

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

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Objectives

The present study aims to clarify the phylogenetic positions of *Cetrariastrum*, *Everniastrum* and *Parmelinopsis* and also test the hypothesis that the morphological characters have evolved independently within the clade as adaptations to ecological conditions.

Material and methods

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.

Results

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., the latter 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.

Conclusions

As a consequence, the genera *Cetrariastrum*, *Everniastrum*, and *Parmelinopsis* are reduced to synonymy with *Hypotrachyna*. Further, 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. *Longiloba*, *Hypotrachyna* subgen. *Parmelinopsis*, and *Hypotrachyna* subgen. *Sinuosa*. Forty nine new combinations are proposed.