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nature portfolio

Nature. 2024 Apr 24. doi: 10.1038/s41586-024-07324-0. Online ahead of print.

Phylogenomics and the rise of the angiosperms

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PMID: 38658746 DOI: [10.1038/s41586-024-07324-0](https://doi.org/10.1038/s41586-024-07324-0)

Abstract

Angiosperms are the cornerstone of most terrestrial ecosystems and human livelihoods^{1,2}. A robust understanding of angiosperm evolution is required to explain their rise to ecological dominance. So far, the angiosperm tree of life has been determined primarily by means of analyses of the plastid genome^{3,4}. Many studies have drawn on this foundational work, such as classification and first insights into angiosperm diversification since their Mesozoic origins⁵⁻⁷. However, the limited and biased sampling of both taxa and genomes undermines confidence in the tree and its implications. Here, we build the tree of life for almost 8,000 (about 60%) angiosperm genera using a standardized set of 353 nuclear genes⁸. This 15-fold increase in genus-level sampling relative to comparable nuclear studies⁹ provides a critical test of earlier results and brings notable change to key groups, especially in rosids, while substantiating many previously predicted relationships. Scaling this tree to time using 200 fossils, we discovered that early angiosperm evolution was characterized by high gene tree conflict and explosive diversification, giving rise to more than 80% of extant angiosperm orders. Steady diversification ensued through the remaining Mesozoic Era until rates resurged in the Cenozoic Era, concurrent with decreasing global temperatures and tightly linked with gene tree conflict. Taken together, our extensive sampling combined with advanced phylogenomic methods shows the deep history and full complexity in the evolution of a megadiverse clade.

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