

Resilient Forests (RES-FOR): Climate, Pests & Policy - Genomic Applications



Barb Thomas
University of Alberta
Feb. 15, 2019
Oklahoma

Genome Canada LSARP Grant

Resilient Forests (RES-FOR): Climate, Pests & Policy

– Genomic Applications

October 2016 – September 2020

- Integrating traditional tree improvement with new ***genomics based selection***
- Introducing new high throughput phenotypic (phenomics) measures for assessing responses to biotic (insect) and abiotic (drought) stresses
 - Eg: terpenes, metabolomics, ecophysiology
- Outreach, collaboration, policy, economics & understanding social acceptance of this emerging application in forest tree breeding
 - typically a conservative bunch

Project Lead, Co-Leads & Manager



Barb Thomas



Nadir Erbilgin



Yousry El-Kassaby



Stacy Bergheim

RES-
FOR
Team

End-Users & Collaborators



Lee Charleson



Barry White



Shane Sadoway



Vashti Dunham



Jeff Morris



Dave Swindlehurst



Andy Benowicz



Deo Rweyongeza

Natural Science Researchers



Charles Chen



David Wishart



Andreas Hamann



Shawn Mansfield



Uwe Hacke

Social Science Researchers



Debra Davidson



Gwen Blue



Julie Cool



Henry An



Chris Gaston

RES-FOR Staff & HQP Update

Name	Role	Supervisor
University of Alberta		
Stacy Bergheim	Project Coordinator	Barb Thomas
Xiaojing Wei	PDF	Barb Thomas
Jana Bockstette	Research Assistant	Barb Thomas
Ryota Kawamura	Research Assistant	Barb Thomas
Jennifer Klutsch	PDF	Nadir Erbilgin
Guncha Ishangulyyeva	Research Technician	Nadir Erbilgin
Chris Arbter	Research Assistant	Nadir Erbilgin
Sudarshana Bhumireddy	PDF	David Wishart
Carin Li	RF-LIMS Bioinformatician	David Wishart
Anthony Fisher	MSc Student	Debra Davidson
Hannah Cunningham	MSc Student	Debra Davidson
Shuo Wang	MSc Complete	Henry An
University of Calgary		
Kristy Myles	MSc Student	Gwendolyn Blue
University of British Columbia		
Wei-Yew Chang	Research Associate	Julie Cool
Letitia Da Ros	PDF (gone)	Shawn Mansfield
Blaise Ratcliffe	PhD Candidate	Yousry El-Kassaby
Eduardo Cappa	Research Associate	Yousry El-Kassaby
Oklahoma State University		



Agriculture
and Forestry



GenomeAlberta



GenomeCanada



GenomeBritishColumbia

\$5.6M total funding



BLUE RIDGE LUMBER INC.
A SUBSIDIARY OF WEST FRASER MILLS LTD.



Grande Prairie Timberlands
Pembina Timberlands



West Fraser Mills Ltd.

Hinton Wood Products



The Motivation.....

✓ CLIMATE CHANGE & MAINTAINING FIBRE SUPPLY

- Declining forests, extreme events
 - Fall-down effect from surge cutting after MPB (25%?)
 - Energy sector development and Caribou

✓ TIME

- Long rotations in the boreal regions (80-110yrs)
 - Traditionally long testing period for TI programs (14-25 yrs)
 - Running out..... need to adjust more quickly

✓ COST

- Long rotations (80-110yrs)
 - Long testing period in TI programs (14-25 yrs)
 - Slow gains

The Opportunity.....

✓ COLLABORATIONS

- Univ + Industry + Govt
- Funding: Genome Canada/Alberta/BC/ABInn+ others

✓ TIME

- Ideal to put research into practice (1st gen to 2nd gen)
- Technological advancements in sequencing
- Modeling of GEBV developed in the Ag. sector

✓ COST

- Genotyping is (relatively) cheap!
- Savings by reduced selection time (~20yrs) for 2nd gen.

✓ PROVIDE SOLUTIONS

- Keep industrial forestry on the landbase in Alberta

Tree Improvement is also...

- A method to manage risk
 - Reduce the time to harvest (rotation)
 - Testing to understand resilience of populations
 - Climate change, reclamation challenges (eg: salty sites)
 - Biotic – insects and diseases
 - Control of parentage from ‘preferred’ regions and tested populations
 - Science based seed transfer guidelines (progeny & provenance trials)

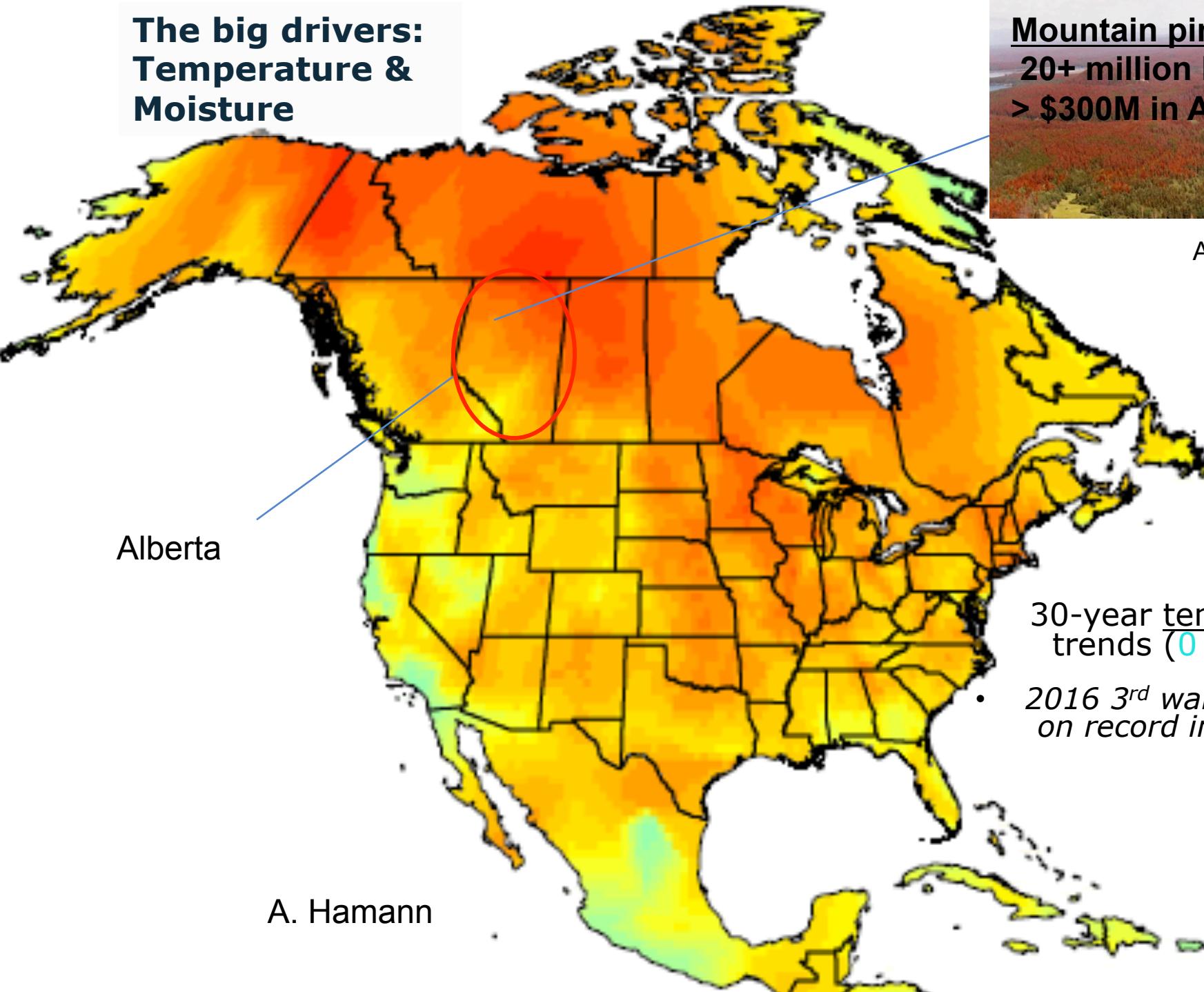


**Diminishing land-base with largest
oil sands deposits in the world in**



Rob Soroya

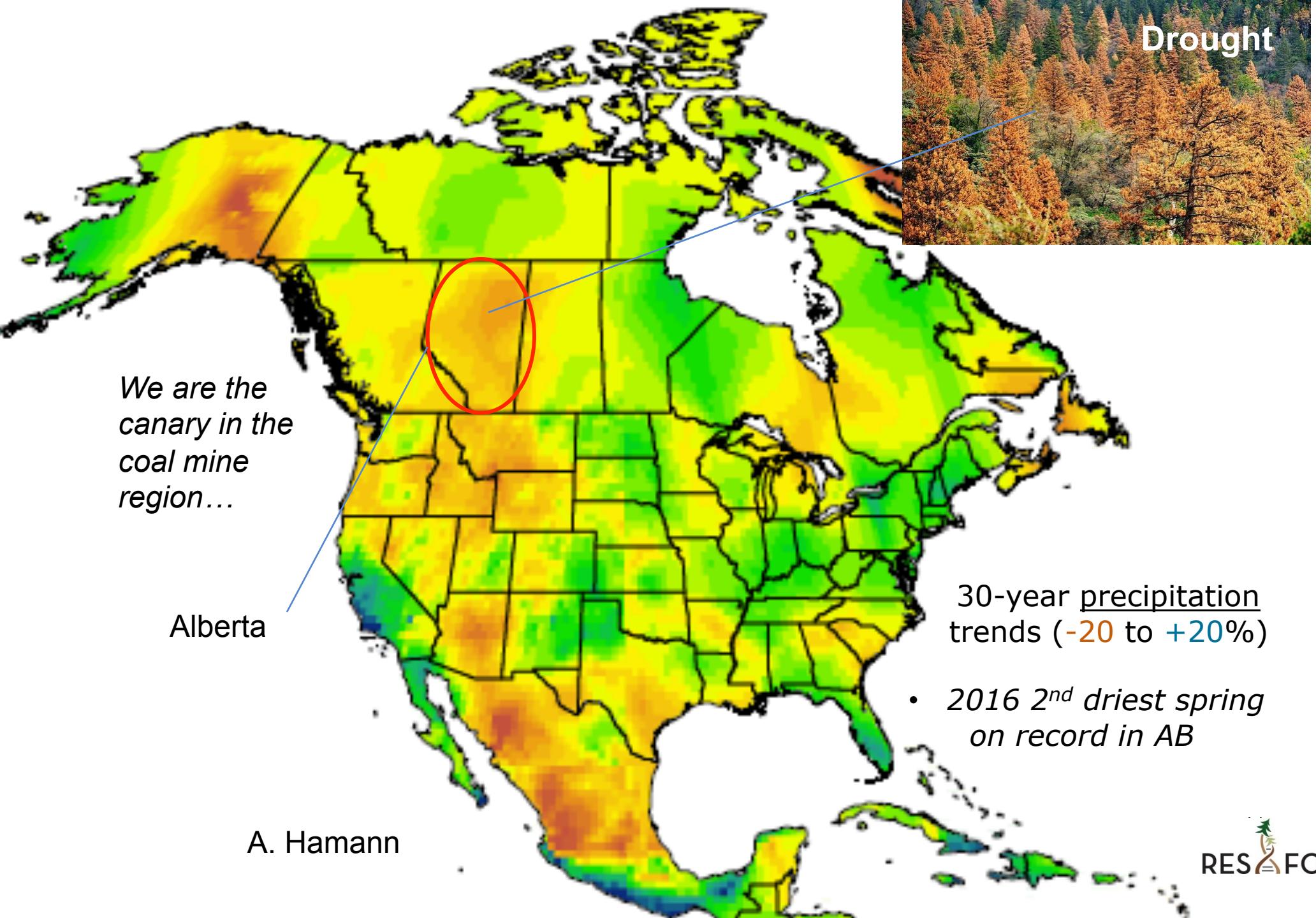
**The big drivers:
Temperature &
Moisture**



Mountain pine beetle:
20+ million ha
> \$300M in AB alone



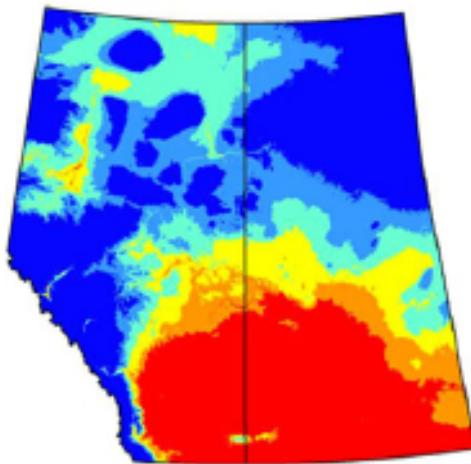
Allen et al. 2010



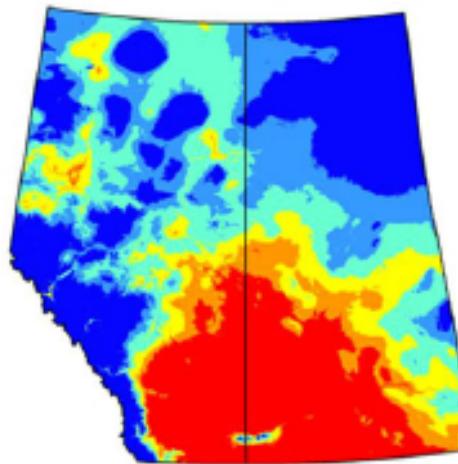
CMI = P – PET (precipitation – potential evapotranspiration)

+ve values = sufficient H₂O to sustain a closed canopy forest

(a) CMI 1961-1990



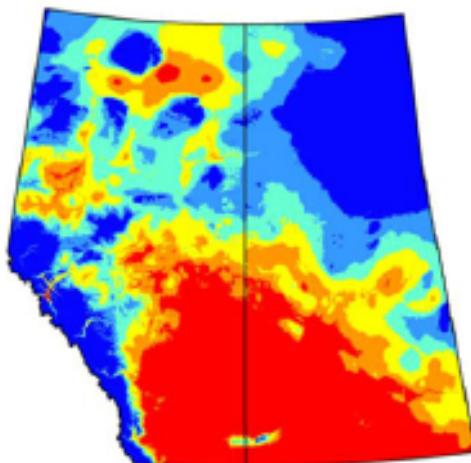
(b) CMI 1991-2000



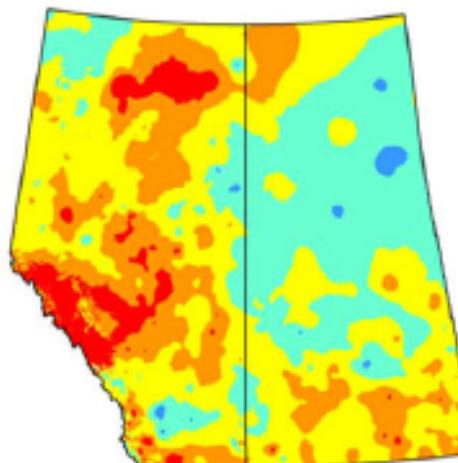
CMI

- <-10
- 10 to -5
- 5 to 0
- 0 to +5
- +5 to +10
- >+10

(c) CMI 2001-2010



(d) ΔCMI



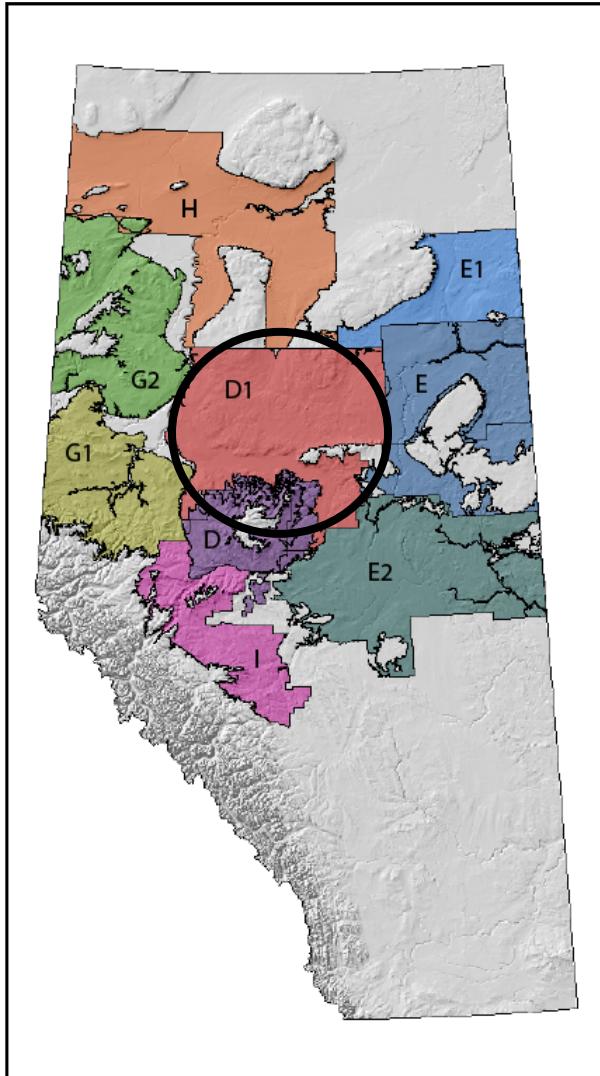
ΔCMI

- <-10
- 10 to -5
- 5 to 0
- 0 to +5
- +5 to +10
- >+10

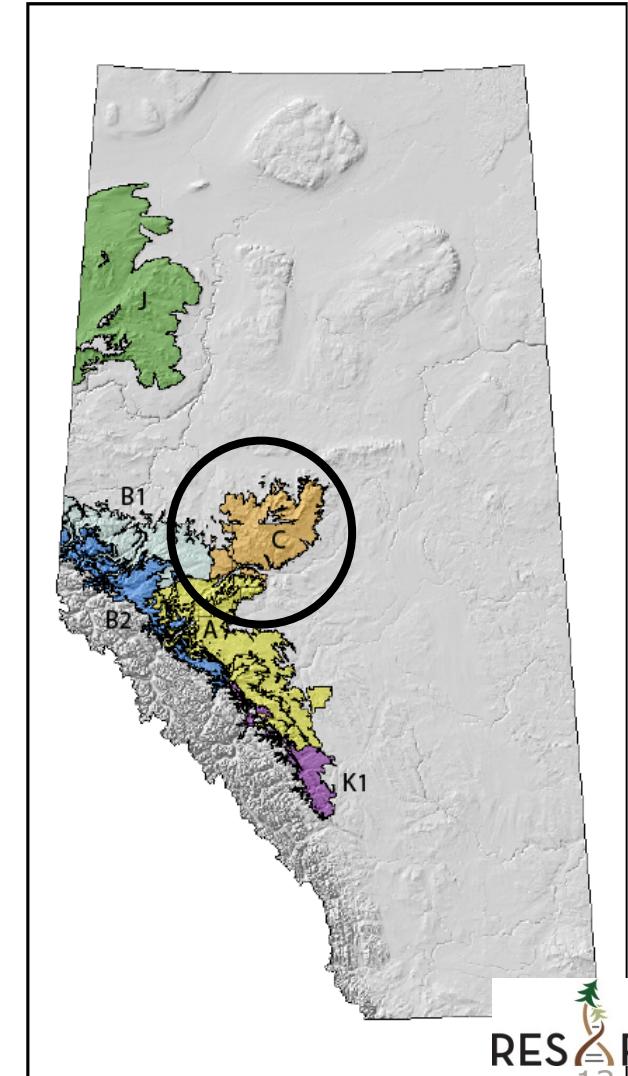
Spruce – Region D1(AAF)

Pine – Region C (BRL)

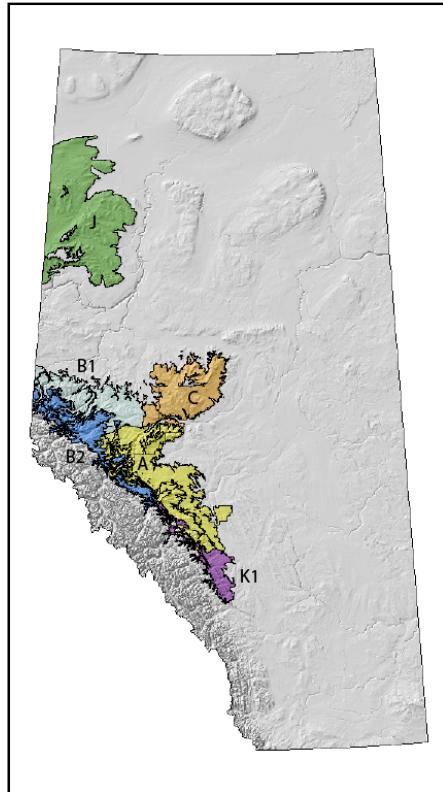
Existing programs needed:



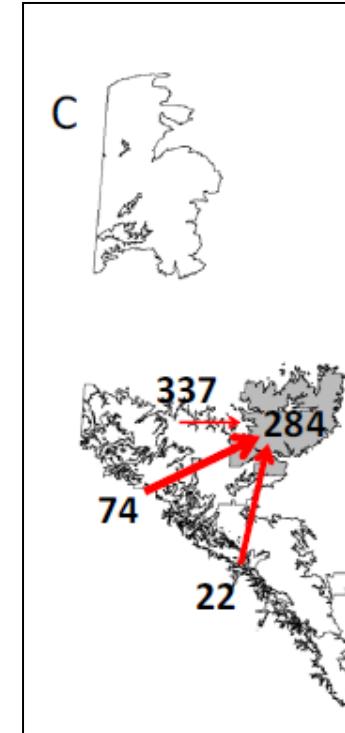
- ✓ 100+ families/species
- ✓ Existing breeding values for height
- ✓ 2+ progeny tests
- ✓ 30+ years of age
- ✓ Parent seed available for greenhouse trials
- ✓ Programs ready for (genomic) selection



Region C Lodgepole Pine

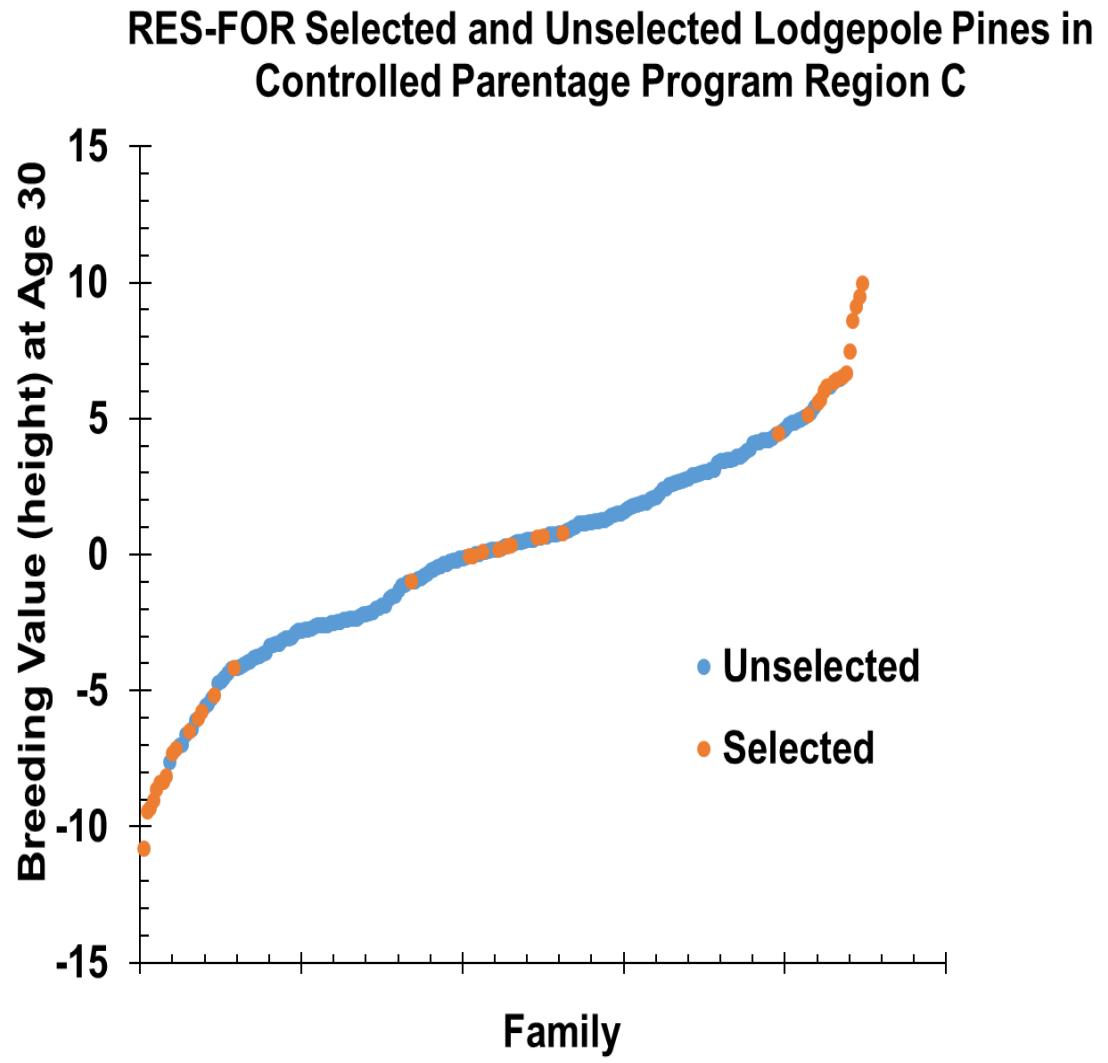
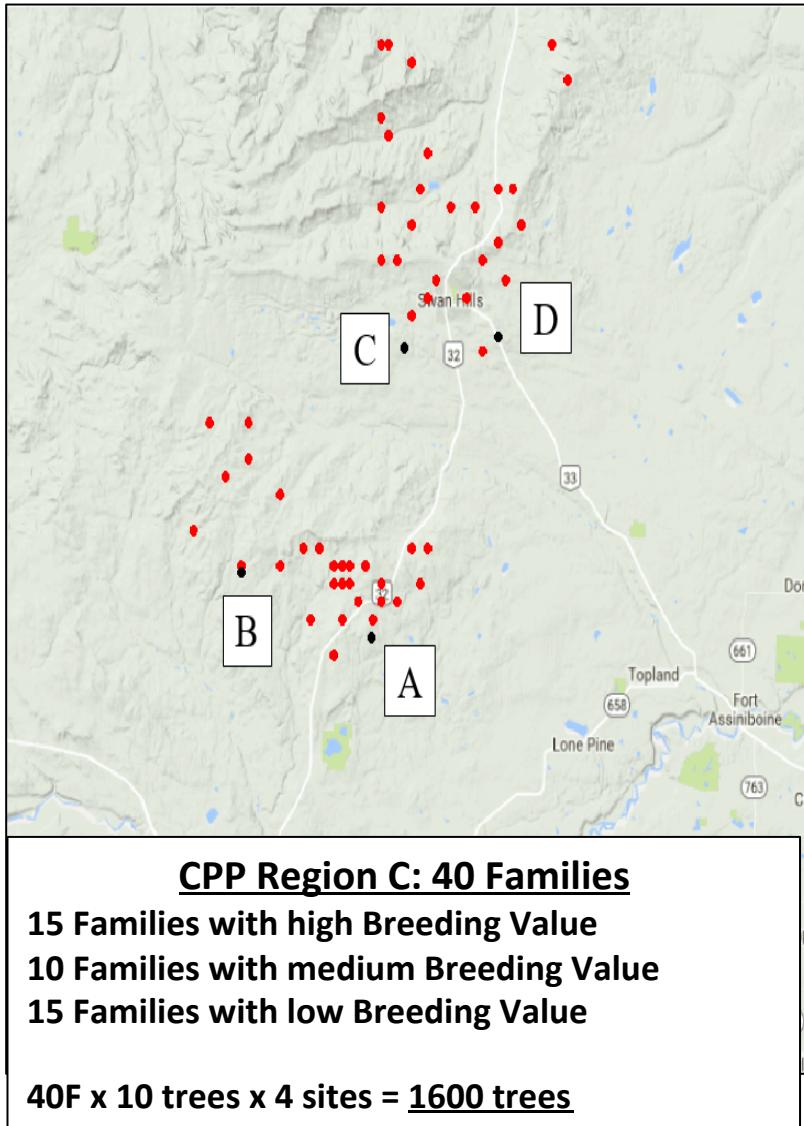


Gray *et al.* F. Ecol.
Mngt. 2016



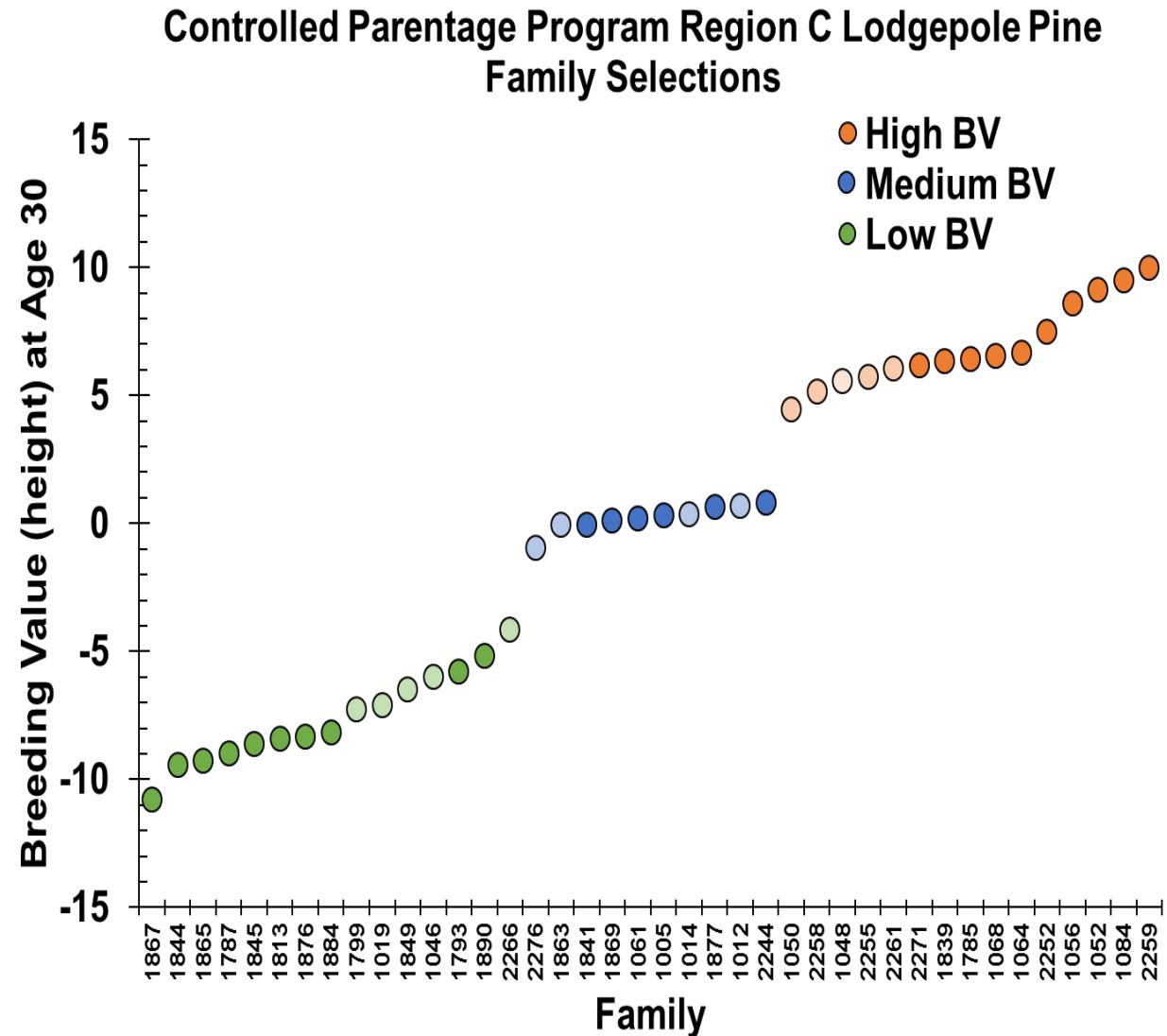
Understand & exploit what we have in our existing populations.

Seedlot Selections: Region C Lodgepole Pine (114 Fam.)



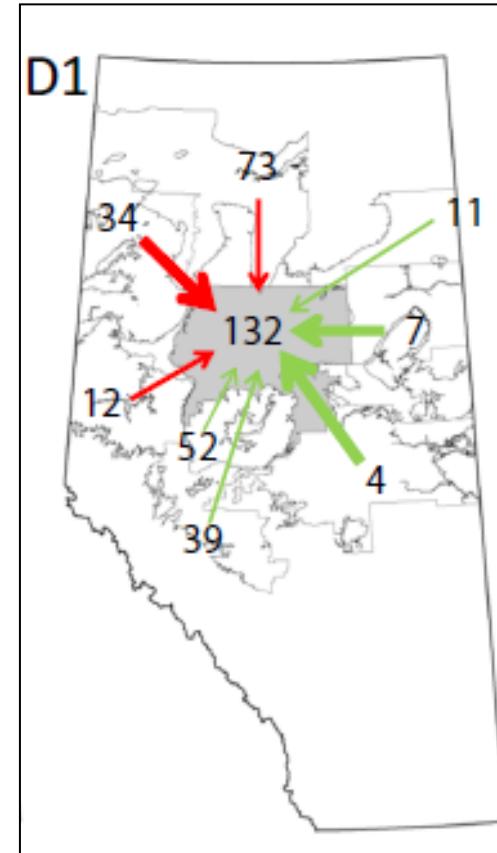
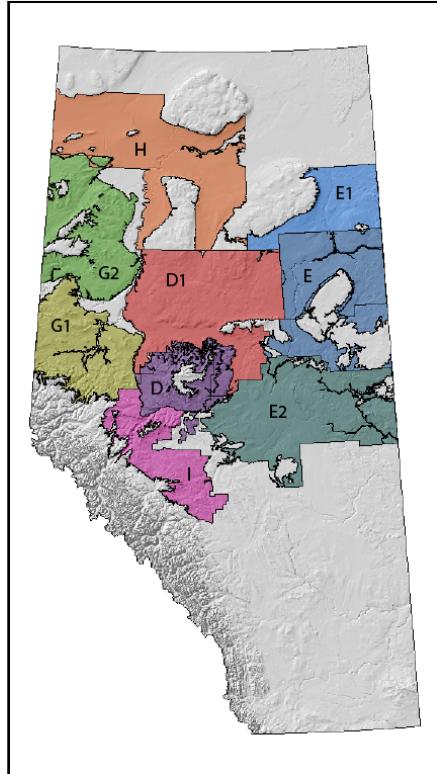
Seedlot Selections: Region C Lodgepole Pine

<u>Greenhouse Selections:</u>	
<u>20 families from 40</u>	
11 (8)	Families with high Breeding Value
6 (4)	Families with medium Breeding Value
10 (8)	Families with low Breeding Value
From darker dots selected: 8-4-8 target	



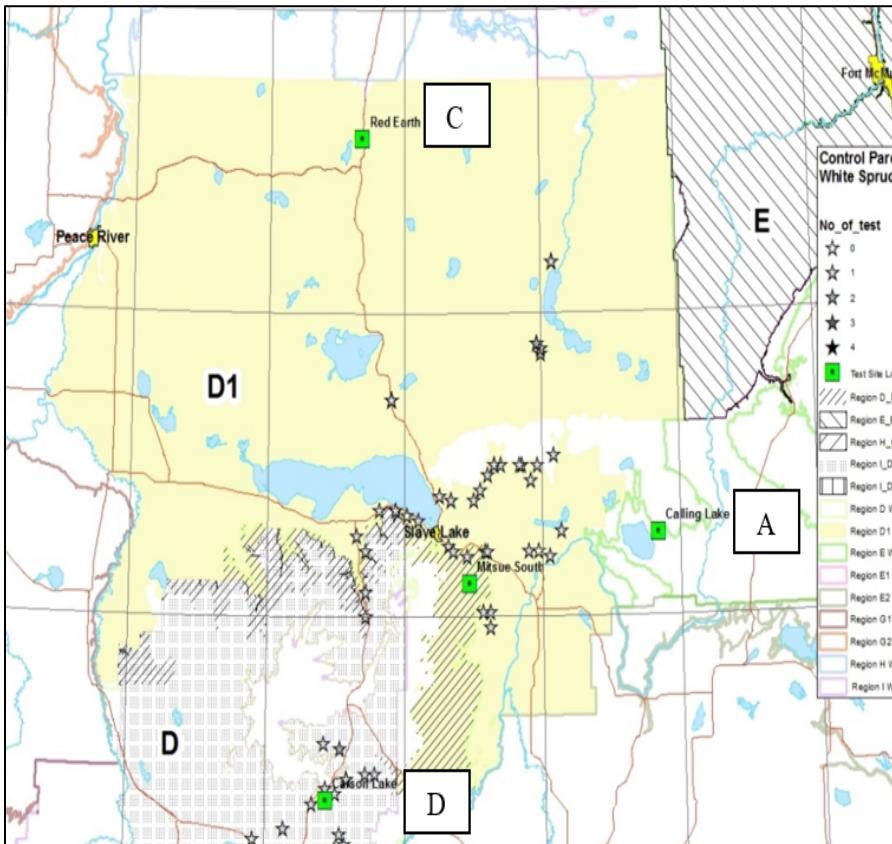
Region D1 White Spruce

Gray *et al.*
Tree Gen. & Genomes 2016



Understand & exploiting what we have in
our existing populations.

Seedlot Selections: Region D1 White Spruce (150 Fam.)

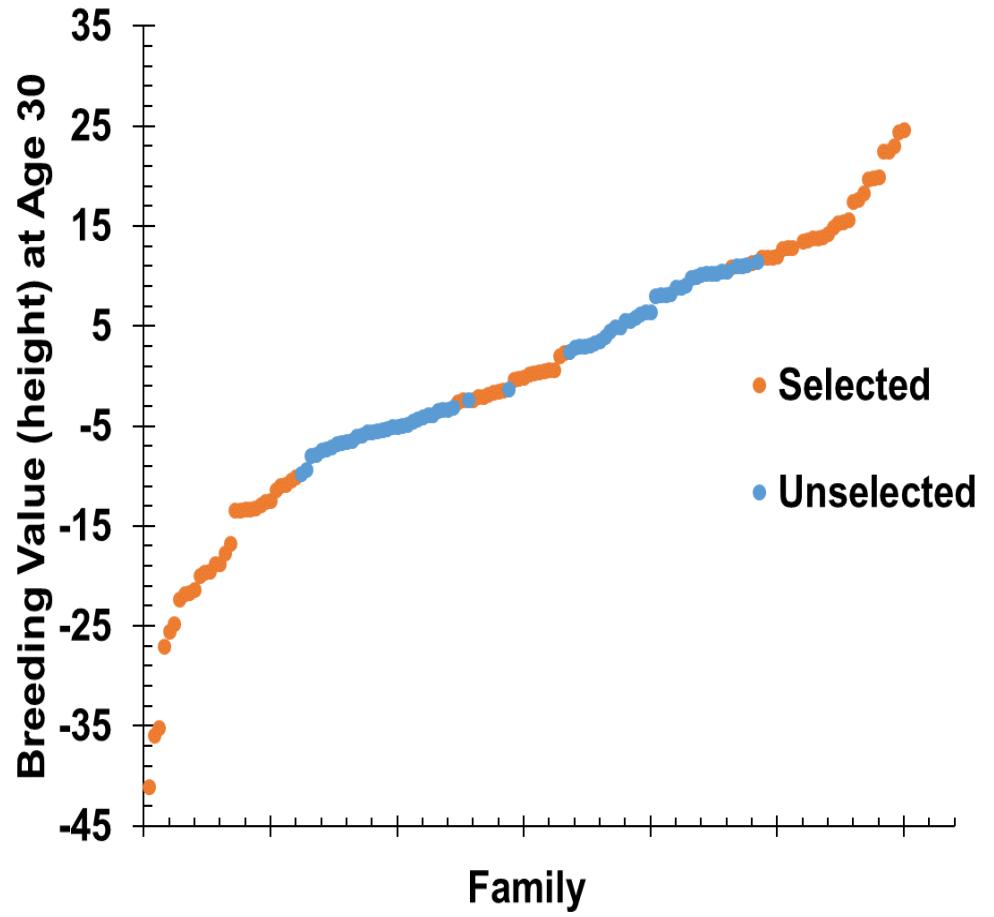


CPP Region D1: 80 Families

- 30 Families with high Breeding Value
- 20 Families with medium Breeding Value
- 30 Families with low Breeding Value

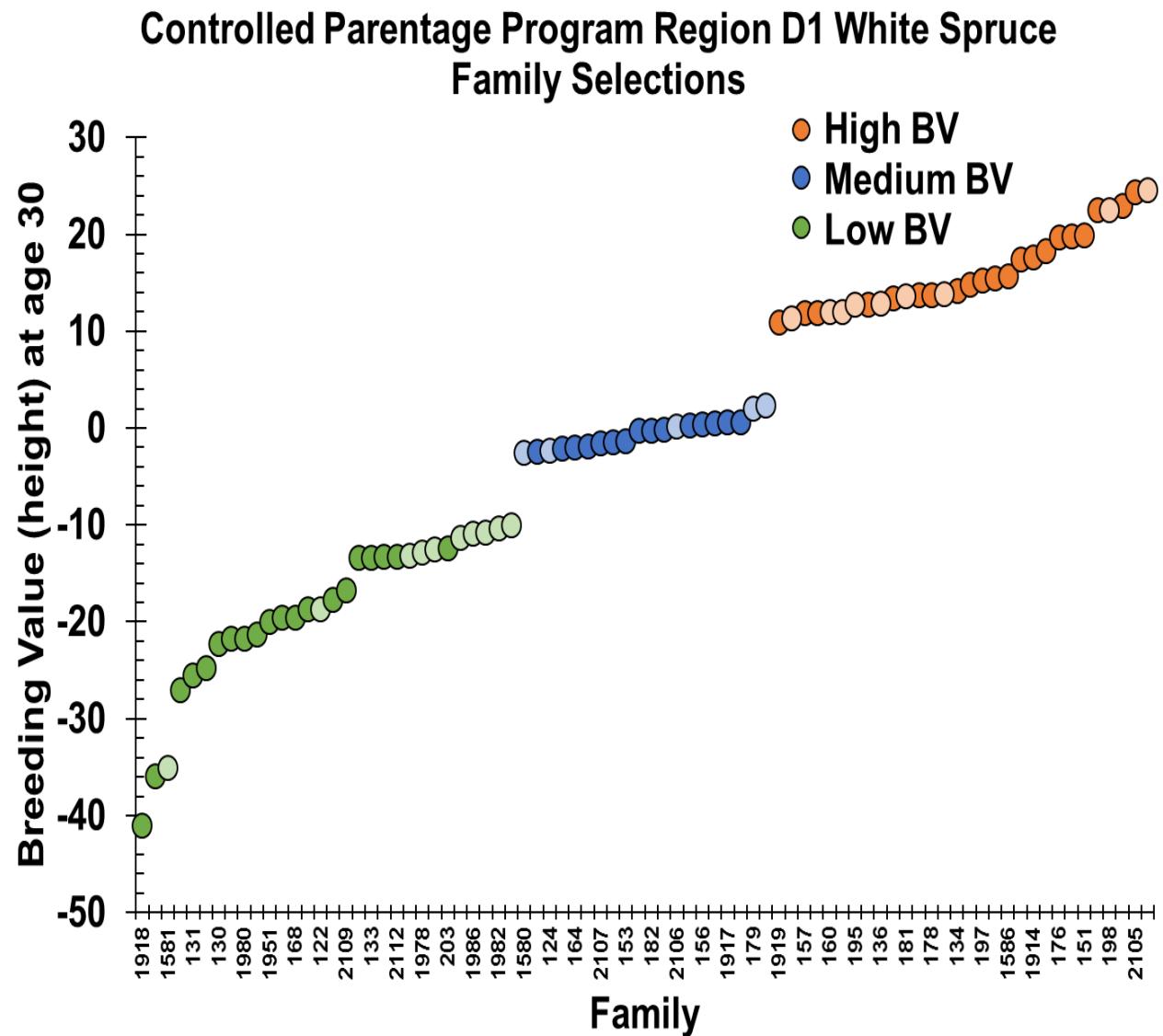
$$80F \times 8 \text{ trees} \times 2 \text{ sites} + 80F \times 4 \text{ trees} \times 1 \text{ site} = \underline{1600 \text{ trees}}$$

RES-FOR Selected and Unselected White Spruce in Controlled Parentage Program Region D1



Seedlot Selections: Region D1 White Spruce

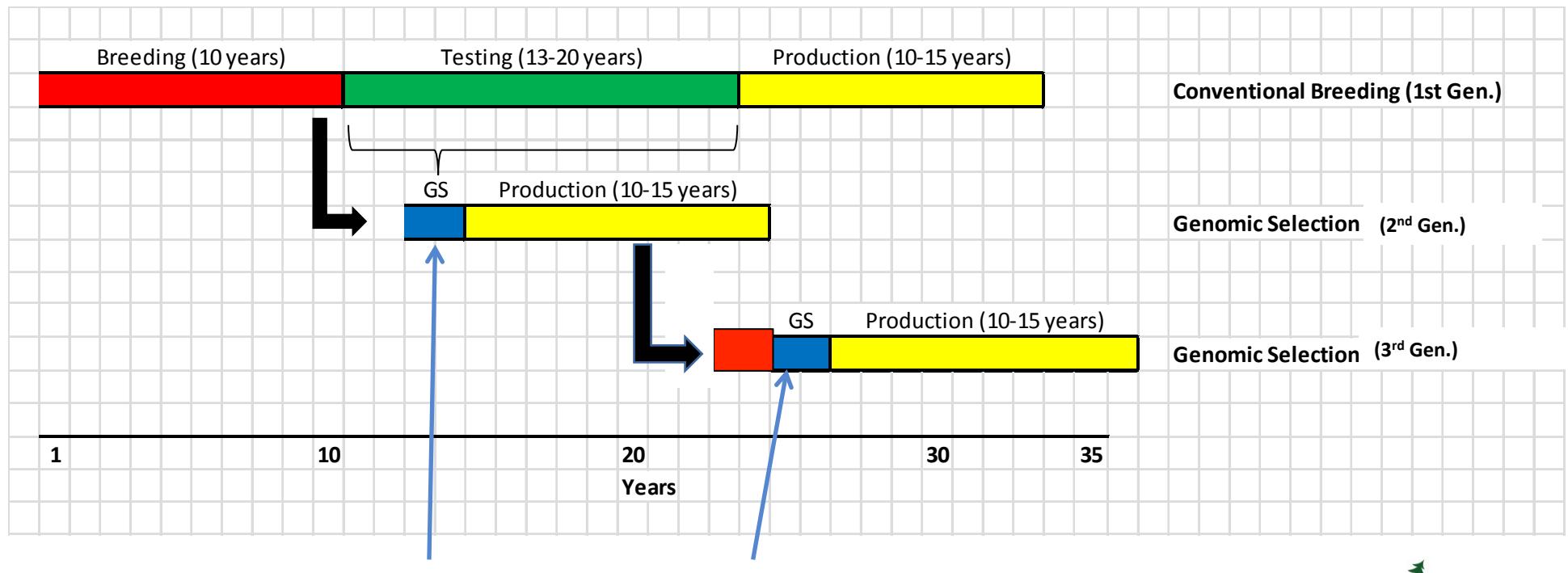
<u>Greenhouse Selections: 40 Families of 80</u>	
21 (15)	Families with high Breeding Value
15 (10)	Families with medium Breeding Value
20 (15)	Families with low Breeding Value
From darker dots selected: 15-10-15 target	



Application of Genomic Selection (GS)

-rapid response to selection with predictive models-
-timing ideal with existing C & D1 programs-

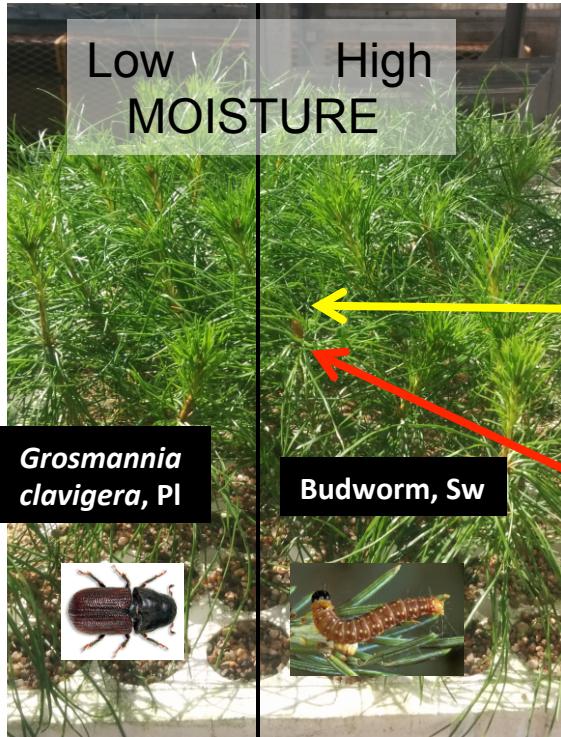
Can develop models for all phenotyping



[Replaces phenotyping with genotyping]

Genotyping & Phenotyping

Validation Population



- Height & caliper
- Drought
- Herbivory MPB & SBW } Induced responses
- Control – **Constitutive responses**
- Physiological, metabolomics
- Physical traits
- 500 Pl, 1000 Sw

40-80 families/sp

Genotyping

20-40 selected families/species

Training Population



- Height & DBH
- 3-4 progeny trials
- ~1600 trees/species
- Physiology, defensive & physical traits, ¹³C
- Wood density & MFA

RES-FOR Phenotyping



Conventional	Unconventional
<ul style="list-style-type: none">• Height• DBH• Wood density• Micro fibril angle	<ul style="list-style-type: none">• Constitutive vs induced chemical responses• ^{13}C (integrated WUE)• Ecophysiological assessments• Resin ducts• metabolomics• Exposure to biotic and abiotic stresses of original parent families (GH)

Data – All complete sets for GS

2017 Field Measurements – 3186 (Pine-40 families; Spruce-80 families)	
Full Set	Sub-set
DNA tissue	Gas Exchange – Ps, Gs, WUE
Height (All Progeny)	Resin Ducts (Sw-160/Pl-200; 20 families each)
DBH (All Progeny)	Global Metabolic Profiles (Sw-160/Pl-200; 20 families each)
Western Gall Rust (All Pine Progeny)	
Wood Density	
Microfibril Angle	5 mm cores
C13 – Integrated WUE	
Constitutive Chemistry (Terpenes/Phenolics)	

2018 Greenhouse Measurements – 1500 (500 pine – 20 families; 1000 spruce – 40 families)

Full Set	Sub-set
DNA tissue	Gas Exchange – Ps, Gs, WUE
Height	Resin Ducts (10 families each Sw & Pl)
Root Collar Diameter	
C13 – Integrated WUE	
Constitutive/Induced Chemistry	
Metabolic Profiles – 3 time intervals (Pl; 20 fam)	Metabolic Profiles – 3 time intervals (Sw; 20 fam)
Chlorophyll Fluorescence – 3 time intervals (Pl)	Chlorophyll Fluorescence – 3 time intervals (Sw)
Biomass	

Field data – Training populations

- Pine

- ✓ Four sites – All Height, DBH & WGR data cleaned, entered and uploaded to LIMS (~20,000 trees)
- ✓ DNA sequence (GBS) on ~1,600 trees

- Spruce

- ✓ Three sites – All Height, DBH & SBW data cleaned, entered and uploaded to LIMS (~15,000 trees)
- ✓ DNA sequence (GBS) on ~1,600 trees

✓ *All field sites re-walked and checked. Data is clean*

Unique Tree Number = Each tree will have a unique number as per the following table:

Pine RES-FOR Field Progeny	5000-6999
Pine Greenhouse Seedlings	7000-7999
Pine All remaining NON-RES-FOR Field Progeny	30000-50127

Unique Tree Number = Each tree will have a unique number as per the following table:

Spruce RES-FOR Field Progeny	1000-2999
Spruce Greenhouse Seedlings	3000-4999
Spruce All remaining NON-RES-FOR Field Progeny	10000-25071



Jesse Shirton collecting tissue





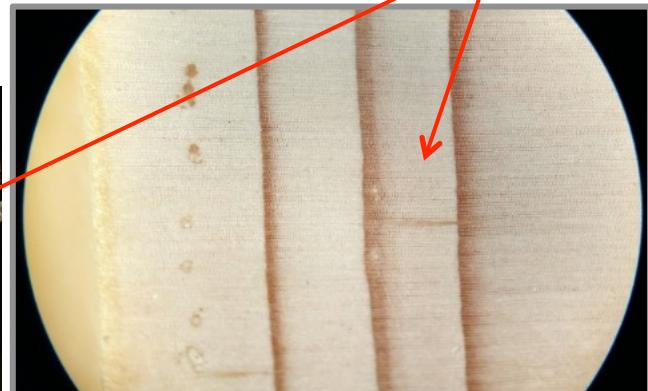
DNA sampling & extraction

>17,000 samples taken on ~ 3200 trees

(photos from the RES-FOR team)



Coring & cores



GH trial data – Verification populations

- Pine

- ✓ 500 trees in trial (All DNA sequenced)
 - ✓ All biomass weighing completed & data entry for roots/stems/needles

- Spruce

- ✓ 1000 trees in trial (All DNA sequenced)
 - ✓ All biomass dried & being weighed (R/S/N)

- ✓ All height, RCD measurements & VWC entered



Unique Tree Number = Each tree will have a unique number as per the following table:

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Spruce RES-FOR Field Progeny	1000-2999
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Greenhouse (2018)

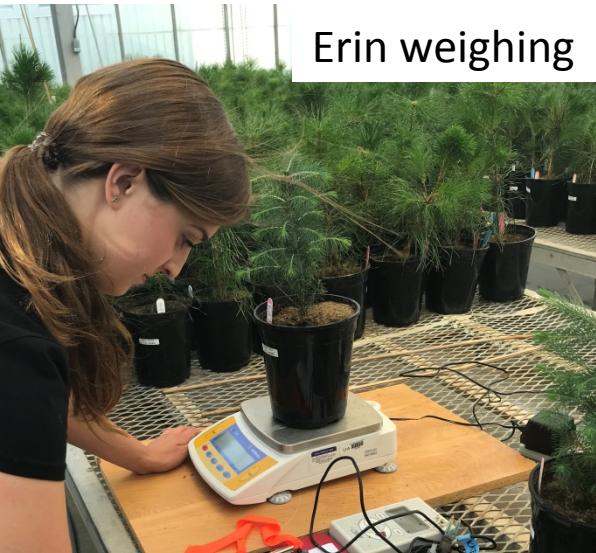
Fungal lesion
on pine



Chen with net for SBW



Erin weighing



Morgan harvesting



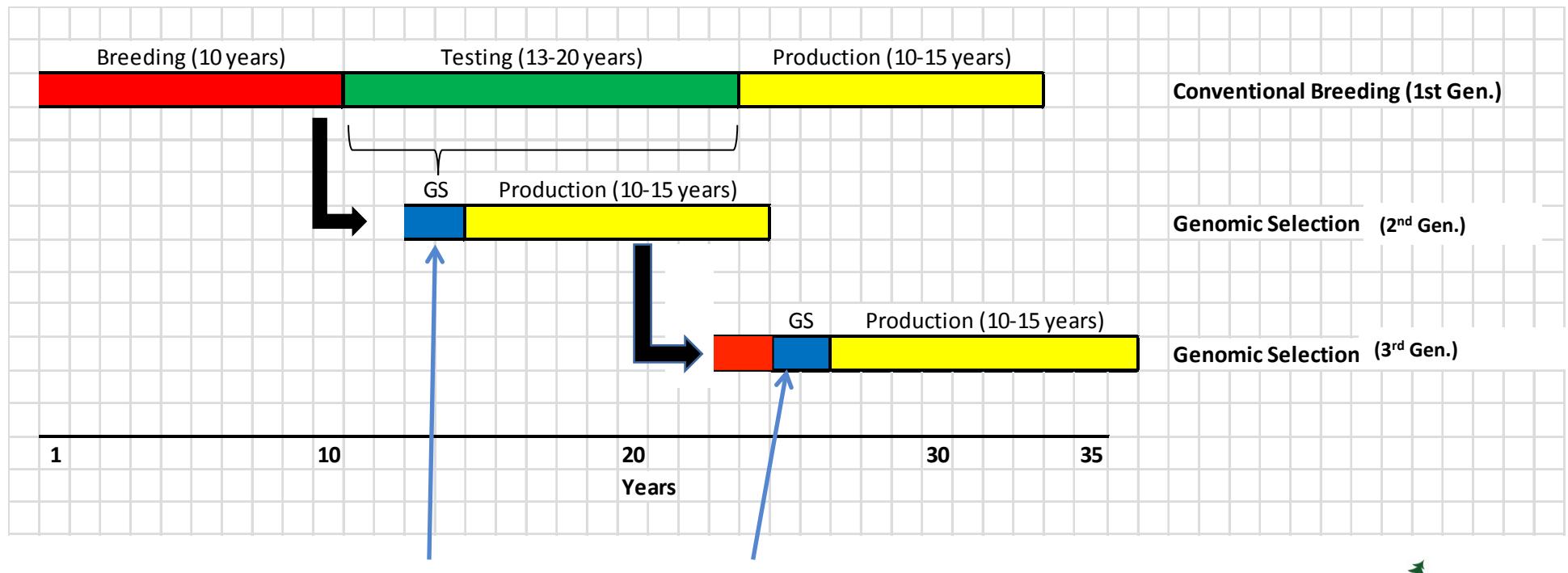
DNA collecting



Application of Genomic Selection (GS)

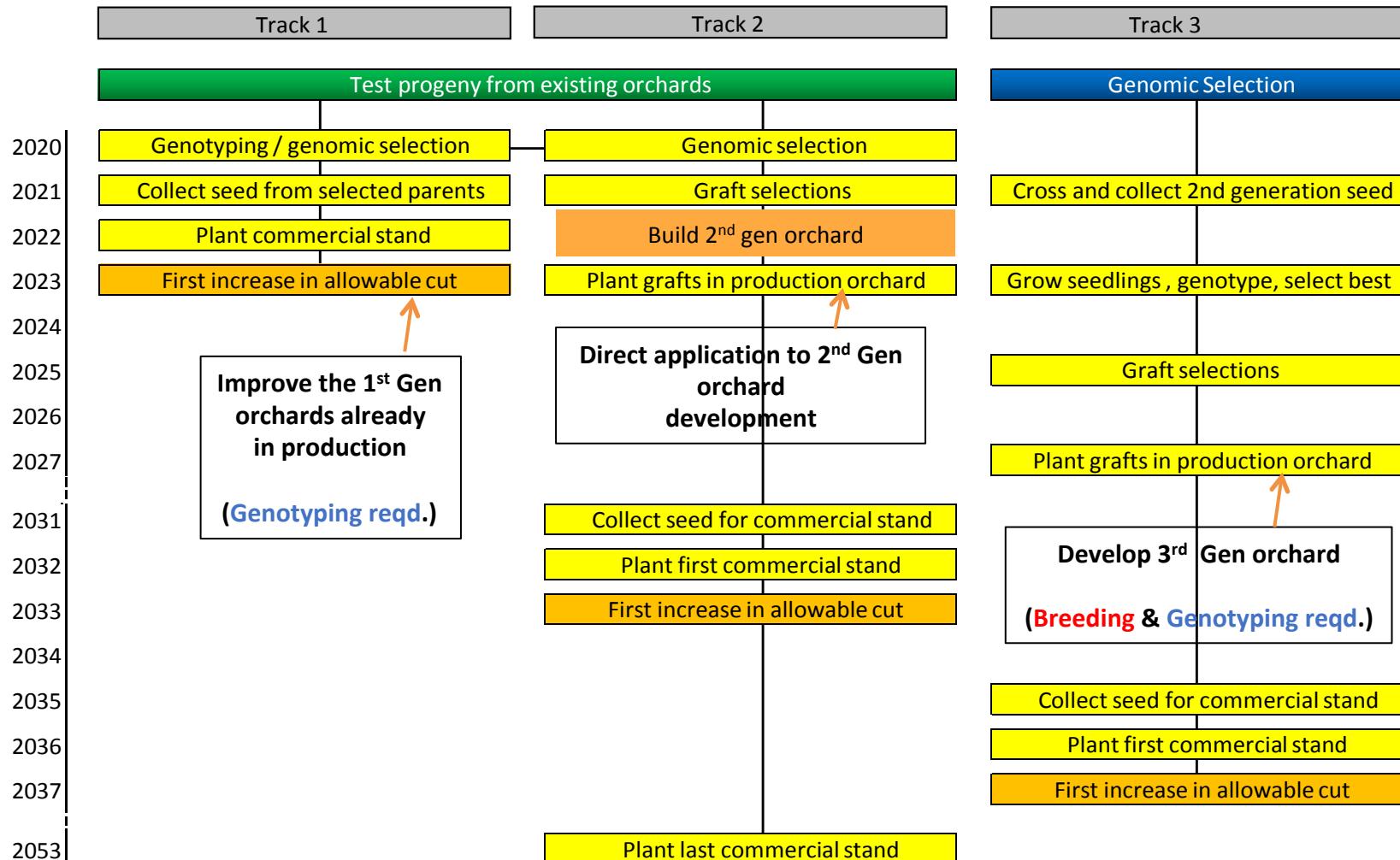
-rapid response to selection with predictive models-
-timing ideal with existing C & D1 programs-

Can develop models for all phenotyping



[Replaces phenotyping with genotyping]

Direct application through Track 2 in Alberta



This work will establish an entirely new platform for tree improvement in Alberta that could expedite decision making and deployment in programs at the cusp of moving from their first- to second-generation orchards.

Delivery....

Drought resistance in Alberta is being increasingly viewed as a critical growth-limiting trait in light of projected climate change in the province over the next 50-80 years. It is imperative that a more comprehensive approach for scoring key traits be taken when selecting parent trees used for production of improved seed in this province.

RES-FOR Deliverables

1. Novel 'omics'-based tree breeding technologies.
 - ✓ Providing SNP profiles for pine and spruce linking genotypes with a wide range of phenotypes.
2. Genomics-based heritabilities & breeding values for key economic traits.
 - ✓ Genomics based breeding values will increase the accuracy & precision for ranking individuals.
3. Improved knowledge sharing & decision-making processes.
 - ✓ GELS informed workshops, reports & guidelines for improved collaboration & understanding social factors.
4. Quantitative economic impact models for tree improvement programs.
 - ✓ GATB economic models impacting demand and supply & forecasting the impact of planting resilient, quality trees.
5. Interactive tree genomics & phenomics resource website.
 - ✓ On-going access to all data, SNP profiles, predictive models.
6. End-user oriented technology & policy workshops.
 - ✓ Investigator and collaborator hosted genomic breeding policy workshops.

Industrial Partner Comments

“Its pretty exciting and heady stuff and will fast track the selection process to meet the forecasted needs of orchard development.”

- Weyerhaeuser (Greg Behuniak)

“...the most exciting aspect... being able to adapt our programs FAR sooner in response to new issues as more is known - will be huge.”

- West Fraser - BRL (Shane Sadoway)



QUESTIONS?

& THANKS!!