



ENVIRONMENTAL DNA SEQUENCING PROVIDES INSIGHTS INTO HOW DIVERSITY, COMPOSITIONAL DYNAMICS AND HABITAT PREFERENCE OF ECTOMYCORRHIZAL FUNGI ARE SHAPED BY EDAPHIC AND TOPOGRAPHIC FACTORS IN PANNONIAN FOREST TYPES

Ektomikorrhizas gombaközösségek diverzitásának és összetételének tájökölógiai jellemzése a Bükk hegység erdőtípusaiban környezeti DNS-minták alapján

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Ectomycorrhizal (ECM) fungi are among the most important fungi in temperate forest ecosystems both ecologically and culturally. They are crucial for ecosystem functioning and resilience towards disturbance, as most forest trees, particularly the representatives of Betulaceae, Fagaceae, and Pinaceae, are dependent on ECM associations for survival. In the Carpathian Basin, ECM fungi have mostly been studied based on sporocarps and it is already apparent that they represent a diverse group of fungi. However, the diversity and community composition of ECM fungi and the environmental factors shaping them in many Pannonian forest types are still unexplored. We provide here unprecedented insights into the diversity, compositional dynamics and habitat preference of ECM fungi among numerous forest types on a landscape scale in the Bükk Mountains, using soil DNA metabarcoding. We detected 1427 genotypes of 57 ECM fungal genera in the 62 sampling sites representing 11 forest types. Our findings, based on multivariate statistical analyses, suggest that ECM fungal community composition differs markedly among forest types and is influenced primarily by mesoclimatic and edaphic factors, such as soil pH, Ca content, and moisture. In addition, in some phylogenetic lineages, ASV richness different significantly among forest types. Overall, our results suggest that the distribution of ECM fungi at landscape scales are driven by local environmental conditions, which offers possibilities for biological monitoring, habitat characterization and periodic assessments.