

Researchers find evidence of early genome duplications in conifers and other plants

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Larix (golden), Abies (central foreground) and Pinus (right foreground) Credit: Marshmallow from Seattle, WA, USA - Flickr/Wikipedia

(Phys.org)—A team of researchers from several academic institutions in the U.S. has found that contrary to popular belief, conifers have experienced at least two complete genome duplication events over the course of their evolutionary history. In their paper published in the journal *Science Advances*, the team describes their sequencing study of three types of plants and the comparisons they made with other plants that had been previously sequenced, and why they believe that what they found might help such trees survive as the planet warms.

Two years ago, a team of researchers in Sweden published a report that indicated that the genome for the common spruce had not been duplicated, a process known as polyploidy. In this new effort, the researchers wondered if the team in Sweden had missed something, so they decided to conduct a study of their own. They obtained frozen leaf samples of *Ophioglossum petiolatum*, *Gnetum gnemon* and *Ephedra frustillata* and conducted Roche 454 transcriptome sequencing on just their genes. They also looked at prior sequencing of 22

gymnosperm or vascular plant species. Next, they made use of a bioinformatics-based approach to figure out the ages of gene paralogs that came about due to duplications. After that, they created and then used an algorithm called Multi-Axon Paleopolyploidy Search to help them verify duplication events in the ancestry of the plants. The team reports that the results of their efforts have led to the discovery of two duplications that occurred in the conifers they studied, one in the ancestry of all Pinaceae, which includes spruces, pines and firs, and the other in cupressophytes, which includes junipers, redwoods and yew.

Such [genome duplications](#) are believed to drive evolution, which the team reports, helps explain the wide genetic diversity of conifers, which together make up the world's oldest, thickest and tallest trees. Their finding of the genome duplication could be helpful to other researchers looking at ways to genetically alter trees to help fortify them against a warming planet, which might be critical—such trees together account for producing approximately half of all lumber used by humans, and perhaps more importantly they are also the largest atmospheric carbon sink the planet has to offer.

More information: Z. Li et al. Early genome duplications in conifers and other seed plants, *Science Advances* (2015). [DOI: 10.1126/sciadv.1501084](#)

Abstract

Polyploidy is a common mode of speciation and evolution in angiosperms (flowering plants). In contrast, there is little evidence to date that whole genome duplication (WGD) has played a significant role in the evolution of their putative extant sister lineage, the gymnosperms. Recent analyses of the spruce genome, the first published conifer genome, failed to detect evidence of WGDs in gene age distributions and attributed many aspects of conifer biology to a lack of WGDs. We present evidence for three ancient genome duplications during the

evolution of gymnosperms, based on phylogenomic analyses of transcriptomes from 24 gymnosperms and 3 outgroups. We use a new algorithm to place these WGD events in phylogenetic context: two in the ancestry of major conifer clades (Pinaceae and cupressophyte conifers) and one in *Welwitschia* (Gnetales). We also confirm that a WGD hypothesized to be restricted to seed plants is indeed not shared with ferns and relatives (monilophytes), a result that was unclear in earlier studies. Contrary to previous genomic research that reported an absence of polyploidy in the ancestry of contemporary gymnosperms, our analyses indicate that polyploidy has contributed to the evolution of conifers and other gymnosperms. As in the flowering plants, the evolution of the large genome sizes of gymnosperms involved both polyploidy and repetitive element activity.

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