

Using Genomic Selection for Tree Improvement

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Breeding healthy and resilient seedlings is a key part of successful reforestation. Selecting the best trees as a seed source is a key part of this process. However, **conventional tree improvement methods** are struggling to keep up with a rapidly-changing climate and frequent insect outbreaks. After decades of genetics research, **genomic selection** has emerged as a tool that could provide well-adapted seedlings in a much shorter time frame. This technology represents a paradigm shift from a phenotype-driven, to a genomics-based data-driven process.

What is Genomic Selection?

Genomic selection is a method that predicts associations between genetic markers and phenotypic traits of interest (e.g., height, insect resistance) based on models. This method allows tree breeders to precisely identify which trees have the most desirable genetic characteristics to produce seed for reforestation.



How Does Genomic Selection Compare to Other Methods of Selecting Trees?

NATURAL REGENERATION

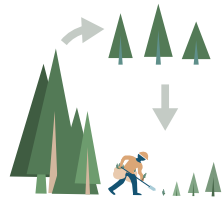


NATURAL REGENERATION

- Trees recolonize the site naturally.

ARTIFICIAL REGENERATION

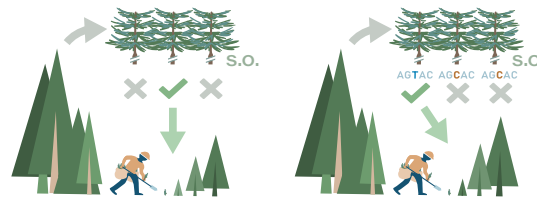
WILD SEED COLLECTIONS FROM SEED ZONES



PLANT WILD SEEDS AS-IS

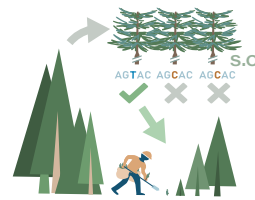
- Seedlings are produced from wild seeds and planted.
- *i.e., Stream 1 seed.*

IMPROVED SEED COLLECTIONS FROM SEED ORCHARDS (S.O.)



CONVENTIONAL BREEDING

- Repeated cycles of breeding and progeny testing to select for desired traits.
- Trees are selected for breeding based on phenotype and statistical models.
- Testing times are long, with breeding, testing and selecting taking decades.
- *i.e., Stream 2 seed.*



GENOMIC SELECTION

- Uses phenotyping and genotyping to find associations between genetic markers and desired traits.
- Trees are selected based on a more detailed understanding of the genetics in candidate trees.
- Bypasses the additional progeny testing of at least one subsequent generation in the tree improvement cycle.
- *i.e., Stream 2 seed.*

GENETIC ENGINEERING



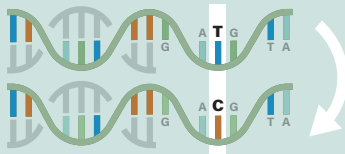
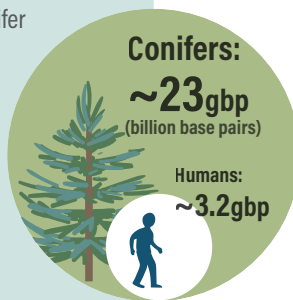
GENETIC ENGINEERING

- **NOT** a part of the genomic selection process.
- Involves directly manipulating DNA (e.g., inserting genes from another species) to produce a modified organism.
- Currently not allowed in Alberta for trees.

How Does Genomic Selection Work?

A genome is the entire genetic material of an organism. As a human, your genome comprises all of the DNA in all of your 23 pairs of chromosomes. Conifer trees typically have fewer chromosomes than humans — e.g., 12 — however, their chromosomes are much larger than ours.

Genomic selection involves examining tree genomes for SNPs: single nucleotide polymorphisms. A SNP is a place in the genome where one nucleotide differs between individuals.



These two DNA strands differ by a single nucleotide — known as a SNP.

While many SNPs have no effect on phenotype, some may affect observable traits directly or, more frequently, be closely associated with nearby regions of DNA that affect a given trait. In a few cases, the presence of a single SNP in an individual's genome might reliably predict their appearance, such as what eye colour they might have. However, most traits of interest in tree improvement, such as height, are the result of the complex interplay of many genes and their environment. This complexity makes it difficult to predict how traits will pass down from one generation to the next. Genomic selection allows us to find out what combinations of SNPs are associated with an individual's genome and trait phenotype.

By modeling these associations through an intensive computer process, we can predict the future phenotype of a seedling (e.g., its height or wood density) simply by knowing what combination of SNPs it has. Similar modeling of SNPs is used in DNA ancestry testing, testing for genetic diseases and in animal and plant breeding.

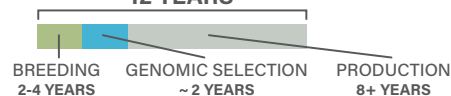
What Can Genomic Tools Offer?

- **A dramatically shortened breeding cycle.** By cutting out potentially one generation of progeny testing, genomic selection can accelerate the tree improvement process by up to 20 years. This improved efficiency could result in economic savings over the long term and more rapid selection and deployment of drought resilient and insect resistant seedlings for reforestation.

CONVENTIONAL BREEDING CYCLE: ~ 30 YEARS



GENOMIC SELECTION CYCLE: ~ 12 YEARS



- **The ability to select for additional traits** we couldn't select for before, particularly those traits that cannot be measured in young trees (e.g., wood density, insect resistance).
- **Increase forest productivity and health** by selection of trees from a larger population of candidate trees.
- **Better understanding of family relationships** among trees (i.e., which trees descended from which parents), can enhance the assessment of genetic traits, genetic progress across generations and genetic diversity.