

[The constant genome of our Christmas trees](#)

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Conifers such as the spruce, pine, and fir are familiar sights in sitting rooms at this time of year, but what is perhaps less familiar is that the genomes of these [Christmas trees](#) have remained relatively stable for the last 100 million years, according to [Jean Bousquet](#) and his group at the [Université Laval Québec](#).



Conifers are one of four sub-groups of [cone-bearing plants](#). The genome sequences of several [flowering plants](#) have been completed, and these have shown that [whole-genome duplications](#) (more than two paired sets of chromosomes) have greatly contributed to the expansion of plant genomes and gene families, giving flowering plants the advantage of genetic diversity to help them supplant cone-bearing plants as the dominant form.

All flowering plant species sequenced so far have at least one whole genome duplication in their evolutionary history, but only 1-5% of conifers have whole genome duplications. The question is, when did these conifer duplications occur? Do they pre- or post-date the divergence of flowering and cone-bearing plants 300 million years ago?

To find out, Bousquet's group used a [phylogenomic](#) approach to compare whole or large parts of genomes between flowering plants and cone-bearing plants (including conifers and black and white spruce). The researchers found ancient duplications and compared the frequency of ancient to more recent duplications.

Using this approach, together with [gene mapping](#) (the assignment of DNA fragments to chromosomes), they could ask if the spread of gene families within cone-bearing plants is more likely for ancient duplicates pre-dating the flowering plant/cone-bearing plant split than more recent duplicates.

The researchers found that 527 of the spruce genes were split into 157 gene families across diverse molecular functions. Of these, 78.4% diverged before the flowering plant/cone-bearing plant split and 9.9% diverged after the split (11.3% could not be accounted for). In other words, there were about eight ancient duplications for each recent one. Most of the genes before the split had [translocated](#) (swapped positions) and moved, but the genes duplicated after the split were still close to each other on the same chromosome, and often organized in tandem.

This relative stability in the cone-bearing plants, including conifers, go towards explaining the amazing 100 million year stability of the 'Christmas tree', and the remarkable similarity between the decorated trees in our living rooms and the ancient fossils – except perhaps for the fairy and the baubles!