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RESEARCH BRIEFINGS | 21 August 2024

Largest genomic tree of life of flowering plants to date includes almost 8,000 genera

A tree of life based on genes from across the nuclear genome and containing nearly 60% of all angiosperm genera unveils the complex evolutionary history of flowering plants. This tree both corroborates and challenges existing knowledge on angiosperm relationships and classification, and reveals two diversification surges, underpinned by many contrasting histories in individual plant lineages.

This is a summary of: [Zuntini, A. R. *et al.* Phylogenomics and the rise of the angiosperms. *Nature* **629**, 843–850 \(2024\).](#)

The problem

Almost all life depends on plants, 90% of which are angiosperms, or flowering plants. Angiosperms are fundamental to the structure, function and evolution of terrestrial ecosystems and provide countless resources to humans, such as food, medicine and shelter. For the past three decades, scientists have used DNA sequences to reconstruct the angiosperm tree of life, transforming our understanding of their evolution.

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— the organelle in the plant cell responsible for photosynthesis. Today, plastid data are abundant in public repositories and underpin a wealth of biological research, including the classification of flowering plants¹. However, plastid genes are tightly linked together and are usually inherited through the maternal line, which can prevent them from fully representing evolutionary history².

By contrast, phylogenomic studies use data from many unlinked genes across the entire genome to infer relationships between organisms and can therefore generate a more complete picture than conventional phylogenetics can. Thus, data from the vastly larger nuclear genome of angiosperms are needed, but they remain difficult and costly to generate at scale, owing to a lack of appropriate DNA-sequencing techniques.

The solution

By exploiting advances in high-throughput sequencing, we built a tree of life for angiosperms that includes 15 times more genera than comparable studies³ and represents all 64 orders and all 416 families. We targeted 353 nuclear genes using a universal genomic toolkit designed for this study (Angiosperms353)⁴, which enables the sequencing of up to 270,000 base pairs per sample for any angiosperm. This method can be used with poor-quality DNA and can be applied even to preserved plant materials (for example, herbarium specimens) that are centuries old.

We devised a data-analysis pipeline that reconciles conflicting molecular evolutionary histories, which often arise between nuclear genes. The lengths of the tree branches, which are determined by molecular variables, were then adjusted to absolute timescales by using 200 fossils as calibration points. This enabled us to perform an in-depth exploration of the dynamics of angiosperm diversification since their origins in the Mesozoic era (around 150 million years ago) (Fig. 1).

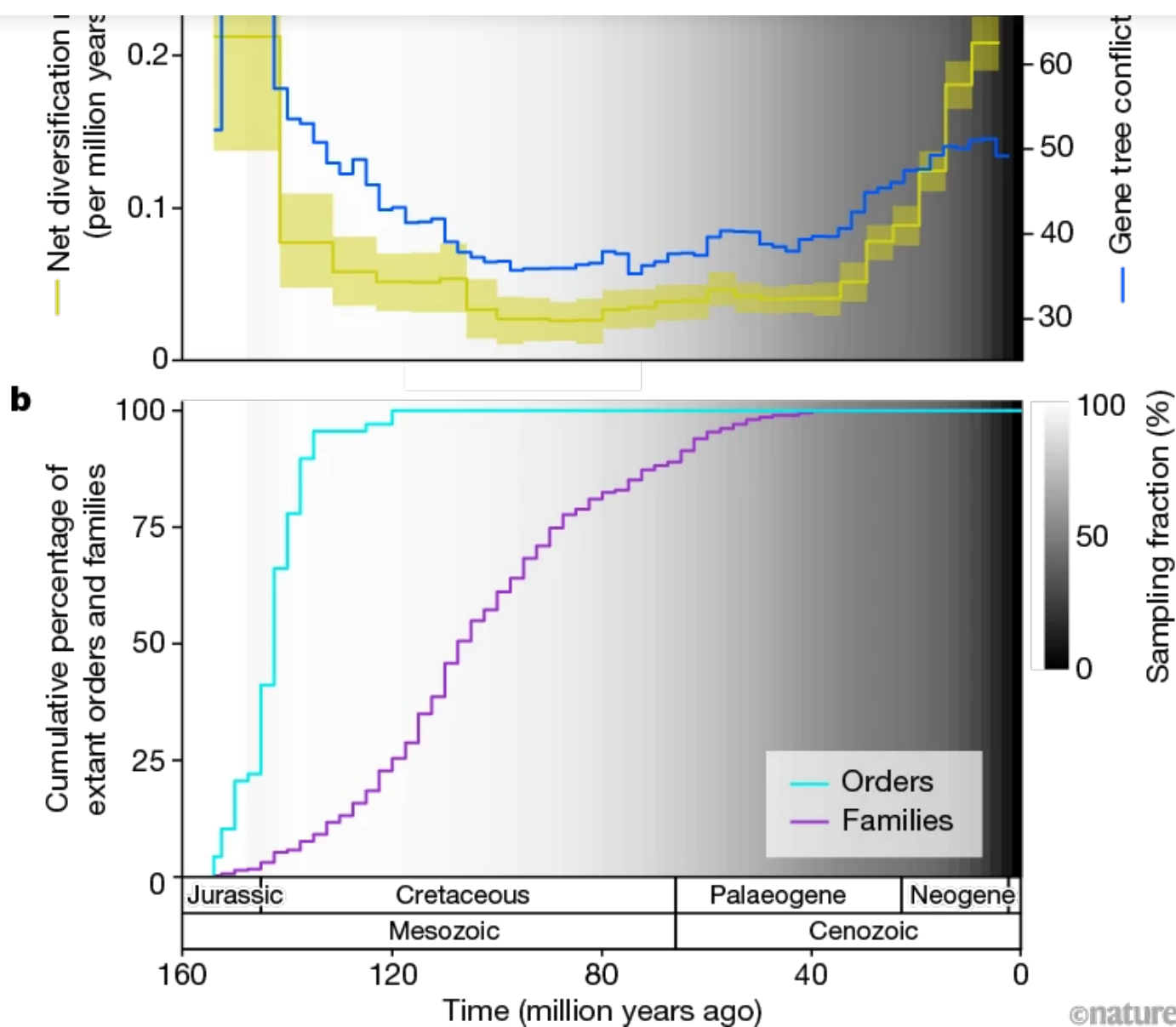
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Figure 1 | Angiosperm diversification dynamics through time. a, Diversification rate (yellow, left y axis) and the level of conflict between gene histories over time (blue, right y axis). **b**, Accumulation of surviving, or extant, orders and families over time. In **a** and **b**, the background greyscale gradient indicates the percentage of extant lineages represented in our tree. Credit: Zuntini, A. R. *et al.*/*Nature* (CC BY 4.0)

Our nuclear-genome-based angiosperm tree of life is remarkably consistent with relationships predicted by plastid data and the classification derived from them, increasing confidence in earlier studies. Many previously undescribed relationships

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previous phylogenetic studies. We found that angiosperms underwent two large bursts of diversification, the first shortly after their origins and the second more than 100 million years later in the Cenozoic era. Both surges coincided with high levels of conflict between the evolutionary stories told by individual genes (Fig. 1). Underlying these general patterns is a complex tapestry of diversification histories across the main angiosperm lineages.

The implications

Our findings showcase the transformative potential of nuclear genomic methods to reveal the history and evolutionary complexity of a megadiverse group, such as angiosperms. By using a standardized set of nuclear genes through openly available, affordable and universal tools, this study paves the way for collaborations and data integration across the plant-science community. Uptake of this approach is already accelerating, and large volumes of new, compatible data are routinely becoming available.

Nevertheless, some challenges remain. First, conflicting phylogenetic signals (patterns in molecular changes that inform the reconstruction of phylogenetic trees) among genes render some branches of the tree unresolvable, owing to biological events such as ancient hybridization or whole-genome duplication. Second, dating and diversification analyses are fraught with uncertainty, and all results should be interpreted with this caveat in mind. Last, sampling at the species level is highly incomplete, limiting our understanding of angiosperms' evolutionary history in the past 20 million years or so.

The framework presented here is the result of an ongoing initiative⁵ to complete the tree of life for all 13,600 angiosperm genera. It sets the scene for a global effort to deliver a species-level tree of all 330,000 species. — **William J. Baker and Alexandre**

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Expert opinion

This is an unprecedented exploration of evolutionary relationships among angiosperms, using the most richly sampled data set to date. The results will be of major interest to the plant systematics, evolution and ecology communities, but also of broader interest to those studying animal, fungal and microbial systems across myriad disciplines, given the enormous impact flowering plants have had on the history of life on Earth over the past 150 million years or so. – **Craig Barrett is at West Virginia University, Morgantown, West Virginia, USA.**

Behind the paper

The success of our mission to complete the angiosperm tree of life⁵ rests on three pillars: designing a solution for universal genomic analyses across flowering plants, establishing a global botanical partnership and harnessing information from the world's botanical collections. Through Angiosperms353⁴, we created an open-source DNA-sequencing toolkit that can be applied to any flowering plant, thus meeting the project's requirements and removing barriers to genomic research for the botanical community. The project partnership grew from inside this community, and brought together essential taxonomic expertise, materials and sequences, and resulted in numerous research papers. For example, our partnership with the Genomics for Australian Plants consortium flourished through its uptake of Angiosperms353 and a programme of reciprocal data sharing and collaborative research. Overall, more than half of the data generated by this project were obtained from herbarium specimens, highlighting the extraordinary value of botanical collections and uses for them that

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From the editor

The authors have built a phylogenomic tree of 9,506 flowering plant species (representing 7,923 genera), which they have calibrated using 200 fossils. The scale of this data set is impressive and the paper is expected to provide a reference for scientists interested in plant biology, evolution, genetics and beyond for years to come. – **Michelle Trenkmann, Senior Editor, *Nature***

doi: <https://doi.org/10.1038/d41586-024-02631-y>

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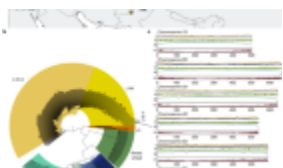
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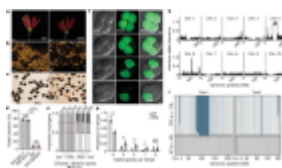
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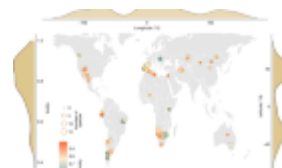
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Nature (*Nature*) | ISSN 1476-4687 (online) | ISSN 0028-0836 (print)