



NEW DATA ON THE DIVERSITY OF LEPIOTOID MACROFUNGI IN HUNGARY

Újabb adatok a hazai lepiotoid nagygyombák diverzitásához

Ágnes Radnóti^{1*}, Bálint Dima², Lajos Benedek¹ & Viktor Papp¹

¹Department of Botany, Institute of Agronomy, Hungarian University of Agriculture and Life Sciences, Budapest, Hungary; ²Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Budapest, Hungary;

*E-mail: radnoti.agnes@gmail.com

The lepiotoid macrofungi (including the genera *Lepiota*, *Macrolepiota*, *Leucoagaricus*, *Leucocoprinus*, *Echinoderma*, *Cystolepiota*) are saprotrophic fungi that represent an important part of the fungal community. They cannot be neglected from an antropomorphic point of view either since some of the species (e.g. *Macrolepiota procera*) are widely collected by foragers, and other species are extremely poisonous to humans, for example *Lepiota subincarnata* and *L. brunneoincarnata*. These taxa are generally understudied and often overlooked due to the fact that their macromorphological identification is difficult and they tend to grow solitary. The aim of the present work is to start a collection and to get a better understanding of the taxonomy of the lepiotoid macrofungi occurring in Hungary, using morphological and molecular methods.

Apart from our own collections we leant on citizen science, involving the public in collecting specimens, thus we have a collection from many different habitats, which extend across several regions in Hungary: Őrség, the Transdanubian Mountains (Bakony Mts, Vértes Mts, Buda Hills), the North Hungarian Mountains (Mátra Mts, Zemplén Mts) and the Great Hungarian Plain. We have collected 191 samples so far from which 28 species have been identified with macro- and microscopic determination methods. Some of the more interesting species are *Cystolepiota bucknalli*, *Lepiota castanea*, *L. cystophora*, *L. forquignonii*, *L. griseovirens*, *L. ignivolvata*, *L. oreadiformis* and *L. pseudolilacea*. Further identification of some of the undetermined specimens by sequencing the ITS nrDNA region has already been started.