IRC2/Project 4 - Fall 2021

SNP-BASED ANALYSIS FOR THE WHITE SPRUCE REGION I TREE IMPROVEMENT PROGRAM

Why it is important to perform genomic analysis in breeding programs?

Genomic analysis reveals the relationships between individuals (family structure) in the most precise method currently available (Fig.1A), allowing for the estimation of effective population size, pollen contamination, or for detecting errors. Also, genomic information more accurately identifies the differences between individuals within a family compared to pedigree analysis, and breeding values for each tree within a family can also be predicted with high precision (Fig.1B). These analyses will help ensure that only the best progeny is selected for further breeding and orchard development.

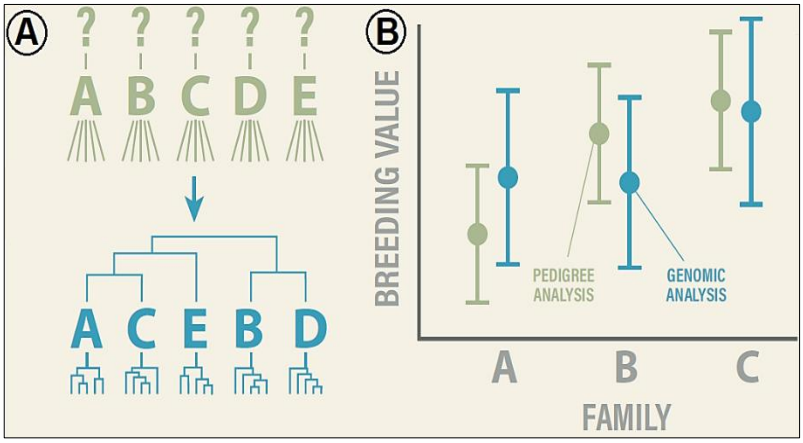

Figure 1. Schematic representation of two advantages when using genomic analysis: (A) identify precise family structure, (B) predict accurate individual breeding values within a family. https://resfor.ualberta.ca/resources/res-for-infographics/

2021 update

Sampling Region I parents

The Region I white spruce program has a single clonal orchard (G333) at HASOC, planted in 1998 with 174 genotypes (2,071 trees), and with an approved genetic gain of 2.0% height at rotation. In 2015, a total of 41 genotypes (496 trees) were rogued, increasing the genetic gain to 2.6% (height at rotation). The roguing was done based on 14-year-old progeny trial data. The orchard currently has 133 genotypes and 1,575 ramets. One hundred and seventy-four parent tree needle samples were collected in June 2021 from the G218B clone bank located at ATISC (Fig.2A). Newly flushed needles were collected using pole pruners (Fig.2B) and scissors cleaned with a 5% beach solution, and nitrile gloves to avoid contamination (Fig.2C). The samples were placed in pre-labelled plastic bags (Fig.2D) and stored in a cooler containing freezer packs (Fig. 2C). All samples were delivered to the Molecular Biology Services Unit (MBSU) at the University of Alberta for DNA extraction in July 2021.

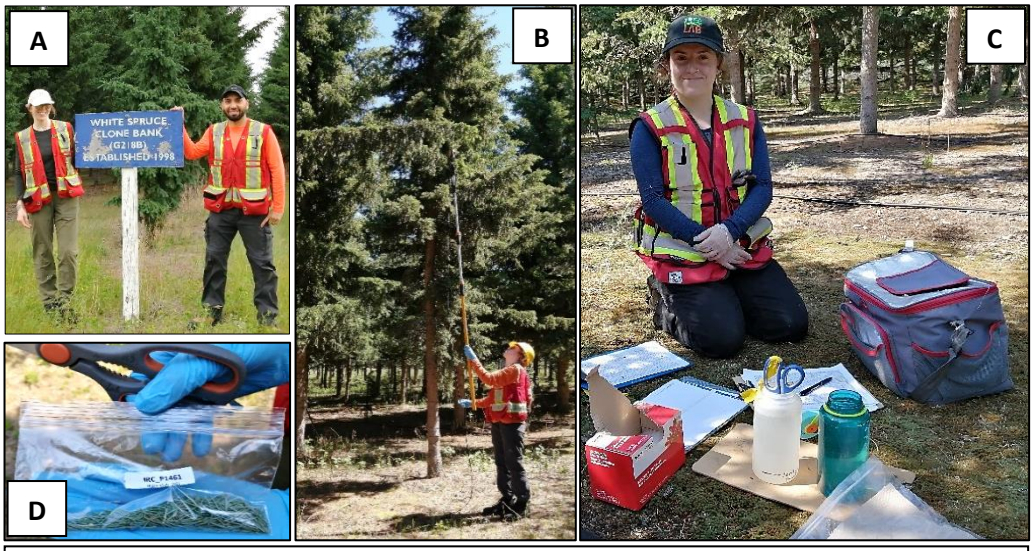

Figure 2. (A) Kennedy Mitchell (summer technician, left) and Esteban Galeano (Research Associate UofA, right) at the G218B clone bank, (B) Kennedy using the pole pruner, (C) Romy Suliteanu (summer technician) using the different materials for the needle collection, (D) Needle sample.

Sampling Region I progeny trial

There are five progeny trials (G354A-E) associated with the Region I program (phase 1) that were established in 2001, with 306 seedlots (46 seedlots are not part of the breeding population). In April 2021, the Thomas lab selected the top 70 families based on the breeding values obtained from Andy Benowicz's (Government of Alberta) analysis using the 14-year-old progeny trial data (2015). Between June-August 2021, we labelled each tree selected (Fig.3) and collected needles as described above (Fig.2C, Fig.3C). In total, we collected 10 trees/family at the G354E trial (Linaria farm). We had originally planned to collect from two progeny trial sites (G354D&E), however, trees at the G354D site were heavily infested with needle rust thereby compromising the DNA collections from this site. All 700 samples were delivered to the MBSU for DNA extraction in August 2021.

Figure 3. A) G354E trial, Linaria farm. (B) Labelling of sampled trees. (C) Esteban using the pole pruner.

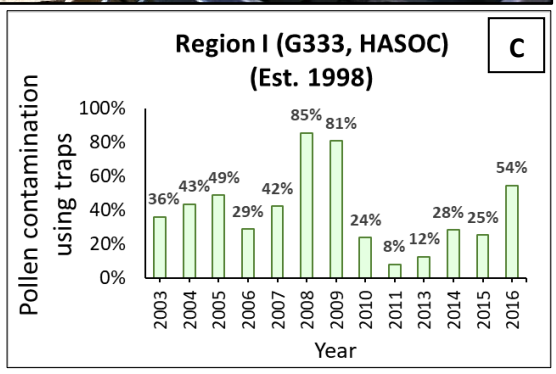

Figure 4. A) Seedlings from the Region I orchard, grown from May to August 2021, from the 2006, 2009, 2010, 2011, 2013, 2015 seedlots. (B) Each seedling was harvested for DNA extraction. (C) Pollen contamination levels from the Region I orchard, estimated using pollen traps, between years 2003-2016. Est.=year of establishment.

Greenhouse seedling samples

A total of six seedlots from the G333 orchard (seeds provided by ATISC), corresponding to the 2006, 2009, 2010, 2011, 2013, 2015 years were sown the first week of May 2021 at the Plant Growth Facility (PGF), Agriculture/Forestry Centre, University of Alberta (Fig. 4A-B). From each year, approximately 120 seedlings were harvested after four months of growth and delivered to the MBSU for DNA extraction in August 2021.

What are the next steps?

The DNA extracted from all 1,594 samples will be delivered to Neogen in November for genotyping. In 2022, we will identify parentage to enhance genetic parameter estimates and genomic estimated breeding values, using the genotyping from parents and the progeny trial. We will also estimate the effective population size in each of the six open-pollinated seedlots, and verify the pollen contamination levels reported previously (Fig.4C), using the genotyping from parents and seedlots. The additional information provided through the adoption of molecular tools will continue to enhance breeding program development in Alberta increasing the accuracy of BVs, pollen contamination and effective population size estimates.

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