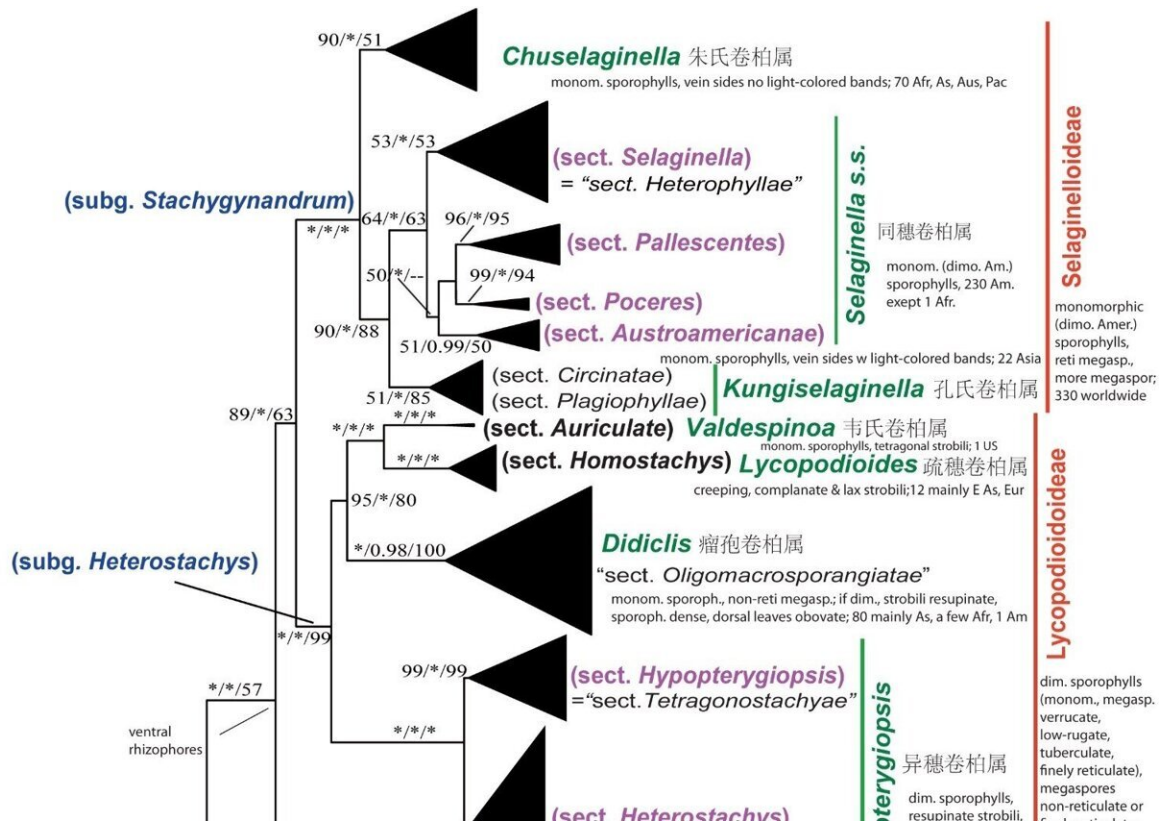


One of the oldest land plant lineages, clubmosses (*Selaginella*), re-classified

September 13 2023



Simplified maximum likelihood phylogeny of Selaginellaceae based on plastid *rbcL* and five nuclear markers. The sizes of black triangles are in proportion to the sample sizes of individual clades. Support values (maximum likelihood bootstrap support, maximum parsimony jackknife support, and posterior probability) are shown along the branches. “*” indicates a 100% support value. Red and green names indicate the 7 subfamilies and 19 genera, respectively, recognized in the current classification. Blue and black Latin names indicate the subgenera and sections recognized by Zhou and Zhang (2015). Black Chinese

names indicate Chinese vernacular names of the genera. Purple names indicate the 6 sections recognized by Zhou and Zhang (2015) and this study at the same rank. Credit: Xin-Mao Zhou, Yunnan University, China, Li-Bing Zhang, Missouri Botanical Garden

Clubmosses (*Selaginella sensu lato*) emerged over 383 million years ago in the Devonian Period, predating dinosaurs. These ancient vascular plants hold significant value in unraveling land plant evolution. Presently, *Selaginella* stands as the sole member of the Selaginellaceae family and Selaginellales order.

Notably, this order/family within pteridophytes (ferns and lycophytes) boasts a remarkable distinction, encompassing 750 or more species. The adoption of the broadly defined *Selaginella* is notably attributed to two key factors. Firstly, the current type species of the [genus](#), *S. selaginoides*, stands within a two-species subset devoid of rhizophores, a stark departure from all other genus members.

Adopting distinct genera would necessitate renaming all except these two non-rhizophore species. Secondly, the adoption of the broadly defined *Selaginella* is rooted in the complexity of phylogenetic relationships within the genus. Despite earlier phylogenetic studies, the uncertainty persists, and morphological homoplasy remains insufficiently evaluated within an appropriate phylogenetic framework.

In a recent study, one American and one Chinese researcher employed DNA sequences from 1 nuclear and 5 chloroplast genes across 684 global clubmoss samples. This encompassed approximately 300 species (40% of the total). The aim was to elucidate familial relationships and, notably, to pioneer the examination of 10 morphological traits' evolutionary patterns.

The researchers discovered that clubmosses were consistently grouped into seven primary clades, with four of these further branching into 3, 3, 4, and 6 subclades. By combining [molecular evidence](#) with morphological attributes, spore characteristics and distribution data, the study led to the classification of clubmosses into 7 subfamilies and 19 genera, with 12 newly described genera.

Considering these 19 genera as subgenera or sections within Selaginella is an alternative approach, albeit one that's largely disregarded except by seasoned plant systematists. Furthermore, relying on [species](#) names, which include the genus, is more effective in highlighting relationships, whether distant (distinct genus names) or close (shared genus name).

Moreover, the division of Selaginella s.l. into distinct and manageable genera offers numerous advantages for analysis, communication and conservation objectives. This novel classification stands to encourage further research in this important lineage of land plants.

The paper is published in the journal *Plant Diversity*.

More information: Xin-Mao Zhou et al, Phylogeny, character evolution, and classification of Selaginellaceae (lycophytes), *Plant Diversity* (2023). [DOI: 10.1016/j.pld.2023.07.003](https://doi.org/10.1016/j.pld.2023.07.003)

Provided by KeAi Communications Co.

Citation: One of the oldest land plant lineages, clubmosses (Selaginella), re-classified (2023, September 13) retrieved 21 May 2024 from <https://phys.org/news/2023-09-oldest-lineages-clubmosses-selaginella-re-classified.html>

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