

A simple Christmas tree, a very complex genome

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This giant Christmas tree in a Paris department store is worthy of the fabulous decorations it's adorned with: it has a genome as complicated as that in humans.

CHARLES PLATIAU/REUTERS

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Who knew that deciphering the genome of a Christmas tree would be a vexing scientific endeavour?

Scientists in the U.S., Canada and Sweden are doggedly working away, trying to identify the building blocks of life within conifer trees.

It turns out that spruce, fir, pine, cypress and cedars have monstrous-sized genomes — the DNA sequences that constitute the instruction manuals of living things.

Scientists want to pull apart the genomes of these trees to figure out the effects of climate change on plants and to improve forest management.

Laval University's John MacKay has been part of a team that recently released preliminary data on conifer genomes. A Swedish group is trying to sequence a Norway spruce.

"Our estimates are that they have the same number of genes as humans," MacKay said on Thursday from Quebec City.

Humans have about 23,000 genes. MacKay estimates conifers have about 33,000. His team is tackling the white spruce.

Scientists are surprised by the monstrous size of the conifer genome. Compared to a simple oak tree, the conifer is far more complex.

"An oak tree's genome would be 30 to 40 times smaller than a conifer," he said.

Evolution may be playing a role here. "There are repetitive sequences that are not genes and have caused them to expand and repeat. They are very ancient in evolutionary terms and that might be part of it as well," he said.

David Neale of the University of California, Davis said new technologies that make it cheaper, faster and easier to analyze a genetic code have changed the world for conifer genetics.

"(The field is) entering the modern era," he said.

While a completely sequenced conifer genome is not expected any time soon, partial versions are helping scientists and those in the forestry industry to understand the mysterious trees.

Conifers have "these large regions I think we will never be able to piece together" with existing technologies, said Par Ingvarsson of Umea University in Sweden, who is leading the Norway spruce project.

The tree's genome is so much larger because it also contains an abundance of non-gene DNA with no obvious function, Ingvarsson said.

The main reason why they wanted to tackle the conifer genome was to fill a conspicuous gap in the list of sequenced plants.

"It was like the one missing piece," he said. "We just need this final piece to say something about how all the plant kingdom has evolved over the last billion years or so."

With files from The Associated Press