



## The application of molecular data to the phylogenetic delimitation of species in bryophytes: A note of caution

ALAIN VANDERPOORTEN<sup>1</sup> & A. JONATHAN SHAW<sup>2</sup>

<sup>1</sup>University of Liège, Institute of Botany, B22 Sart Tilman, B-4000 Liège, Belgium. E-mail: a.vanderpoorten@ulg.ac.be

<sup>2</sup>Duke University, Department of Biology, Durham, NC 27708, USA. E-mail: shaw@duke.edu

### Abstract

Molecular phylogenetics has been of prime importance in revisiting traditional taxonomic hypotheses, and this is especially true in taxa with reduced morphologies like bryophytes. Sequence identity at one or a few loci, as well as evidence for species para- or polyphyly, have been increasingly used to lump species. While sequence identity at loci that are usually variable within the group of interest can provide some incentive for additional study of such species, it does by no means alone provide sufficient evidence for synonymization. Similarly, the strict requirement that all species must be demonstrably monophyletic is equivalent to adopting an uncompromising view that reproductive isolation (i.e., the biological species concept) is the only valid evidence for species status, and that all species have to be 100% isolated. Some modes of speciation lead to paraphyletic species or even phylogenetic networks. We therefore encourage case by case evaluation of all available data rather than applying a single criterion such as monophyly. We make some suggestions about how to use molecular data in the circumscription of bryophyte species.

**Key words:** species concept; parphyly; budding speciation; monophyly

### Introduction

The species concept has long been a central issue in systematic biology. Mayden (1997) listed no less than 24 different, potentially conflicting species definitions. The reason that different criteria lead to incompatible species concepts is that various aspects of lineage divergence arise at different times during the process of speciation (De Queiroz 2007). Daughter species progressively diverge with time, but the acquisition of the different properties defining them (when they become phenotypically diagnosable, reciprocally monophyletic, reproductively incompatible, ecologically distinct, etc.) is not simultaneous. Before the acquisition of any one of those properties, everyone will agree that there is a single species, and after the acquisition of all, everyone will agree that there are two. In between, however, there will be disagreement.

In the large and taxonomically difficult moss genus *Bryum* Hedw. for instance, phylogenetic patterns uncovered by molecular analyses correspond poorly to traditional classifications based on morphology (Holyoak & Pedersen 2007). Arguing that molecular data provide a more accurate representation of phylogenetic history and relationships than do morphological characters, Holyoak & Pedersen (2007) concluded that any 'classification of the Bryaceae based on morphological characters alone cannot be defended'. Incongruence between inferences derived from molecules versus morphology in *Bryum* relates both to species delimitation and the resolution of multispecies clades. It has in fact become increasingly evident that bryophyte species, due to the limited availability of characters defining them, the focus on a few key-characters, and the influence of the environment in the evolution of those characters, render many morphologically defined species vulnerable to refutation by phylogenetic analyses (Vanderpoorten & Goffinet 2006). A large body of literature thus points to the sometimes severe incongruence between morpho-species concepts and molecular phylogenies (see Heinrichs *et al.* 2009a for review).