Huge DNA code of the Christmas tree being revealed

Malcolm Ritter, AP Science Writer

NEW YORK (AP)—To millions of people, the Christmas tree is a cheerful sight. To scientists who decipher the DNA codes of plants and animals, it's a monster.

We're talking about the conifer, the umbrella term for cone-bearing trees like the spruce, fir, pine, cypress and cedar. Apart from their Yuletide popularity, they play big roles in the lumber industry and in healthy forest ecosystems.

Scientists would love to identify the billions of building blocks that make up the DNA of a conifer. That's called sequencing its genome. Such analysis is a standard tool of biology, and doing it for conifers could reveal genetic secrets useful for basic science, breeding and forest management.
But the conifer genome is dauntingly huge. And like a big price tag on a wished-for present, that has put it out of reach.

Now, as Christmas approaches, it appears the conifer's role as a genetic Grinch may be ending.

In recent months, scientific teams in the United States and Canada have released preliminary, patchy descriptions of conifer genomes. And a Swedish team plans to follow suit soon in its quest for the Norway spruce.

"The world changed for conifer genetics," said David Neale of the University of California, Davis. It's "entering the modern era."

What happened? Credit the same recent technological advances that have some doctors predicting that someday, people will have their genomes sequenced routinely as part of medical care. The technology for that has gotten faster and much cheaper.

"Until just a few years ago, the idea of sequencing even a single conifer genome seemed impossible," said John MacKay of the University of Laval in Quebec City, who co-directs a multi-institution Canadian project that's tackling the white spruce. The new technologies changed that, he said.

How big is a conifer genome? Consider the 80-foot Christmas tree at Rockefeller Center in New York. It's a Norway spruce, so its genome is six times bigger than that of anybody skating below it. Other conifer genomes are even larger.

Nobody expects a perfect, finished conifer genome anytime soon. MacKay and others say that reaching that goal would probably require some advances in technology. But even partial versions can help tree breeders and basic scientists, researchers say.

Why bother doing this?

For breeders, "genomes can really help you speed up the process and simply do a better job of selecting trees, if you understand the genetic architecture of the traits you want to breed for," MacKay said.

The prospect of climate change brings another dimension. As forest managers select trees to plant after a fire or tree harvesting, genetic information might help them pick varieties that can adapt to climate trends in coming decades, Neale said.

It's all about "giving them a tree that will be healthy into the future," he said.

To sequence a genome, scientists start by chopping DNA into small bits, and let their machines sequence each bit. That's the part that has become much faster and cheaper in recent years. But then comes the task of re-assembling these bits back into the long DNA chains found in trees. And that is a huge challenge with conifers, because their DNA chains contain many repeated sequences that make the assembly a lot harder.

As a result, conifers present "these large regions I think we will never be able to piece together" with current technologies, said Par Ingvarsson of Umea University in Sweden, who is leading the Norway spruce project.

Will scientists develop new technologies to overcome that problem?

"You should never say never in this game," Ingvarsson said.

This past summer, Neale's group presented partial results for the genome sequence of loblolly pine, based on DNA extracted from a single pine nut. It includes about a million disconnected chunks of DNA, and altogether it covers well over half the

tree's genome.

Neale figures it will take his team until 2016 to complete genomes of the loblolly, Douglas-fir and sugar pine. The project is financed by the U.S. Department of Agriculture.

Mackay's group recently released its early results on DNA taken from a single white spruce.

As for the Swedish project on Norway spruce, Ingvarsson said its results will be made public early next year. The 2 million DNA pieces have captured most of the estimated 35,000 to 40,000 genes in the tree, even if researchers don't know just where those genes go in the overall genome sequence, he said.

People have about 23,000 genes, not much different from a conifer. The tree's genome so much bigger because it also contains an abundance of non-gene DNA with no obvious function, Ingvarsson said.

He said his chief reason for tackling conifer genomes was to fill a conspicuous vacancy 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."

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