Diversity of cultivable mycorrhizal fungi in temperate orchid species: variation in their phylogeny and functional traits

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Résumé

All orchid species rely on orchid mycorrhizal fungi (OMF) for seed germination, seedling growth and nutrition supplies at plant maturity stage. Although most orchids are associated with several OMF simultaneously, mycorrhizal specificity varies among orchid species due to host preference, but can be also influenced by environmental conditions. In photosynthetic orchids, OMF belong mostly to the polyphyletic rhizoctonian group, which besides forming orchid mycorrhizae can live as saprotrophs in the soil. However, their ability to utilize different nutrient sources is not yet well studied, and the isolation and identification of OMF remain challenging as many fungi cannot be cultivated. In the first study, we tested the efficiency of both culture-dependent (cultivation of isolates) and culture-independent methods (next-generation sequencing of colonized roots) to assess the root-associated fungal communities and any phylogenetic patterns of cultivability across multiple temperate orchids from Southern France and the Czech Republic. Additionally in the second study, we selected nine isolates representing the key rhizoctonian families (Ceratobasidiaceae, Tulasnellaceae and Serendipitaceae) and tested their ability to utilize carbon (C), nitrogen (N) and phosphorus (P) sources *in vitro* in both liquid and solid media. We found that the culture-independent method revealed greater fungal diversity than the culture-dependent one, but despite the lower detection, the isolated fungal strains were in majority the most abundant OMF in adult roots. The orchid host had a greater impact than locality (habitat conditions) on the variability in fungal communities. The nine isolates showed significant inter- and intra-familiar variability in nutrient utilization, most notably in N sources. The largest amount of biomass was produced by Ceratobasidiaceae isolates on most sources in both medium types. Interestingly, we detected a phylogenetic pattern in both studies for Tulasnellaceae family, as strains from a clade (A) with *Tulasnella helicospora* grew more slowly, produced a lower amount of biomass, and utilized a narrower spectrum of nutrients compared to isolates from clade (B) with *T. calospora* and *T. irregularis*. Simultaneously, other strains of the clade (A) failed in cultivation, though they were dominant in orchid hosts. Our results suggest the importance of combining different methods to learn more about this intimate association and provide useful highlights on factors involved in structuring OMF community across several orchid host species. A better understanding of OMF phylogeny and functional trait is crucial for investigating the aboveground orchid species assemblages.

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Mots-Clés: Orchidaceae, mycorrhizal fungi, Tulasnellaceae, Ceratobasidiaceae, Serendipitaceae, metabarcoding, culture, independent and, dependent methods, nutrient utilization, fungal phylogeny