ground of tropical ecosystem.

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