



Towards a monophyletic classification of Lejeuneaceae I: subtribe Leptolejeuneinae subtr. nov.

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Abstract

We employed sequences of two chloroplast regions (*trnL-trnF*, *rbcL*) and the nuclear ribosomal ITS region of seven accessions of *Leptolejeunea* to explore its phylogenetic position. Maximum parsimony and maximum likelihood analyses led to similar topologies but deeper nodes received good bootstrap support only with maximum likelihood methods. *Leptolejeunea* formed an early diverging, robust monophyletic lineage within Lejeuneaceae tribe Lejeuneae. Contrary to earlier belief, it is not closely related to *Drepanolejeunea*. To amend the current classification of Lejeuneae into subtribes, we propose Leptolejeuneinae, subtr. nov.

Key words: epiphyll, Lejeuneae, *Leptolejeunea*, liverwort, Porellales, taxonomy

Introduction

Lejeuneaceae are a nearly cosmopolitan family with the majority of species in the humid tropics, where they form a major component of the epiphytic, especially epiphyllous diversity (Pócs 1996). Species numbers are still unclear, with recent estimates ranging from 750 (Wilson *et al.* 2007a) to 1700 species (He & Zhu 2011). An equally controversial topic is the supraspecific classification, especially when considering exclusively morphological and chemical evidence (Gradstein *et al.* 2003). These challenges are now increasingly addressed in studies using DNA sequence data to reconstruct relationships. The application of this molecular phylogenetic approach has improved our understanding of evolutionary patterns within Lejeuneaceae (e.g., Wilson *et al.* 2004, 2007b, Dong *et al.* 2012, 2013, Heinrichs *et al.* 2013, 2014, Yu *et al.* 2013), and has led to a considerable reduction of genera from some 90 to 68 (Gradstein *et al.* 2006, Heinrichs *et al.* 2012a, 2012b, Ye *et al.* 2013).

Based on the hitherto published molecular phylogenies of Lejeuneaceae, Gradstein (2013) proposed a new classification of Lejeuneaceae. However, he deemed this classification “somewhat preliminary” because not all genera of Lejeuneaceae have been studied using DNA sequence data, and many are represented only by a single or a few species in published molecular datasets. This holds especially true for Lejeuneae, the most diverse tribe of Lejeuneaceae. Gradstein (2013) classified tribe Lejeuneae into eight subtribes but felt unable to assign seven of its 40 genera to any of them due to a lack or paucity of molecular data. One of these “unassigned” genera is the largely epiphyllous genus *Leptolejeunea* (Spruce 1884: 193) Schiffner (1893: 126) (Pócs 1996), of which a single species was included in previous molecular phylogenetic analyses of Lejeuneaceae (Wilson *et al.* 2007b). In that study, it was resolved in an early diverging clade of Lejeuneae.

Here, we test the monophyly of *Leptolejeunea* by sequencing chloroplast and nuclear markers of seven Neotropical or Paleotropical accessions and including them in a large alignment of published Lejeuneae sequences. Based on maximum parsimony and maximum likelihood analyses of this dataset we confirm the monophyly of *Leptolejeunea* and propose a new subtribe, Leptolejeuneinae Heinrichs et Schäf.-Verw.

explore the evolution of ecological preferences within Lejeuneae, and to further amend the current classification, an extension of the molecular data sets, and inclusion of genera such as *Metalejeunea* Grolle (1995: 17), *Schusterolejeunea* Grolle (1980: 105), *Tuyamaella* Hattori (1951: 60), and *Vitalianthus* Schuster & Giancotti (1993: 447) is required. Work to obtain these data is under way.

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