



A molecular perspective on generic concepts in the *Hypotrachyna* clade (Parmeliaceae, Ascomycota)

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Abstract

Recently, molecular phylogenetic studies have revolutionized the generic concepts in Parmeliaceae and in lichen forming fungi in general. In the present study, the generic delimitation in the *Hypotrachyna* clade is revised using a molecular phylogeny of nuclear ITS, LSU and mitochondrial SSU rDNA sequences of 88 hypotrachynoid taxa. Morphological and chemical features are also revised in each group. 118 sequences are newly generated for this study. Our phylogenetic analyses show the polyphyly of *Hypotrachyna* as currently circumscribed which falls into four well-supported and one unsupported clade. *Cetrariastrum*, *Everniastrum* and *Parmelinopsis* are nested within *Hypotrachyna* s. lat., *Parmelinopsis* being also polyphyletic and nested in one of the *Hypotrachyna* clades. *Cetrariastrum* is monophyletic but clustered within *Everniastrum*. Two alternative hypotheses tests significantly rejected the monophyly of these three genera. As a consequence, the genera *Cetrariastrum*, *Everniastrum*, and *Parmelinopsis* are reduced to synonymy with *Hypotrachyna*. Furthermore, we here propose an alternative classification to recognize the well-supported clades at subgeneric level and leave the remaining species unclassified within the genus. Five new subgenera are proposed: *Hypotrachyna* subgen. *Cetrariastrum*, *Hypotrachyna* subgen. *Everniastrum*, *Hypotrachyna* subgen. *Longilobae*, *Hypotrachyna* subgen. *Parmelinopsis*, and *Hypotrachyna* subgen. *Sinuosae*. Forty-nine new combinations are proposed.

Key words: generic classification, lichens, molecular systematics, parmelioid lichens, taxonomy

Introduction

Traditionally, the generic classification in lichenised fungi is based on morphological, anatomical and chemical characters. In Parmeliaceae, morphology of vegetative thalli have traditionally played an important role in circumscribing genera with a number of generic segregates being described over the last three decades (Culberson & Culberson 1981; Elix 1993b; Elix & Hale 1987; Elix et al. 1986; Hale 1974a, 1974b, 1984, 1986a, 1986b; Krog 1982; Kurokawa 1991; Sipman 1980; Sipman 1986). However, in recent years a number of taxonomic re-evaluations, mainly based on molecular phylogenies, have been proposed (Amo de Paz et al. 2010a; Amo de Paz et al. 2010b; Blanco et al. 2005; Blanco et al. 2004b; Crespo et al. 2010b; Crespo et al. 2007; Divakar et al. 2006; Divakar et al. 2010; Divakar et al. 2012; Thell et al. 2006; Wirtz et al. 2006). These studies revealed that the taxonomic significance of phenotypical characters of the vegetative thallus was overestimated in several groups. As a consequence, some former segregates were synonymized, such as *Rimeliella* Kurokawa (1991: 1) within *Canomaculina* Elix & Hale (1987: 239); nine genera in