

Genomic Selection in Western Redcedar Breeding Program in BC: From Proof of Concept to Application

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Objective

Deliver elite selections to industry seed orchards decades ahead of traditional breeding methods using GS.

WRC Improvement Program in British Columbia

- **Growth** (selection age 7-year-old)
- **Heartwood durability**: Phenotyping for durability related heartwood extractives (selection age **25-year-old**)
- **Deer browsing resistance**: Phenotyping for resistance related foliar extractives (selection age 1-year-old)

Project Description

FITTING models

Training population (PX progeny trial, 21 males)

- 45 Parents trees
- 1,520 trees (26 PX: polycross families)
- 3 sites
- Phenotyped (3 traits) + genotypes

VALIDATING models

- A. Training population (cross-validation) All traits
- B. Target population (independent-validation) Foliar extractives

PREDICTING growth & heartwood traits

Target population (1-year-old)

- 3,000 seedlings (168 FS families)
- Phenotyped (foliar extractives) + genotypes
- Each seedling in the target population is sharing one or both parents with the training population
- 45K filtered SNPs (genic and non-genic)

1. Pedigree Reconstruction Using Genomic Relationship Matrix

- To convert the **training population** (N=1520) from **PX to FS** (Full-Sib) by identifying male parent
- Results revealed unequal contribution for the 21 males (Range: 7-187 offspring/male, mean = 68)
- We identified **438** unbalanced small FS families (Range: 1-15 offspring/FS family, mean= 3.3)

2. Compare Traditional PX-pedigree Analysis (ABLUP) to Genomic (GBLUP) in Training Population

Genomic analysis resulted in:

- Increasing the **selection intensity** for **backward selection** (selection from parents), as now we have the male breeding values too.
- Increasing breeding values accuracy by up to 22% and expected **genetic gain** by up to 35% for **forward selection** (selection from offspring).

3. GS Prediction Model (GBLUP) Validation in Training Population

A. Random 10% cross-validation (pooled sites)

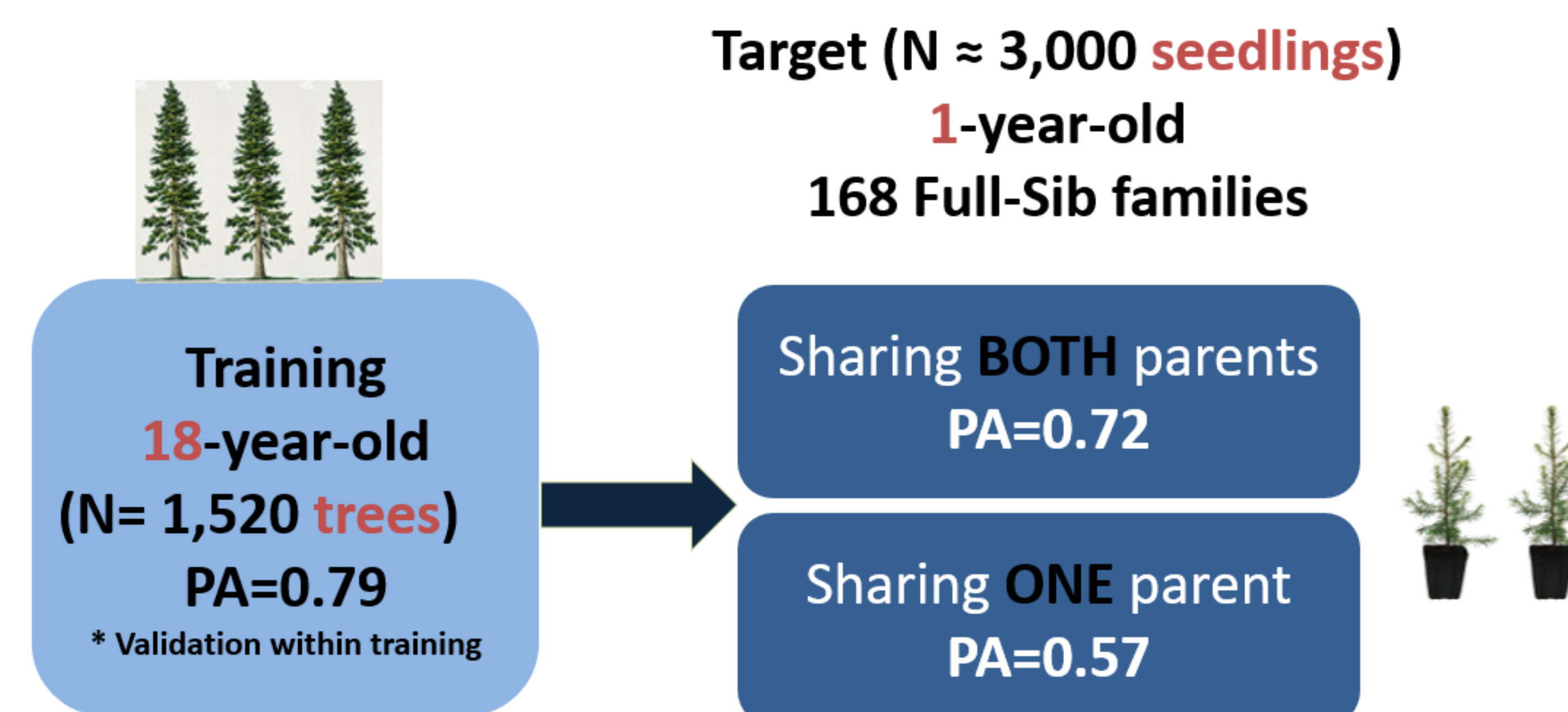
90% of the data were used to fit the model and 10 % to test the model

Trait	Height	Heartwood extractives	Foliar extractives
Prediction Accuracy (SE)	0.85 (0.001)	0.80 (0.002)	0.83 (0.001)
Heritability (SE)	0.13 (0.04)	0.20 (0.05)	0.25 (0.05)

B. Across-sites, -generations, and -ages cross validation

Small decrease in prediction accuracy

4. GS Prediction Model (GBLUP) Validation in Target Population



*Prediction Accuracy (PA): Correlation between measured and predicted phenotype for validation population

GS application

1. **Predicting breeding values (BVs) for growth and wood** resistance traits for the target seedling population
2. **Multi-trait selection** (Selection index: GROWTH, WOOD, foliar)
3. **Optimal selection** for best 100 individuals for seed orchard and field testing

Conclusions

As a general conclusion, **GS (molecular breeding)**, has two main advantages:

1. **Training population** → In the presence of measured phenotypes from an old progeny trial, genomic analysis resulted in **increasing BV accuracy** and genetic gain. In our project we overcome the limitation of **PX** mating design, which is only designed for **backward selection** from the female parents, but now we can select from the dad's parents too, and due to the significant increase in offspring BV accuracy we used it for **forward selection**, which was not possible in traditional pedigree analysis.
2. **Target population** → **Predicting BV** at the seedling phase for **early selection** to eliminate the time required for progeny trials. In our project this advantage coupled with the fact that western redcedar **seedlings younger than one year can be reproductively induced, reduced the breeding cycle from 25 to only 2 years**, which increases the expected gain.

Acknowledgement

- Dr. Inanc Birol
- Mack Yuen
- Dr. Rod Stirling
- Dr. Jeremy Schmutz
- Dr. Jesse Breinholt
- Dr. Leandro Neves



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