



CRYPTIC SPECIES IN THE BASKET: A TAXONOMIC REVISION OF CHESTNUT BOLETES (*GYROPORUS CASTANEUS* S.L.) COLLECTED AS EDIBLE IN HUNGARY

Kriptikus fajok a kosárban: az ehetőként gyűjtött hazai gesztenyebarna
űregestinóruk (*Gyroporus castaneus* s.l.) taxonómiai revíziója

Noémi Kiss^{1*}, Regina Csáky², László Albert³, Viktor Papp^{1,2} & Bálint Dima²

¹Department of Botany, Hungarian University of Agriculture and Life Sciences, Villányi út 29–43, H-1118, Budapest, Hungary; ²Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; ³Hungarian Mycological Society, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; *E-mail: noe.mimi.kiss@gmail.com

Clarifying the taxonomy of the edible Chestnut Boletes (*Gyroporus castaneus* sensu lato) collected for consumption in Hungary is important for both mycological research and food safety. Our study presents an integrative taxonomic revision of the *Gyroporus castaneus* species complex based on the combined evaluation of morphological and molecular characters. Recent phylogenetic studies have demonstrated that this complex comprise several morphologically similar or cryptic, yet genetically well-supported lineages worldwide. Moreover, poisoning cases have been associated with taxa resembling *Gyroporus castaneus* traditionally regarded as edible in certain geographic regions, highlighting the need to reassess species boundaries and the identification criteria applied in mushroom foraging and inspection.

More than one hundred *Gyroporus* specimens collected in Hungary were examined, together with additional material from several European, African, and Asian countries. Genomic DNA was extracted and multiple molecular markers were amplified, including the nuclear ribosomal ITS and LSU regions, the protein-coding genes *RPB1*, *RPB2*, *TEF1-α*, and the mitochondrial *ATP6* gene. Our sequence dataset comprises own and publicly available sequences downloaded from GenBank, UNITE and BOLD databases, providing broad geographic representation of the investigated taxa. Preliminary results indicate substantial previously unrecognized diversity, with Hungarian specimens distributed among five distinct phylogenetic lineages.

Our results demonstrate that the diversity of *Gyroporus castaneus* species complex occurring in Hungary and collected for consumption is considerably more complex than suggested by traditional morphology-based identification. The integrative approach provides a framework for clarifying species boundaries within the *G. castaneus* complex and for determining the taxonomic identity of the Hungarian lineages. Beyond its taxonomic significance, this revision may provide a more robust scientific basis for mushroom foraging recommendations and official mushroom inspection practices.