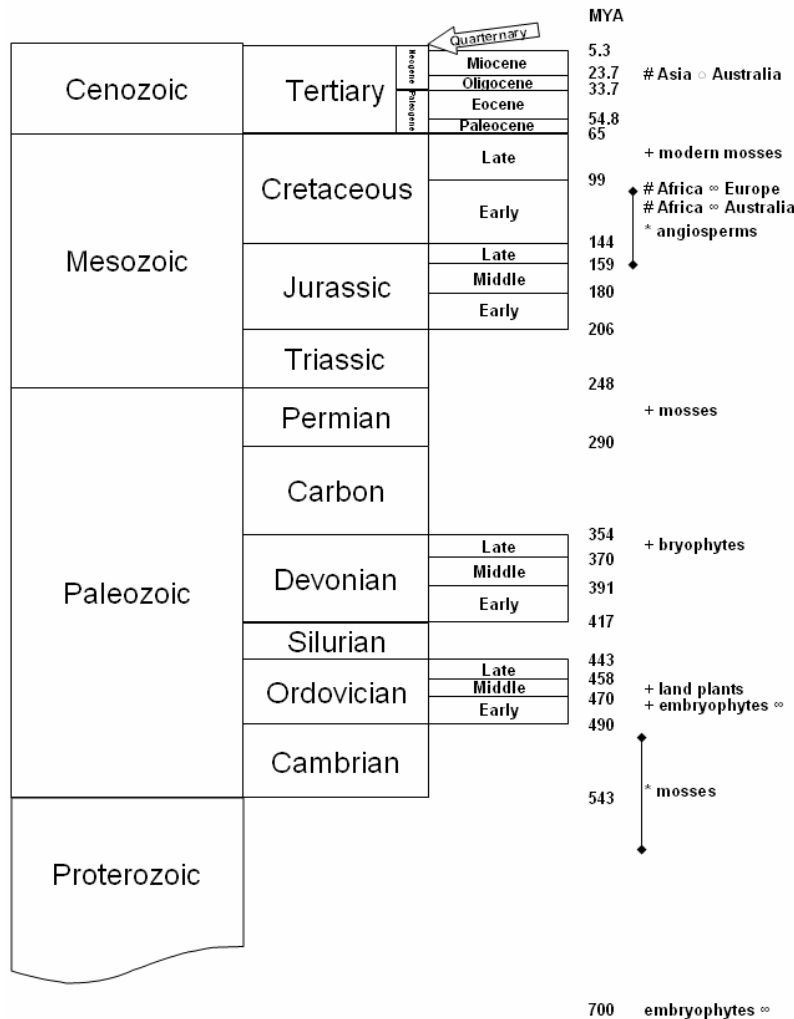


Molecular evidence that *Physcomitrella patens* is a paleopolyploid

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Whole genome duplications have been described as a driving force of eukaryote evolution. Several ancient polyploidization events have been detected based upon calculation of synonymous substitution rates of paralogous gene pairs among diploid flowering plants, revealing them to be paleopolyploids. In this study, we have analysed paralogs of the haploid moss *Physcomitrella patens* and find evidence that it is a paleopolyploid as well. Gene Ontology and pathway association of the retained duplicates revealed biased functional categories and differences in comparison with seed plants, particularly the abundance of metabolic genes in the moss. The rate of fixed nucleotide substitutions among the internal transcribed spacers of the 5.8S rRNA gene from three pairs of *P. patens* accessions was used to calibrate the molecular clock and demonstrates that the mosses evolutionary rate is an order of magnitude slower than those of seed plants. Based on the paralog analysis the large scale duplication event was dated to the Early Cambrian, ~540 million years ago, probably after the divergence of the last common ancestors of mosses and seed plants.



Geologic time scale summarizing data from the fossil record, plate tectonics and genome duplications. Key to symbols: + fossil record, # tectonic drift, * genome duplication, ∞ separation, ○ connection. Financial support by the DFG (Re 837/10-1) is gratefully acknowledged.