

**Erős-Honti, Zs. & Jakucs, E. (2009):
Characterization of beech ectomycorrhizae
formed by species of the Pachyphloeus-
Amylascus lineage. Mycorrhiza 19: 337-345.**

Reference: Erős-Honti, Zs. & Jakucs, E. (2009): Characterization of beech ectomycorrhizae formed by species of the Pachyphloeus-Amylascus lineage. Mycorrhiza 19: 337-345.

Short reference: Erős-Honti & Jakucs (2009)

First author: Erős-Honti Zsolt

Year: 2009

Abstract

Characterization of beech ectomycorrhizae formed by species of the Pachyphloeus-Amylascus lineage
Zsolt Erős-Honti - Erzsébet Jakucs

The hypogeous genus *Pachyphloeus* forms a common phylogenetic lineage with the epigeous *Scabropezia* and the hypogeous *Amylascus*, within the Pezizaceae (Ascomycota). Though the ectomycorrhiza- (EM) forming ability of this group was proposed previously, no detailed description has been published up to now, except for the characterization of EM related to *P. virescens*. During our several-year-long survey on the EM community of a beech forest reserve in Hungary, we found ten EM specimens belonging to the Pachyphloeus-Amylascus lineage. All of them share common morphological and anatomical characters. The densely ramifying whitish-yellow to light-brown mycorrhizal systems are pyramidal with short, stout ends. The EM surface is densely wooly with white or brown, curly hyphae. All mantle layers are pseudoparenchymatous angular, covered by a thick-walled hyphal network. Frequent emanating hyphae are densely septate without clamps. The EM can be sorted into three different morphotypes (Mt) according to their color, specific morphometric traits (cell-wall thickness, diameter of emanating hyphae, septal distance), and certain anatomical characters (structure of the surface net). Molecular identification was accomplished by the phylogenetic analysis of the ITS and LSU regions of the nrDNA, what proved that the sequences clustered into three clades corresponding to the three Mt. With the aid of fruitbody-derived sequences, obtained from GenBank, one of the Mt can be identified as *Pachyphloeus melanoxanthus* and another one as *Pachyphloeus*

citrinus. The third Mt, together with another unidentified EM sequence of the GenBank, forms a distinct branch, which is a sister group to the Pachyphloeus-Scabropezia-Amylascus lineage. In addition to presenting the first detailed anatomical and molecular comparison of the EM related to P. melanoxanthus and P. citrinus, we call the attention to the need for further microscopical investigations amended by molecular taxonomical analyses.

biodiversity: fungus, lichen

habitat: oak-hornbeam forests, beech forests

taxonomy

Notes

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Tartalom:

Introduction

Materials and methods

Sample collection and preparation

Molecular and phylogenetic analyses

Results

Characterization of the ectomycorrhiza of Mt 1 (reference EM specimen: BP 99792)

Differentiating between the three EM morphotypes

Phylogenetic inference

Discussion

Acknowledgements

References

Pezizaceae, Ectomycorrhiza, LSU, ITS, Molecular analysis, Anatomy

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