

Editorial

Molecular data have revolutionized our understanding of evolution and classification of lichenized fungi. In 1998, Mats Wedin, Tor Tonsberg and Dennis Brown edited a seminal issue of the *Lichenologist* (30, 4/5) on “Taxonomy, Evolution and Classifications of Lichens and Related Fungi” and stated in their editorial “Progress in lichen systematics at all taxonomic levels has probably never been so rapid as today”. The speed of progress in systematics of lichenized fungi has undoubtedly further accelerated since then. We are now able to address questions of species delimitations, evolution of characters, and circumscription of taxa in a more rigorous way than imaginable less than two decades ago. *Parmeliaceae* is an ideal family to demonstrate the progress in systematics over the last decade. It is probably the largest family of lichen-forming fungi, has a worldwide distribution, and includes the overwhelming majority of macrolichens. Estimates of the numbers of species in the *Parmeliaceae* range from 2200 to 2500, and they exhibit a remarkable diversity in morphology and chemical products. Moreover, it has become apparent that morphologically defined species frequently harbour more than one phylogenetic lineage; sometimes one that is not immediately related. In addition, the family includes many common and widespread species that are regularly used as bioindicators for atmospheric pollution and others that are of value as indicators of ecological continuity or are responding to recent climatic change.

The idea of presenting together a series of manuscripts on *Parmeliaceae* in a thematic issue of the *Lichenologist* was developed at an Encyclopedia of Life (EOL) Biosync workshop held in the BioSync Center of the Field Museum in Chicago in May 2010 entitled “*Parmeliaceae*: improving our understanding

of taxonomy, classification and biogeography of the largest family of lichen-forming fungi”. The occasion was organized by Thorsten Lumbsch, Robert Lücking and Ana Crespo, and attended by 30 scientists from 12 countries, with the financial support of EOL. This issue includes 11 contributions, including two reviews. The first review focuses on the progress of the use of internet resources and databases to increase both scientific and outreach capacities (Lücking *et al.*, p. 503), while the second (Crespo *et al.*, p. 511) reviews the changing generic concepts in parmelioid lichens, how these have been revised as a result of accruing molecular evidence, and considers the phylogenetic informativeness of different characters.

The original contributions include four papers dealing with phylogenetic relationships at the generic level, and four addressing species delimitations in different groups of *Parmeliaceae*. The studies at generic and species-group levels include ones on cetrarioid genera (Nelsen *et al.*, p. 537), neuropogonoid lichens (Lumbsch & Wirtz, p. 553), a new subgenus in the genus *Parmotrema* (Hawksworth, p. 647), and a study on the crustose genus *Protoparmelia* and allied groups (Papong *et al.*, p. 561). The species delimitation studies address the taxonomic status of currently accepted species and the detection of cryptic species in parmelioid lichens (Del Prado *et al.*, p. 569; Molina *et al.*, p. 585; Nunez-Zapata *et al.*, p. 603), and the genus *Bryoria* (Myllys *et al.*, p. 617). In addition, an update to the checklist of parmelioid lichens in Europe and adjacent areas first published in 2008 is included (Hawksworth *et al.*, p. 639).

Although the focus here is on representatives of a single family, in view of the intensity and depth of study it has received as a result of international collaborative research over

the last ten years in particular, it can be expected to have pointers to situations that may occur in other less-studied families and an indication as to which kinds of characters are the most valuable for generic and species delimitations. Our experience with this family also leaves us convinced that, in the 21st century, major systematic revisions are only likely to be achieved through a combination of formal and informal collegial co-operations; and further a willingness to share results and debate possible explanations so that a consensus that can be expected to be of lasting value can emerge. We have also come to recognize that to make changes in classifications on the basis of small data sets from a limited number of species, and with few samples of those species, may often be unwise.

In presenting this series of contributions together, it is also our hope that it will serve to demonstrate to field lichenologists: 1) why classifications even in such conspicuous

lichens have been changed, 2) the complexity of the evolutionary situations now emerging and 3) the issues that systematists have to address when translating research results into classifications for general use.

Finally, this Editorial gives us the opportunity to thank the EOL Biosync initiative for their support and great work in the logistics of the meeting. We also want to thank Robert Lücking for his help in organizing the EOL Biosync Meeting.

REFERENCE

- Crespo, A., Kauff, F., Divakar, P. K., del Prado, R., Pérez-Ortega, S., Amo de Paz, G., Ferencova, Z., Blanco, O., Roca-Valiente, B., Núñez-Zapata, J. *et al.* (2010) Phylogenetic generic classification of parmelioid lichens (*Parmeliaceae*, *Ascomycota*) based on molecular, morphological and chemical evidence. *Taxon* **59**: 1735–1753.

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