An evolutionary view of the taxonomy and ecology of *Inocybe (Agaricales)*

with new perspectives gleaned from GenBank metadata

Martin Ryberg, 2009

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Dissertation Abstract

Martin Ryberg (2009). An evolutionary view of the taxonomy and ecology of *Inocybe* (*Agaricales*) with new perspectives gleaned from GenBank metadata.

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Inocybe (*Inocybaceae*) is one of the most speciose genera among the gilled mushrooms (*Agaricales*) but large parts of its taxonomy and evolutionary history remain poorly explored. The present thesis shows that the traditional infrageneric classification of *Inocybe* does not fully reflect evolutionary relationships and that the two most commonly used taxonomic characters, spore shape and presence of a cortina, have not evolved in such a way as to define unique monophyletic groups. The section *Rimosae*, in its traditional circumscription, is divided into two separate clades by the present analyses, and *Rimosae* s.str. does not group with the subgenus *Inosperma* - where it is commonly placed - but forms a separate clade more closely related to the subgenus *Inocybe*. Also the sections of the subgenus *Inocybe*, the largest of the subgenera, should in general be interpreted in a strict sense if they are to reflect monophyletic groups. Such a view-point would leave many species with an uncertain placement. On the species level it is shown that many of the traditionally accepted taxa are insufficiently characterized in terms of circumscription and morphological variation.

This thesis also explores metadata associated with DNA sequences from molecular ecological studies. These sequences represent a large part of the fungal internal transcribed spacer sequences (ITS) in GenBank that are relatively well annotated regarding ecological and geographical data. They are, however, seldom used as sources of such information. One reason is that they typically lack precise taxonomic annotation and therefore are hard to search in a systematic context. To facilitate the exploration of such sequences, the software suite *emerencia* (www.emerencia.org) was developed and is presented as a component of this thesis. The *emerencia* software was employed to explore the distribution and ecology of *Inocybe* and was found to have the capacity to significantly expand on our knowledge of the world-wide distribution of the genus and of the ecology of its individual species. This new information was compiled together with information from other sources to explore whether host preference and three characters coding for preference for particular soil conditions are correlated to the phylogeny. This was done using ancestral state reconstruction methods. The results show that while soil moisture preference is not, host preference, preference for calcareous soils, and preference in soil nutritional status are indeed correlated to the phylogeny. This indicates that a well formulated taxonomy that is reflective of phylogenetic relationships can have predictive values for these ecological traits.

Key words: *Inocybe*, *Inocybaceae*, *emerencia*, GenBank, insufficiently identified sequences (IIS).

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