Canadian Wood Fibre Centre

Impact Assessment: Genomic Selection

CWFC researchers examined the benefits of genomic selection technology for improving fibre traits and growth rates in white spruce seedlings.

Genomic selection identifies superior trees with desirable traits five to seven times faster than traditional methods. Early selection for wood traits by using DNA markers was successfully demonstrated in this work.

The Canadian Wood Fibre Centre (CWFC) researched the white spruce (*Picea glauca*) genome to discover if DNA markers can be used to make seedling selection possible. These markers are pieces of DNA that may be linked directly or indirectly to specific traits such as density, elasticity, stiffness and growth rate. Using DNA markers distributed along the tree genome for this selection process is called genomic-assisted selection, or genomic selection (GS).

While traditional tree breeding methods take decades, GS can allow breeders to identify trees with desirable traits much earlier in the trees' development and so shorten breeding cycles. Identifying desirable traits earlier will provide the forest industry with plantation-grown seedlings that produce sought-after fibre attributes more rapidly than is possible with current tree improvement methods.

As well, GS could enable reforestation with selected trees. For instance, a grower could produce tree varieties that have certain combinations of traits (e.g. growth and wood quality) that will better fit requirements of the products sought by the customers.

Researchers hope to obtain maximum value from GS by quickly deploying new tree varieties that have desirable attributes, together with cutting-edge vegetative propagation methods developed by the Canadian Forest Service.

Need

For Canada's forest sector, the main need is better and faster-grown wood. With traditional tree improvement processes, the selection of some wood characteristics that have a strong impact on the strength and stiffness of lumber (such as wood density and microfibril angle) can occur only 15 to 20 years after planting. Most breeding programs do not yet predict or select for these important wood traits in their plantation-grown trees because of this long lead time and the very high costs of the associated assessment. Consequently, the wood characteristics of mature plantation-grown trees cannot be predicted.

Canadian Wood Fibre Centre
Working together to optimize wood fibre value – creating forest sector solutions with **FPInnovations**

Canada

The ability to predict the attributes of mature trees at planting time will enable foresters to better plan their future outputs and will result in less waste and, ultimately, cheaper wood.

The Canadian forest sector would benefit considerably from finding ways to reduce both wood trait testing time and assessment costs. There is an urgent need to supply reforestation programs as quickly as possible with a stock of high-quality seedlings for which both growth and wood quality potential can be predicted. Improving this supply would boost the competitiveness of the Canadian forest industry – as would the ability to grow stands with more uniform wood fibre closer to the sawmills.

A goal of this project was therefore to enable breeders to make seedling-stage selections of fast-growing trees that possess desirable wood quality traits.

White spruce was studied because spruce trees represent 56 percent of Canada's annual tree plantings, with 300 million trees being planted across the country every year. These seedlings represent the next generation of trees for Canada's forest harvest. White spruce in particular is a major component of reforestation programs in most provinces.

Approach

GS research focuses on techniques to identify and select trees with desirable traits in order to tailor the growth of those selections to market demands. These techniques use tree "fingerprints." These fingerprints are obtained by using many DNA markers to predict the genetic value of each tree tested for physical traits such as wood density or growth rate. The ultimate objective is to identify which trees should be retained for the reforestation program.

Researchers studied the genome (the entire set of DNA for all of the trees) of the white spruce, which allowed them to localize natural variations in DNA (DNA markers) observed between various trees. Mathematical models were developed to predict the desired wood traits of a tree based on information from its DNA markers.

In this study, the trees examined were from a population obtained through crossing superior trees that came from Quebec's white spruce breeding program. These 1,700 trees

were full-siblings, with both parents matching, belonging to 59 families. About 7,000 DNA markers were used to predict the value of four growth and wood traits among the 1,700 trees.

Wood core samples were collected from each of the trees. Wood traits were assessed using microdensitometry and X-ray diffraction. These processes closely examine the sample under ordinary or X-ray light to evaluate the desired properties in the wood. Microdensitometry evaluates the density of the wood, which is a strong indicator of its strength. X-ray diffraction reveals a great deal about the structure and other qualities of the wood. Microfibril angle, for instance, can help to predict how well a piece of wood can hold a screw.

Benefits

It currently takes 15 to 20 years to identify desirable traits in white spruce by using traditional breeding methods and 30 to 35 years to develop seed orchards to produce the genetically improved seed. GS is much faster: superior trees with desirable traits can be identified after only one to two years, which represents a five- to seven-fold reduction in time. Moreover, GS allows reducing the breeding cycles by about two-thirds, making genetically superior material accessible within 10 years and generating at least twice the genetic gains per year of breeding effort compared with traditional breeding.

Improving Canada's white spruce stock could benefit the next generation of foresters and consumers of forest products by providing cheaper trees more rapidly and in response to market demand. In addition, more rapidly growing trees could allow an increase in annual allowable cuts granted to foresters.

High-tech forest management applications have a huge impact on the performance of the forest value chain. Understanding how to efficiently reproduce desired fibre attributes from the current forest resource requires using several tools. These tools include selecting and breeding the strongest seedlings and developing varieties of tree species to take advantage of local growing conditions. GS will be the newest in this suite of tools that will help to grow the forest of the future and to expand the present forest land base by using afforestation and plantation management systems.

Research indicates that early selection for wood traits by using DNA markers could indeed be successfully implemented in white spruce breeding programs. Many genes are linked to each growth and wood quality trait so a single DNA marker is insufficient to explain the variation of any trait among trees. However, GS can significantly improve the accuracy of predictions to about 80 percent when using full-siblings because it uses all the markers simultaneously to predict the growth or wood trait.

Furthermore, when GS is used to select only the top 5 percent of trees for a given trait, it can identify those seedlings with an accuracy that is nearly equal to that of traditional methods without having to wait 20 years for the trees to mature.

In a similar experiment on unrelated trees, using DNA markers to predict the genetic makeup of the top trees produced weaker results and was less accurate. This means that GS is of most value in tree populations where the pedigree of the trees is well established, such as breeding populations.

It is not possible to say with certainty what impact GS will have on the Canadian forest sector because the technology is so new. The CWFC is taking the next step in advancing its use by searching for partners with which to trial this technology on an operational scale. The aims are to gain a better understanding of the economics of GS and to introduce it to the marketplace. The CWFC has already solved the science behind GS so it will focus on best practices to make it a viable business proposition over the long term and on obtaining solid operational data on how best to employ it.

Future uses for this technology could include screening trees in existing seed orchards with DNA markers and thinning trees that are predicted to have less desirable traits. Seed produced by the remaining trees could be used in standard reforestation programs. Stands comprised of select trees – trees with desirable growth and wood traits – could conceivably reduce demand on other sources of wood and fibre. In the medium term, tree varietals could be selected for site conditions or for other traits, such as disease and pest resistance.

Competition

The main alternative to GS is the traditional method of selecting and breeding seedlings and waiting for them to grow, which is current practice. It requires little initial capital investment and is still more accurate for predicting wood and growth traits but it requires a much longer lead time.

Other techniques are also being developed to reproduce highly valued, fast-growing trees on a commercial scale. These techniques may be used with GS to improve its efficiency or they may be used separately. Somatic embryogenesis is one technique that allows for the production of unlimited quantities of identical genetic copies from a single seed embryo. Combined with the GS technique, this technique will allow rapid identification and mass production of high-quality seedlings.

Why this matters

The forest industry is moving away from treating individual trees as commodities. The future of the business is marketing particular traits as required by end-users, instead of organizing logs by grade and species.

For seed orchards, GS will be an important tool for meeting the demands of this new model in the forest industry. Speeding up the selection of new seedlings allows seed orchards to select seedlings with desirable characteristics according to market demand. Also, they can duplicate trees with those characteristics much more quickly than previously possible. In this way, GS will support the transformation of the forest sector and ensure its continued competitiveness by speeding up response to market demand for particular fibre types.

GS will be a key tool in creating and sustaining the inventory of tomorrow's trees as the forest sector transforms and fibre properties become more important.

January 2015