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News in Brief: Giant genomes felled by DNA sequencing advances

Complete genetic blueprints collected for several conifer species



By Puneet Kollipara

Web edition: May 22, 2013

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Your Christmas tree may dwarf you not only in height but in its genome. At 20 billion bases of DNA, the newly sequenced genome of the Norway spruce, a popular Christmas tree in Europe that can reach heights above 30 meters, is six times larger than the human genome. The sheer size made it no small task to sequence.

The genome of *Picea abies*, one of the largest ever sequenced, appears May 22 in *Nature* and is one of several that have been read out recently from trees known as gymnosperms — seed-bearing plants that don't produce flowers. The group includes conifers, cycads and ginkgos.

This month, researchers presented the 24-billion-base genome of the loblolly pine, *Pinus taeda*, at a conference ([SN Online: 5/16/13](#)). A May 22 *Bioinformatics* report provides the sequence of the 21-billion-base genome of the white spruce, *Picea glauca*.

To sequence the enormous genomes, researchers used powerful sequencers and new sequence-analyzing software. The genomes could help breeders produce trees with better wood quality and insect resistance, says John MacKay of Laval University in Quebec, who worked on both spruce genomes.

The spruces likely piled up duplicates of existing DNA sequences over hundreds of millions of years. Other plants and animals tend to eliminate these duplicates.

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CITATIONS

B. Nystedt et al. The Norway spruce genome sequence and conifer genome evolution. *Nature*. Published online May 22, 2013. doi: 10.1038/nature12211. [[Go to](#)]

I. Birol et al. Assembling the 20 Gb white spruce (*Picea glauca*) genome from whole-genome shotgun sequencing data. *Bioinformatics*. Published online May 22, 2013. doi: 10.1093/bioinformatics/btt178. [[Go to](#)]



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The genetic sequence of the Norway spruce (shown) could shed light on the evolution of the seed-bearing plants called gymnosperms.

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