CEDaR: Cedar Enhanced Durability and Resistance

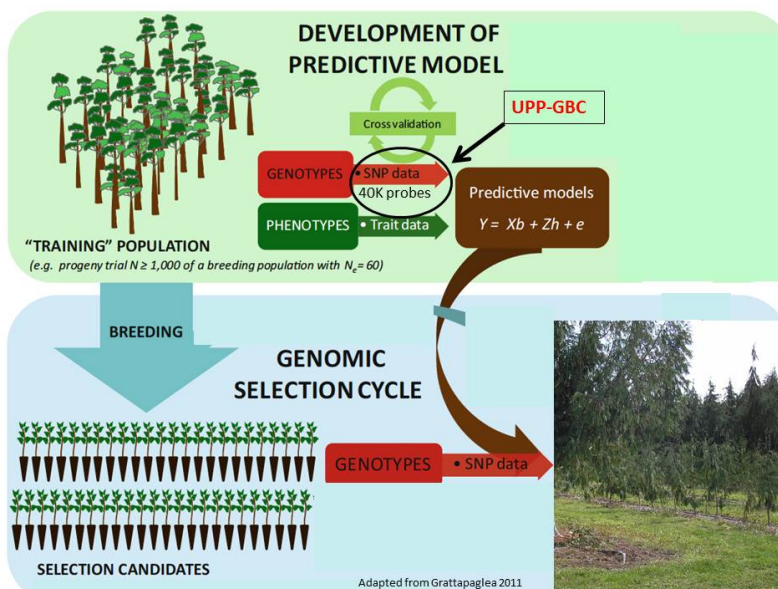Western redcedar (cedar) is a long-lived tree species and known as the "Tree of Life" to Coastal First Nations peoples. Cedar's unique wood characteristics, including low weight and rot resistance, make it superior for outdoor products such as roofing, decks, fences and siding. Its durability is derived from extractives deposited in heartwood, which takes decades to develop. Second-growth stands therefore contain less durable wood and less volume per hectare compared to old-growth forests. Pathogens, ungulate damage, and climate change also threaten the sustainability of cedar and the $1.3B export industry it supports.

Dr. John Russell, the Ministry's cedar geneticist, and Dr. Joerg Bohlmann, Professor Michael Smith Laboratories, UBC, have partnered with Genome Canada, Genome BC, Interfor, Island Timberlands, TimberWest, Western Forest Products, and FPInnovations to improve the genetic quality of the ~8M cedar seedlings planted annually on BC's west coast.

This CeDAR project aims to develop genomic selection (GS) predictive models and apply them to the second-generation breeding population to identify trees with faster growth, more extractives, and better pest resistance. Recent advancements make GS more feasible, faster, and cheaper than traditional breeding methods – which can take 30-40 years to test and select trees for mature wood traits in large expensive field-tests.

Genomic-selected trees will be incorporated into cedar seed orchards managed by the project's partners and used to produce seed for reforestation. Planting GS seedlings will save forest companies ~$30M/year in browse protection and site rehabilitation costs. GS seedlings will also increase the resilience, productivity, and value of BC's cedar forests for future generations.

For more information on the CeDAR project, visit http://mrjeff.net/cedar/

DEVELOPMENT OF PREDICTIVE MODEL

Cross validation — UPP-GBC

GENOTYPES • SNP data 40K probes

PHENOTYPES • Trait data

Predictive models $Y = Xb + Zh + e$

"TRAINING" POPULATION
(e.g. progeny trial N ≥ 1,000 of a breeding population with N_e = 60)

BREEDING

GENOMIC SELECTION CYCLE

GENOTYPES • SNP data

SELECTION CANDIDATES

Adapted from Grattapaglea 2011

What is genomic selection?

Genomic selection (GS) consists of extracting and screening the DNA of 1000s of individuals in a large "training population" to identify single nucleotide polymorphisms (SNPs) associated with desired phenotypic traits observed in that population. A predictive model is developed and used to select seedlings based exclusively on their genotype in a target, related population. GS has been successfully used in animal breeding, notably dairy cattle, and eucalyptus and loblolly pine, and is under development for white spruce, Douglas-fir and other pines. (UPP-GBC = Genome BC's User Partnership Program.)

Top left: Heartwood rot in cedar logs.

Top right: Dr. John Russell examining a cedar progeny trial.

Bottom: Collecting foliage for DNA from target population seedlings.

Photos: John Russell