



## Moss diversity: A molecular phylogenetic analysis of genera

CYMON J. COX,<sup>1,3,5</sup> BERNARD GOFFINET,<sup>2</sup> NORMAN J. WICKETT<sup>2,4</sup>, SANDRA B. BOLES<sup>1</sup> & A. JONATHAN SHAW<sup>1</sup>

<sup>1</sup> Department of Biology, Duke University, Durham, North Carolina 27708, U.S.A.

<sup>2</sup> Department of Ecology and Evolutionary Biology, University of Connecticut, Connecticut 06269, U.S.A.

<sup>3</sup> Current address: Centro de Ciências do Mar (CCMAR), Universidade do Algarve, 8005-139 Faro, Portugal.

<sup>4</sup> Current address: Department of Biology, Pennsylvania State University, Pennsylvania 16802, U.S.A.

<sup>5</sup> Author for correspondence (cymon.cox@googlemail.com)

### Abstract

In this study we present phylogenetic and molecular phylogenetic diversity analyses of moss taxa from a total of 655 genera of mosses. Three loci were sampled: chloroplast ribosomal small protein 4, the intronic region of the mitochondrial NADH dehydrogenase subunit 5, and partial sequences of the nuclear 26S ribosomal RNA. Maximum likelihood and Bayesian phylogenetic analyses were performed on individual loci and on multilocus data sets. A measure of phylogenetic diversity was calculated and contrasted among major lineages of mosses. We reveal many instances of incongruence among genomic partitions, but, overall, our analyses describe relationships largely congruent with previous studies of the major groups of mosses. Moreover, our greater sampling highlights the possible non-monophyly of many taxonomic families, particularly in the haplolepideous and pleurocarpous mosses. Comparisons of taxic and phylogenetic diversity among genera indicate that the Dicranidae (haplolepideous taxa) include about 15% of moss genera, but nearly 30% of the phylogenetic diversity. By contrast, the Hypnanae (hypnalian pleurocarps) contain about 45% of moss genera, but a lower percentage of phylogenetic diversity. Agreement between numbers of genera and phylogenetic diversity within other moss clades are remarkably consistent.

**Key words:** mosses, Bryopsida, phylogeny, phylogenetic diversity, Bayesian phylogenetic analysis

### Introduction

Mosses (Bryophyta) are a diverse clade with over 12,700 species in more than 800 genera (Crosby *et al.* 1999) and are conspicuous floristic components in all terrestrial habitats suitable for plant growth — from the cold and barely hospitable antarctic to lush tropical rainforests. Mosses have many ecological functions, and one group, the peat mosses (*Sphagnum*), perform an important role in the global biogeochemical cycling of carbon where they represent a large reservoir of sequestered carbon in the form of northern boreal peatlands (Wieder & Vitt 2006).

Together with the other two bryophyte lineages, the liverworts (Marchantiophyta) and hornworts (Anthocerotophyta), and the vascular plants (Tracheophyta), mosses are one of the primary lineages of land plants (embryophytes) that arose *circa* 470 MYA, after the colonisation of land by an ancestor most closely related to modern-day charophycean algae (Lewis & McCourt 2004). The transition of plants from water to land was accompanied by major morphological, developmental, and physiological innovations most markedly expressed by the intercalation of a multicellular diploid phase into the life cycle (Kenrick 1994, Bateman *et al.* 1998, Graham *et al.* 2000, Renzaglia *et al.* 2000, Hemsley & Poole 2004). Based on extant representatives, the