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## Analysis of mycobiomes to uncover biodiversity: a case study between soil fungi and orchid species in Sweden

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**ABSTRACTS** - Oral Presentations

**Analysis of mycobiomes to uncover biodiversity: a case study between soil fungi and orchid species in Sweden**

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An analytical approach and framework were developed to examine the soil mycobiome associated with orchids in Sweden as a case study and proxy for improved taxonomic placement and understanding of fungal biodiversity. DNA was extracted, amplified, and sequenced using the entire ITS region from soil sampled from eight locations in central Sweden. Sequence data were analyzed using the DADA2 pipeline in order to use the resulting amplicon sequence variants (ASVs) for higher resolution of fungi present in the soil. Initial taxonomic assignments were performed using the UNITE database, and association between fungal order and orchid species was subsequently measured using Chi-square tests. This analysis showed an apparent enrichment of Sebaciales, which are fungi commonly associated with roots of orchids and other plant species. Further taxonomic resolution and insight into trophic behavior of sampled Sebaciales across different host plants was examined using the Tree-Based Alignment Selector (T-BAS) toolkit version 2.1. This analysis was based on a comprehensive Sebaciales phylogeny of the ITS region developed by Oberwinkler and colleagues. Phylogenetic placement showed a clear affinity of putatively sampled *Sebacina* taxa to other Sebaciales reference taxa that represent beneficial endomycorrhizal symbionts of orchids, ectomycorrhizae, and saprobic lifestyles.