MOLECULAR PHYLOGENY OF THE FAMILY RHIZOCARPACEAE

Erik Möller 1 ; Mika Bendiksby 1 ; Einar Timdal 1

1 University of Oslo, Norway

E-mail: erikjmo@uio.no

*Rhizocarpon* (Ramond ex DC.) is a common crustose lichen genus on rock in the boreal and arctic-alpine zones, but also occurs throughout temperate, subtropical, and even tropical regions. It was first described in 1805, and represents one of the oldest described lichen genera. It is globally distributed and, though almost exclusively saxicolous, it is morphologically, chemically and ecologically diverse. Historically, ca 378 species names have been introduced, of which 143 are in use in checklists today. However, new species are regularly discovered and old species concepts redefined. The peripheral phylogeny is poorly known and the backbone has rarely been examined. Huge volumes of material exist in fungaria around the world, and *Rhizocarpon* DNA has proven to be durable. With recent development in DNA methods and molecular phylogenetics it is now easier, cheaper, and perhaps overdue to perform a large scale examination of how the clades are related and how well this correlates with morphology, chemistry and ecology. We aim to evaluate family, genus and some species circumscriptions and update the taxonomy accordingly. In addition, we want to identify informative morphological and chemical characters that can form a basis for an identification key. We will include multiple accessions of species representing the major clades of the family and use both freshly collected and herbarium specimens. A phylogenetic hypothesis of the family will be established, using multiple genetic markers and various phylogenetic and taxon delimitation methods. Morphology and anatomy of relevant specimens will be re-examined in light of the DNA based results. Finally, taxonomic conclusions will be made based on a total evidence approach.