The evolutionary story of birch, told through 80 genomes

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A stand of silver birch trees. Credit: Wikimedia Commons.

Forests of silver birch stretch across Europe, and they are a wonder to behold: stands of slender, white-barked trees sheltering vast swathes of earth.

But these woodlands also have value beyond their beauty: They are an economic asset, generating raw material for papermaking, construction, furniture-building and more.

A new study illuminates the evolutionary history of birch, a tree that has not been studied much by scientists despite its commercial value.

"Birch is one of the major trees for forest products in the Northern Hemisphere. Others, like spruce, pine and poplar, all have genome sequences, but birch did not—until now," says University at Buffalo biologist Victor Albert, who co-led the Finnish-funded project with Jaakko Kangasjärvi, Ykä Helariutta, Petri Auvinen and Jarkko Salojärvi of the University of Helsinki in Finland. Helariutta is also a professor at the University of Cambridge.

"We sequenced about 80 individuals of one species, Betula pendula, the silver birch," says Kangasjärvi. "We sampled populations of this species throughout its range, so up and down Finland, down to Germany, over to Norway and Ireland, and all the way up to Siberia."By analyzing the 80 genomes sequenced, the team was able to identify genetic mutations that may be of interest to industry, including mutations that may affect how well birch trees grow and respond to light at different latitudes and longitudes and under different environmental conditions.

The research could be a starting point for breeding trees that better meet the needs of various industries."What makes a birch tree hardy in different environments? A tree in Finland may die if you plant it in Siberia because plants have local adaptations—specific genetic mutations—that help them survive where they are found," Helariutta says. "An understanding of these natural adaptations can facilitate genetic engineering and artificial selection. That's why our research could be very useful for forest biotechnology."

The study will be published on May 8 in *Nature Genetics*.

Manipulating genes for better growth

In the study, the researchers identified genetic mutations of interest by hunting for distinctive stretches of DNA within the genomes of individual birch trees.

Like people, plants inherit two copies of every gene—one from each parent—and these two copies are slightly different from each other. However, in some spots, an organism may have long strips of identical DNA in both copies of a gene. Such stretches of DNA point to genetic regions that are critical to a species' survival and development, as these regions are the product of "selective sweeps" in which all or most organisms in a geographic location come to depend on a certain genetic trait.

When the scientists analyzed the genomes of 80 birch trees from across Europe, they discovered a rich array of selective sweeps in genes that influence important qualities such as tree growth and wood production.

Moreover, the team found that some selective sweeps appeared to be associated with various environmental conditions. Two genes that help control how birch trees respond to light—PHYC and FRS10—had notable genetic mutations correlating with latitude, longitude and temperature, while the mutations in PHYC were also related to precipitation trends. Similar associations were also identified for two genes tied to wood production—KAK and MED5A. (Mutations in these genes were correlated with latitude, longitude and temperature.)

"The selective sweeps we identified may be the basis for local adaptation for different populations of birch," Salojärvi says. "Trees in Siberia are under different selective pressure from trees in Finland, so genes are being tweaked in different ways in these two places to allow these plants to better adjust to their environment."

"The research points to genetic mutations that could be of interest for genetic manuipulation for forest products," says Auvinen.

More information: Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch, *Nature Genetics* (2017). nature.com/articles/doi:10.1038/ng.3862

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