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Scientists sequence genome of Norway spruce

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Researchers yesterday reported that they had sequenced the genome of the Norway spruce, a giant evergreen native to Europe that had also been planted widely in parts of North America.

Published in the journal *Nature*, scientists say what was notable about the DNA of the tree was its length. The human genome was made up of around 3 billion pairs of DNA base letter, which stored all the genetic information for making a person, but the Norway spruce genome made up of 20 billion base pairs was seven times longer.

Sequencing the DNA posed a technical challenge given the genome included many repetitive segments.

The research showed that despite its huge genome, spruces seemed to have a similar number of protein-encoding genes as humans: on the order of 30,000.

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Why the Norway spruce had so very much other DNA, and whether that DNA played an ongoing role in conifer biology, was a question scientists would explore further, according to the researchers.

Conifers, like spruce, fir and pine trees, were members of a sub-group of seed-producing plants known as gymnosperms, which all had very long genomes. The journal *Bioinformatics* also described another super-long conifer genome, that of the white spruce.

According to University of British Columbia plant biochemist Joerg Bohlmann, a coauthor on both studies, the newly assembled genome sequences would let researchers perfect the way foresters bred trees, focusing on challenges such as "insect resistance, wood quality, growth rates and adaptation to changing climate."

However, researchers say all that extra DNA might have nothing useful to do.

Scientists point out that conifers, technically gymnosperms, include ginkgoes and a few other species are some of the most phenomenally successful organisms on earth.

These have dominated forests for over 200 million years and members of the group include the tallest, heaviest, and oldest things currently alive and they have managed this despite having a massively inefficient genome management style.

Unlike many groups that vary widely in the number of chromosomes their species carried, pretty much all the gymnosperms had a dozen pairs of chromosomes, with all of these chromosomes in the area of 2 billion bases long, or a bit smaller than the human genome. The size was so consistent in fact, that the authors thought the trees might be just about pushing the limits of how much stuff a chromosome could carry and still get it copied and shared between two cells at the time of division.