

Scientists characterize four episodes of large-scale gene duplications in evolutionary past of mosses

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Gene duplications provide genetic raw materials and are considered as important driving forces in diversification and evolution. The evolution of land plants is characterized by recurrent ancestral paleopolyploidy events, i.e. ancestral whole genome duplications.

The duplicated genes in both the model plant *Arabidopsis* and rice can

be traced back to five rounds of polyploidy. Bryophytes (including mosses), which branched away from other [land plants](#) almost 500 million years ago, represented a key group occupying an important phylogenetic position in land plant (embryophyte) [evolution](#).

To resolve an accurate phylogeny of mosses and the phylogenetic positioning of ancestral genomic duplication events, researchers from the Xinjiang Institute of Ecology and Geography (XIEG) of the Chinese Academy of Sciences, Hong Kong Baptist University, The Chinese University of Hong Kong and University of Missouri unveiled and characterized four episodes of large-scale gene duplications in the evolution of mosses.

The study was published in the *Journal of Systematics and Evolution*.

The researchers utilized phylotranscriptomic analyses of nearly 30 moss transcriptomes to probe single-copy gene families and generate reliable species phylogenies. Then they coupled the analyses with a large-scale phylogenomic analysis investigating duplication signals from more than 5,000 gene trees to determine the phylogenetic positioning of ancestral genomic duplication events.

Results showed that two branches with large numbers of gene duplications were elucidated by phylogenomic analyses, one in the ancestry of all mosses and the other before the separation of the Bryopsida, Polytrichopsida, and Tetraphidopsida.

The analysis of the phylogenetic progression of duplicated paralogs retained on genomic syntenic regions in the *Physcomitrella patens* genome confirmed that the whole-genome duplication events WGD1 and WGD2 were re-recognized as the ψ event and the Funarioideae duplication event, respectively. The ψ polyploidy event was tightly associated with the early diversification of Bryopsida, in the ancestor of

Bryidae, Dicranidae, Timmiidae, and Funariidae.

Together, four branches with large numbers of [gene duplications](#) were unveiled in the evolution of *P. patens*. The researchers analyzed and discussed gene retention patterns following the four large-scale duplications in different moss lineages.

Recurrent significant retention of stress-related [genes](#) may have contributed to their adaption to distinct ecological environments and the evolutionary success of this early diverging land plant lineage.

More information: Bei Gao et al. Ancestral gene duplications in mosses characterized by integrated phylogenomic analyses, *Journal of Systematics and Evolution* (2020). [DOI: 10.1111/jse.12683](https://doi.org/10.1111/jse.12683)

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