A NEW COMBINATION IN *BARBILOPHOZIA* FOR *LOPHOZIA HYPERBOREA* SUBSP. *HELOPHILA* (SCAPANIACEAE, MARCHANTIOPHYTA) OF GREENLAND, WITH MACROEVOLUTIONARY JUSTIFICATION

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ABSTRACT

A new combination in the hepatic genus *Barbilophozia* is made for a subspecies of *Neoorthocaulis* (Scapaniaceae) to fit the conservative classification being used for the Flora of North America. Justification is given for avoiding names generated in new molecular classifications.

Volume 29 is the prospective volume of hepatics and hornworts for the FNA Editorial Committee (1993+). The genus *Barbilophozia* Loeske has presented a problem in classification. Rather than following the modern classification for the North American taxa proposed by Stotler and Crandall-Stotler (2017), which recognizes several segregate genera associated with *Barbilophozia* based on recent molecular work by many authors, the older, more inclusive genus is retained for Volume 29. A new combination is required for this conservative classification, which avoids using the molecularly based new genus *Neoorthocaulis* L. Söderstr., De Roo, & Hedd. Justification for this is presented in the discussion section below.

Barbilophozia hyperborea subsp. **helophila** (R.M. Schust. & Damsh.) R.H. Zander, **comb. nov.**
    Basionym: *Lophozia hyperborea* subsp. *helophila* R.M. Schust. & Damsh., Phytologia 63: 325. 1987. *Neoorthocaulis hyperboreus* subsp. *helophilus* (R.M. Schust. & Damsh.) Stotler & Crandall-Stotl., Ann. Missouri Bot. Gard. 102: 659. 2017.

Barbilophozia hyperborea subsp. *helophila* is restricted to southern Greenland. It is distinguished from the typical subspecies by a red cast to the plants, smaller underleaves, and presence of gemmae.

A return to the classical concept of *Barbilophozia* is justified by the uncertainty associated with molecular systematics as nowadays practiced. The genus *Neoorthocaulis* was established by Söderström et al. (2010) to reflect recent molecular studies (Vilnet et al. 2007, 2008, 2010) of the *Lophozia* relationship among Scapaniaceae. This work distinguished *Barbilophozia* sensu stricto from the segregate genera *Orthocaulis* H. Buch, *Neoorthocaulis*, *Schljakovia* Konstant. & Vilnet, and *Schljakovianthus* Konstant. & Vilnet. The molecular studies are here considered negatively biased for the following reasons:

(1) Clades do not model evolution, which is serial, that is, species to species. Clades model series of sets of traits giving rise dichotomously to further split sets of traits, which is not a process in nature, but is a form of cluster analysis. A more realistic model is the dissilient genus concept (Zander 2013: 92, 2018: 170) of descendant species radiating from a central more generalized progenitor, a key organizing principle of macroevolutionary systematics (Zander 2019a).

(2) Metadata reviews (Zander 2019b, c) of molecular systematics studies of mosses in the family Pottiaceae, published by various phylogeneticists, have demonstrated that molecular races are common in species and that they are often molecularly paraphyletic such that any two OTUs within an average of 4.5 nodes has a good chance of one being a direct descendant of the other. Thus, sister

group distribution in a molecular cladogram is highly uncertain within a rather broad topological range. The same appears to be true for hepatics, with examples of multiracial species in the study of Vilnet et al. (2008), which revealed much infraspecific cladistic structure (serial branching), including species-level paraphyly.

(3) Molecular traits are sometimes cited as confirming molecular clades. This presents the statistical problem of multiple testing. A thorough search will usually find some traits that appear to concentrate within a particular molecular clade, usually polythetically (traits partially applicable but in total overlapping among all species). Morphological traits must stand on their own to corroborate molecular results or be considered random coincidences. Thus, there must be demonstrated no reasonable alternative to the putative morphological clustering. Bonferroni correction for multiple tests would be (Zander 2013: 113) to split the alpha in half if there were two morphological alternatives (selected as in flipping a coin), only one of which supports the molecular. This means that the statistical support needed for non-critical applications would be, not 0.94 BPP, but 0.97 BPP for the molecular results. Problematically, the morphological alternative may instead be similar to the classical, quite different clade structure, and with excellent Bayesian support through Shannon-Turing analysis (Zander 2018: 35, 173). In this case a Bayes factor method (Zander 2018: 39) must be used instead, which splits the total support, that is, provides about 0.50 BPP for both morphological and molecular concepts of relationships. The negative biases one and two given above argue for retaining the morphologically based classification.

Until the three objections made here are addressed, classical taxonomic name combinations should be preferred to radical new and different distributions of species into molecularly based genera.

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