

The Mitochondrial Genome of the Moss *Brachythecium rivulare* (Hypnales, Brachytheciaceae)

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Abstract—The mitochondrial genome of the pleurocarpous moss *Brachythecium rivulare* has been sequenced and annotated. The genome consists of 104,460 base pairs and has approximately the same gene set and organization as other bryophyte mitogenomes. Whole mitochondrial genome comparison between *B. rivulare* and *Physcomitrella patens*, *Tetraphis pellucida*, *Anomodon rugelii*, and *Anomodon attenuatus* was performed. The primary cause of bryophyte mitochondrial gene length variation was found to be numerous indels in the introns. Bryophyte mitochondrial gene conservation level was estimated, and it was in a good congruence with the overall phylogeny of bryophytes with the percentage of mitogenome similarity being proportional to the age estimated by phylogenetic analysis. Annotation discrepancies in the analyzed mitogenome sequences were identified. The simple sequence repeat (SSR) content was evaluated, and candidate sites of RNA editing were predicted in the *B. rivulare* mitochondrial genome.

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Bryophytes *sensu lato* are the earliest terrestrial group of plants that still exist on Earth. Bryophyta (*sensu stricto*), or mosses, branched off from the stem of the Embryophyta phylogenetic tree after Marchantiophyta and before the separation of Anthocerotophyta [1–4], although an alternative topology with Anthocerotophyta in the basal position repeatedly appears in analyses [5]. Estimates of the date of moss origin vary greatly from 440 to 710 mya [6]. These nonvascular pioneers of land plants first acquired morphological, biochemical, and physiological adaptations that enabled the transition from aquatic to terrestrial habitats. The primary terrestrial biotopes formed by the bryophytes were important spots for the subsequent colonization of land by other plant evolutionary lineages. However, there is no comprehensive scenario of this crucial step in plant evolution. One approach to clarifying some obscurities of evolution is comparative genomics. Comparative genomics can be

used to investigate the diversity of genome structure across different groups of living beings, to identify genome organization conformities, and to understand the mechanisms and factors of its evolution.

Recently, the development of next generation sequencing (NGS) technologies created new opportunities for genome studies and dramatically changed the methodology of investigation. As a result, many new genome sequences of different organisms have been loaded into the NCBI database. However, bryophyte genomics remains in the early stages of progress in comparison with other groups of plants. Until recently, the nuclear genome sequence was only available for a single moss species, namely *Physcomitrella patens* [7], and for eight species plastid genomes are known. Mitochondrial genomes from 39 moss species from 11 orders have been deposited in the NCBI GenBank (www.ncbi.nlm.nih.gov) to date. This is significantly fewer than for vascular plants, for which sequences of 164 mitochondrial genomes are present in GenBank.

Although moss chondrioms are rather conservative in structure [3, 8–10], the available data are scarce; six orders represented by only single species. The largest

Abbreviations: CDSs, coding sequences; mya, million years ago; NGS, next generation sequencing; ORF, open reading frame; SSR, simple sequence repeat.

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