Evaluation report on the thesis of Mrs Dovilė Barcytė on “Diversity of microalgae from extreme habitats: linking phylogeny and ecology”

Research question of both, basic science (e.g. speciation, dispersal, microbial diversity) and applied science (bioindication, species conservation, ecosystem services) rely on reliable species delimitations – at least for the key organisms. The enormous diversity of protists and its tremendous ecological and economic importance is sharply contrasted by the pronounced lack of knowledge on these organisms. We are only beginning to understand the extent of protist diversity, the mechanisms maintaining these high levels of diversity and their impact on ecosystem stability. The present work deals with the diversity, taxonomy and ecology of microalgae of extreme habitats, providing a valuable and much needed foundation for further research in the field of protist studies.

Following a general introduction, the aims of the thesis and the outline of the papers are discussed. The general part concludes with a short summarizing conclusion. Attached are corresponding stand-alone publications on which the doctoral thesis is based. The thesis comprises eight published manuscripts and two further manuscripts currently under review. They include their own in-depth introductions, methods, results and discussions. The eight published manuscripts are issued in peer-reviewed journals, well known for taxonomic and ecological contents. In the impressive ten listed papers, which belong to this thesis, a large organismic range is dealt with, in morphology as well as in taxonomic affiliation. The focus of the thesis is on coccoid, monoid and saccoderm protists. They belong to the groups of Chlorophyceae, Trebouxiophyceae, Zygnematophyceae and Cyanidiophyceae. A broad range of established methods for taxonomic work is used within the different papers to assess the phylogeny, morphology and ecology of the analyzed isolates. Among them are e.g. Sanger sequencing of different loci, secondary structure analyses of the ITS2, isolation of new algae and morphological techniques including light microscopy and TEM. After ecological, phylogenetic and morphological analyses, taxonomic conclusions were drawn for many analyzed
algae groups. In the intensive and in depth taxonomic studies, different new species were established in already existing genera, e.g. *Coccomyxa silvae-gabretae*, *C. fottii*, *Watanabea acidotolerans*, *Chloromonas arctica*, *Chl. svalbardensis*. In addition, new genera were established if necessary, e.g. *Lunachloris lukesovae* gen. et sp. nov.

In sum, Mrs Dovilė Barcytė applies an impressive broadness of methods and statistical analyses. The diversity of her thesis subjects, her ability to analyze data from different techniques and her ability to work collaboratively, reflect multifaceted qualities required of a Ph.D candidate. The covered aspects are highly relevant for biodiversity, ecology and biogeographic distribution of biota. Both methodology and scientific content match scientific standards. Aside from the scientific quality is the thesis well written with respect to phrasing and stylistic issues. Statements are very clear and comprehensive. The literature review is comprehensive.

I strongly recommend this thesis for defence.

Upon reading this thesis, the following open questions and remarks arose:

A large part of the work deals with taxonomic questions and taxonomic procedures. For example, the establishment of new species and genera. According to which criteria/concepts were new species established? Have the same basic criteria been applied to all taxonomic groups? Why were these specific phylogenetic markers chosen? More and more environmental studies refer to genetic high-throughput studies based on relatively short gene segments. How well can the new species be distinguished from closely related species on the basis of short genetic regions? How variable are, for example, the V4, V9 of the 18S or the ITS regions? In some of the papers the concept of barcoding was mentioned. Were possible barcode regions investigated in the analyses? Which gene regions would you suggest for your analysed groups?

With kind regards

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