

Towards genetically-improved conifers

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Credit: F. D. Richards

Pines are long-lived; between 100 and 1,000 years. And they are a tree species, of high commercial importance. Indeed, they are valued for their timber and wood pulp. Now, a European Research project, called [ProCoGen](#), is planning to unravel the pine genome by 2016. The trouble is that pines have a complex genome—seven times larger than the human genome—with an estimated size of 3.2 billion base pairs. The project's goal is to identify genes and gene networks controlling important traits of ecological and economic relevance. These include traits able to control tree productivity, growth, drought and cold stress, in trees subjected to climate change.

"The main objective of the project is to develop an integrative and

multidisciplinary genomic research in conifers, using high-throughput platforms for sequencing, genotyping and conducting functional analysis," says project co-coordinator Carmen Díaz-Sala, who is also an associate professor at the department of Plant Biology from Alcalá de Henares University in Madrid, Spain.

The project is focusing on the sequencing the genomes of two European conifer species, *Pinus sylvestris* and *Pinus pinaster*. It also integrates the outcomes of international conifer [genome sequencing](#) initiatives. These focuses on *Pinus taeda*, which is the variety of pine mostly used in the US paper industry.

One of the key challenges is to devise strategies to handle high-level information, such as genome assembly. The information generated during the project will thus make it possible to uncover the genome structure. As a result, it will contribute to identify the underlying molecular bases explaining pines' adaptability to external stresses imposed by [climate change](#). The hope to infer information that can be transferred to other conifer species of high importance in European forestry, explains Díaz-Sala.

Experts believe that calling upon genomic tools in forestry can help solve several problems. First, it will contribute to optimise productivity. "We need to produce more biomass with new and improved properties from our forests in order to meet the challenges of the future," says Ove Nilsson, director of the Umeå Plant Science Centre at the Swedish University of Agricultural Sciences, in Sweden, who is not part of the project. He adds: "We want to replace fossil fuels and materials dependent on oil with renewable biomaterials and biofuels."

Second, this research will help produce trees that are adapted to external conditions. "These tools will also help to breed for trees that are better adapted to the [rapid climate change](#) with increased drought resistance,

better water use efficiency and resistance against various insect and fungi pathogens," adds Nilsson.

By acquiring knowledge of all the conifer genes, we can, for instance, help pinpoint, which ones are active in response to changes in photoperiod and temperature and in response to drought or cold. This will, in turn, help identify which of these changes are most important for adaptation to design an efficient breeding program, Nilsson tells CommNet.

Another advantage of the genomic approach, it that is also informs ecological processes and their underlying genetic mechanisms. This is the case, "for example, in species interactions, such as in the mycorrhizal association between trees and fungi," explains Felix Gugerli Künzle, head ecological genetics at Swiss Federal Research Institute WSL, in Birmensdorf, Switzerland. He believes this approach can also help identify the variation between genomes among species and among provenances, through comparative analyses.

Since the project does not to focus on one particular species, but actually tries to find out how genes have evolved in different species, by identifying similarities in patterns and differences in genomic arrangements, it helps "better understand how the genomic composition may also affect local adaptation," concludes Künzle.

For now, one of the main challenges "is to get such a large project involving so many different scientists in different countries to work efficiently," says Nilsson, adding: "This consortium has a reasonably good line-up of people, but they are competing with other scientific environments that are organised in a much more efficient way." The comparison is difficult, if it does not apply to consortia of a similar size to the project team, which includes 22 partners, according to Carmen Díaz-Sala. Besides, she believes that the comparison is difficult if it is

made with teams studying much less complex [trees](#), such as poplars.

"Collaboration is always difficult, because cultural background, political situations in different countries," says Künzle. "On the other hand it's really the complexity of these large genomes, which is more [of a] technical problem; this is probably something that make things a little bit more complicate than in other organisms".

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