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Multi-gene phylogenetic analyses reveal species limits, phylogeographic patterns, and evolutionary histories of key morphological traits in *Entoloma* (*Agaricales*, *Basidiomycota*)

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Species from *Entoloma* subg. *Entoloma* are commonly recorded from both the Northern and Southern Hemispheres and, according to literature, most of them have at least Nearctic-Palearctic distributions. However, these records are based on morphological analysis, and studies relating morphology, molecular data and geographical distribution have not been reported. In this study, we used phylogenetic species recognition criteria through gene genealogical concordance (based on nuclear *ITS*, *LSU*, *rpb2* and mitochondrial *SSU*) to answer specific questions considering species limits in *Entoloma* subg. *Entoloma* and their geographic distribution in Europe, North America and Australasia. The studied morphotaxa belong to sect. *Entoloma*, namely species like the notorious poisonous *E. sinuatum* (*E. lividum* auct.), *E. prunuloides* (type-species of sect. *Entoloma*), *E. nitidum* and the red-listed *E. bloxamii*. With a few exceptions, our results reveal strong phylogeographical partitions that were previously not known. For example, no collection from Australasia proved to be conspecific with the Northern Hemisphere specimens. Almost all North American collections represent distinct and sister taxa to the European ones. And even within Europe, new lineages were uncovered for the red-listed *E. bloxamii*, which were previously unknown due to a broad morphological species concept. Our results clearly demonstrate the power of the phylogenetic species concept to reveal evolutionary units, to redefine the morphological limits of the species addressed and to provide insights into the evolutionary history of key morphological characters for *Entoloma* systematics. New taxa are described, and new combinations are made, including *E. fumosobrunneum*, *E. pseudoprunuloides*, *E. ochreoprululoides* and *E. caesiolumellatum*. Epitypes are selected for *E. prunuloides* and *E. bloxamii*. In addition, complete descriptions are given of some other taxa used in this study for which modern descriptions are lacking, viz. *E. subsinuatum*, *E. whiteae*, *E. flavifolium*, *E. luridum*, *E. bloxamii*, *E. madidum*, *E. corneri*, *E. callidermum* and *E. coeruleoviride*.

Keywords: BIODIVERSITY; DNA BARCODING; ENTOLOMATAEAE; FUNGAL BIOGEOGRAPHY; MOLECULAR SYSTEMATICS; PHYLOGENETIC SPECIES**Document Type:** Research Article

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