



**SPHAGNUM MOSSES HOST TAXONOMICALLY AND FUNCTIONALLY DIVERSE FUNGAL COMMUNITIES**

A tőzegmohák rendszertani és funkcionális értelemben gazdag gombaközösségeknek adnak otthont

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Fungi are ubiquitous in most terrestrial habitats and microhabitats, such as soil, decomposing plant parts, and living plant tissues. Mosses are no exception, and recent studies using DNA sequencing have revealed diverse communities in several lineages of bryophytes. In this pilot study, we provide the first characterization fungal communities in *Sphagnum* species in Hungary, based on ITS2 rDNA sequences generated from living and dead parts of the same individuals. Our results show that fungi from a wide variety of functional groups are found in or on *Sphagnum* mosses. Of these, plant pathogens (25 genera) and soil saprotrophs (17 genera) tend to dominate in terms of diversity and litter and wood saprotrophs ectomycorrhizal fungi and foliar endophytes with respect to abundance. Fungi with the highest DNA sequence abundance included well-known bryophilous taxa, such as *Galerina hybrida* and *G. tibiicystis* (Agaricales, Basidiomycota) as well as several *Hyaloscypha* species (Helotiales, Ascomycota). Of these, the above-mentioned *Galerina* species are known to be specific to *Sphagnum*. We also found several ectomycorrhizal and other root-associated fungi, e.g., *Paxillus involutus*, *Laccaria laccata*, and *Lactarius rufus*, that were represented by several of the forty most abundant sequence types. With respect to community composition, we observed some differences between living and dead parts within peat moss individuals, which suggest certain microhabitat specificity. In addition, there was high community turnover among moss individuals, indicating stochastic components, e.g., the founder effect, resulting from the expected dominance of species and genotypes that are early colonizers of the moss individual in question.