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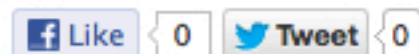


Oh, Christmas Tree, Thy Genome So Unchanging

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Sarah C.P. Williams

The conifer genome hasn't changed much in the last 100 million years, according to a new study. Why is it so relatively stable compared with other plants? Find out...



The Christmas tree that's decorating your home this holiday season not only looks like ancient conifers but also is genetically similar to its ancestors, according to a new study in which researchers analyzed thousands of genes from different conifer species and compared conifer genomes with those of flowering plants.

Scientists knew that conifers—a taxa which includes pine, spruce, and fir trees—had genetic properties that set them apart from other plants. For instance, conifers have massive genomes that contain a significant number of pseudogenes and transposable elements. The spruce genome, for example, is 10 times the size of the human genome and more than 100 times larger than the genome of the model plant *Arabidopsis thaliana*. "We already knew that there was a ballooning effect in conifer genomes that's very different from what we see in other plants" said Jean Bousquet, a forest geneticist at Laval University. Despite this fact, the number of coding genes in the conifer genome is comparable with other organisms.

While the morphological features of flowering plants have changed drastically in the past hundred million years, the ancient fossil record reveals that conifers maintained a similar morphology in the far past, even before the dinosaurs ruled the planet.



The conifer genome hasn't changed much in the last 100 million years, according to a new study. Source: Public Domain Images

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To understand this apparent lack of evolution in conifers, Bousquet's team worked with the Genome Canada SMarTForest Project to sequence the white spruce tree genome and compare hundreds of gene loci between white and black spruces, loblolly pines, and maritime pines. In a paper recently published in *BioMed Central Biology*, they reported that the vast majority of genes appeared in the same order and chromosome locations in all tree species (1).

"You still see some mutations, polymorphisms, small scale duplications and rearrangements, but the large scale architecture of the genome is really very similar," said Bousquet. "You just don't see that in flowering plants."

Based on the known time of divergence of the different conifer species, Bousquet's team estimates that the conifer genome has been relatively stable for the past 100 million years. And when they compared the conifer genes with those from flowering plants, they found that some gene duplications are shared, suggesting that conifer genomes have been stable since before the two taxa split around 300 million years ago.

Another unique characteristic of conifers is that chromosome number did not appear to change due to duplication as is common in flowering plants, but instead relied on fusion or fission. This leads Bousquet to believe that the conifer's massive genome might be related to their lack of evolution. "It might be that when you copy an entire chromosome that's so big, the organism just can't be viable," said Bousquet. If this were the case, selective pressure would maintain genome stability by limiting changes that increased its size.

For now, the authors can only guess at the mechanism for conifer genome stability. But further studies should hint at how organisms avoid large scale genetic changes once they're optimally adapted to their environment.

References

1. Pavy N, Pelgas B, Laroche J, Rigault P, Isabel N, Bousquet J. A spruce gene map infers ancient plant genome reshuffling and subsequent slow evolution in the gymnosperm lineage leading to extant conifers (2012). *BMC Biology* 2012, 10:84.