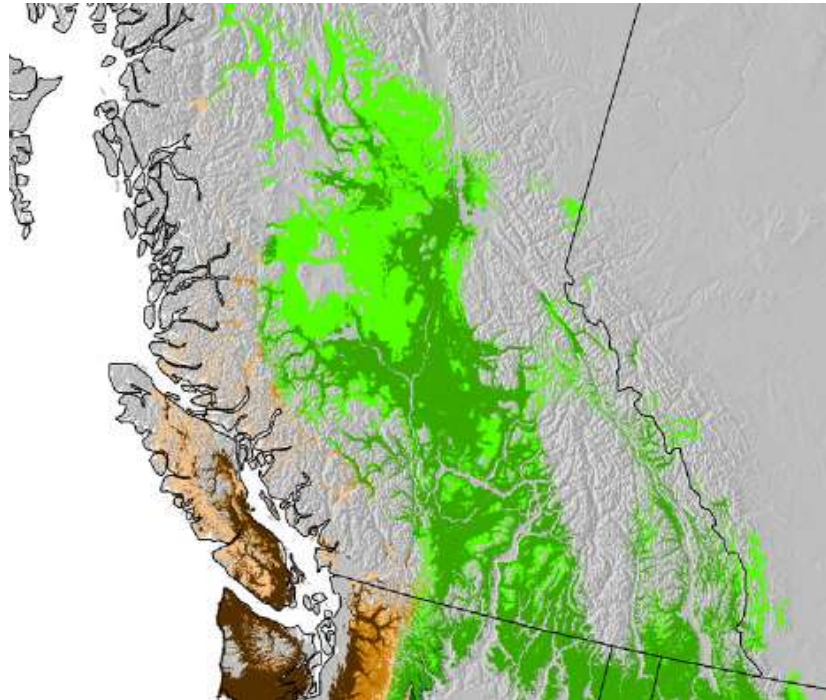


# Informing climate-based seed transfer with genomic and phenotypic tools: AdapTree and CoAdapTree Projects



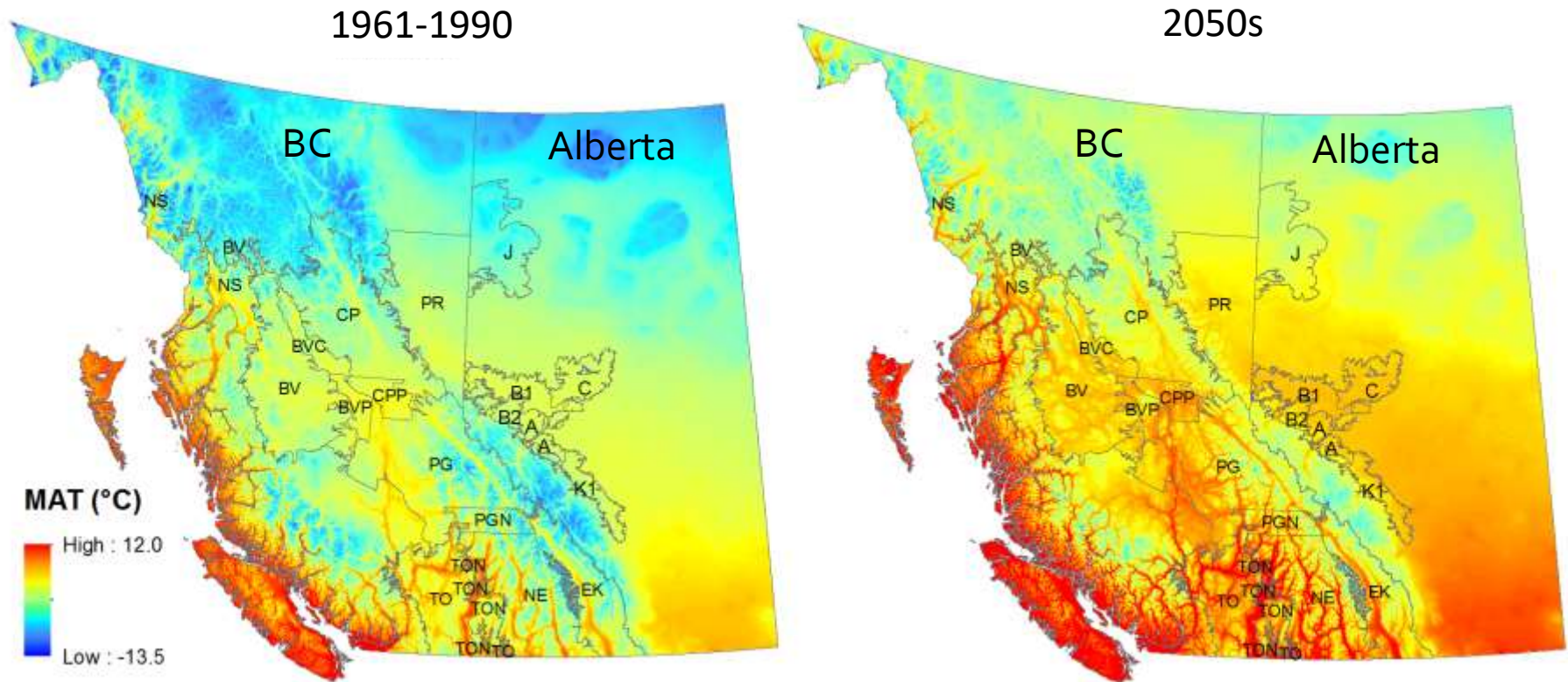
# Shifting distribution of climatic niches of hosts and diseases with climate change



**Figure 4.** Projected climatic niche of Douglas-fir in western Canada in 2060s for coastal (brown) and interior (green) varieties. The lightest colour indicates new areas of climatic suitability outside current species range.



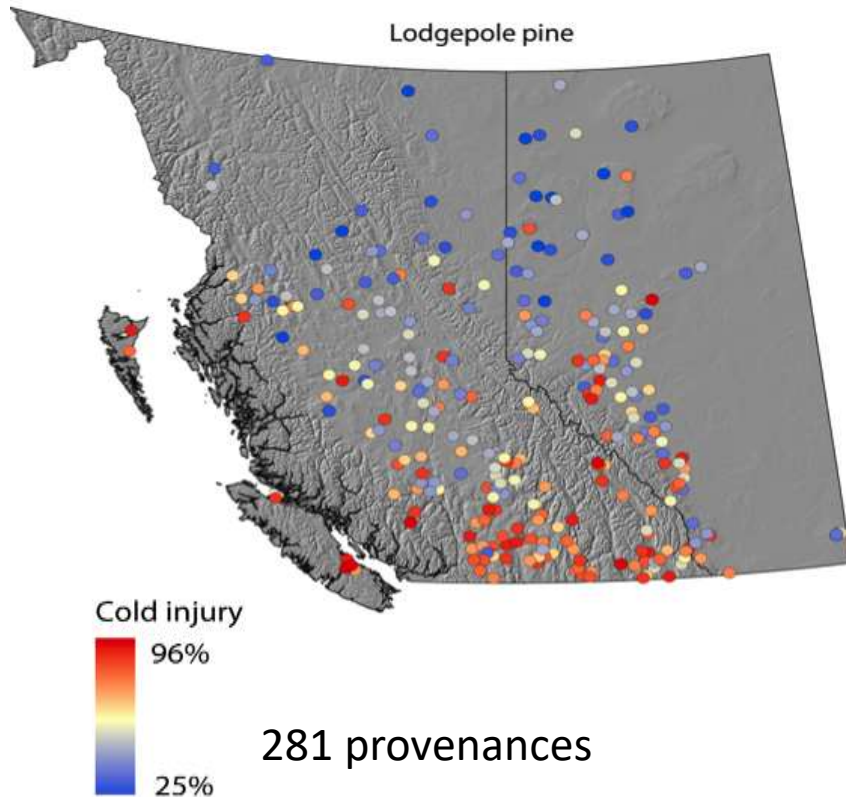
# Realizing gains from breeding programs requires matching trees to new climates



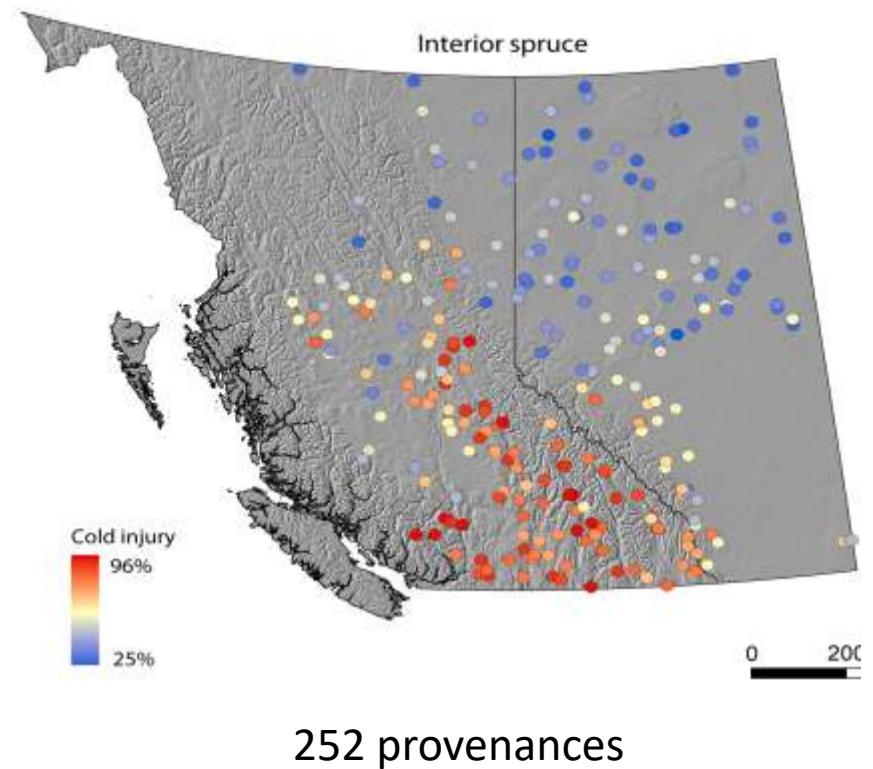
**Breeding zones match recent  
but not future climates**

# Provenance variation in fall cold hardiness

Fall cold injury – lodgepole pine



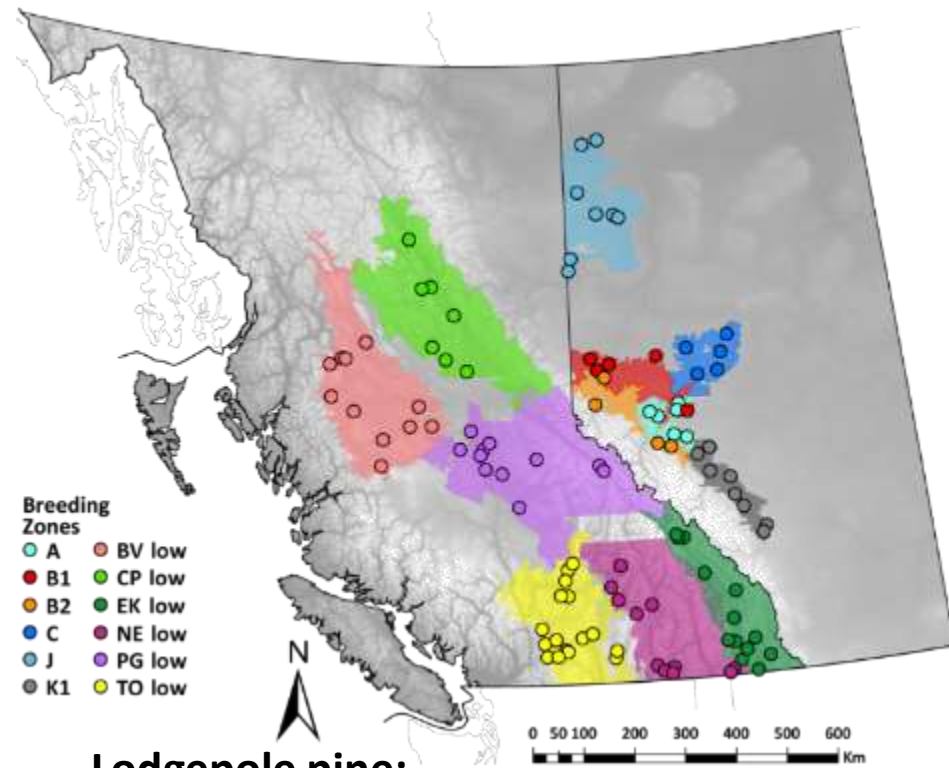
Fall cold injury – interior spruce



# AdapTree: Class B vs Class A climate adaptation



Ian MacLachlan, PhD

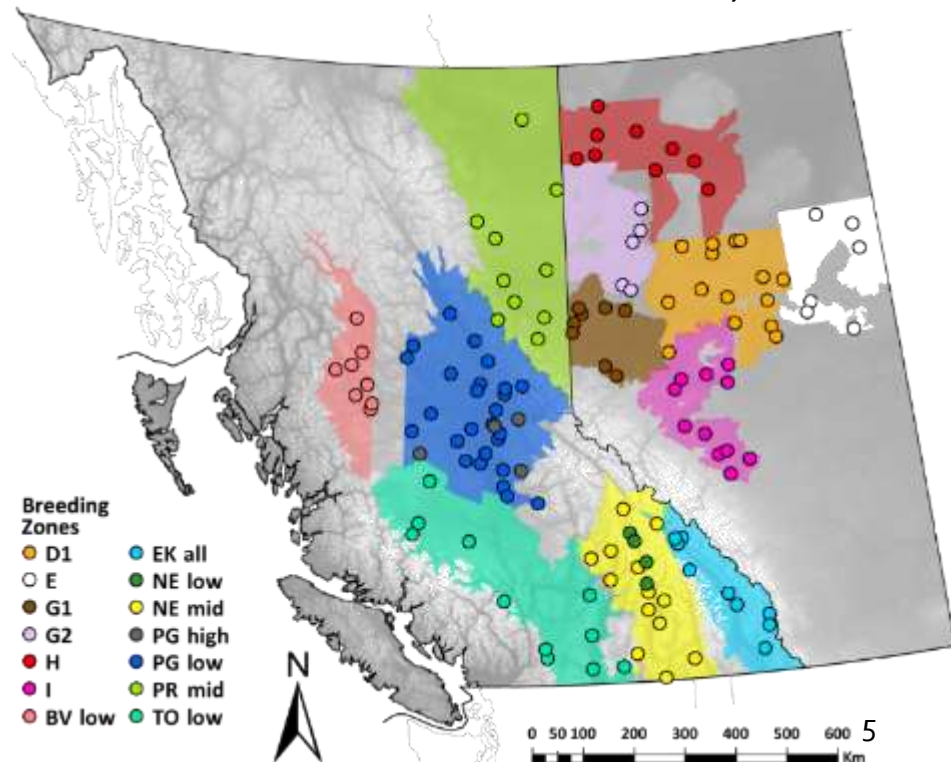


## Lodgepole pine:

2176 seedlings from 12 breeding zones

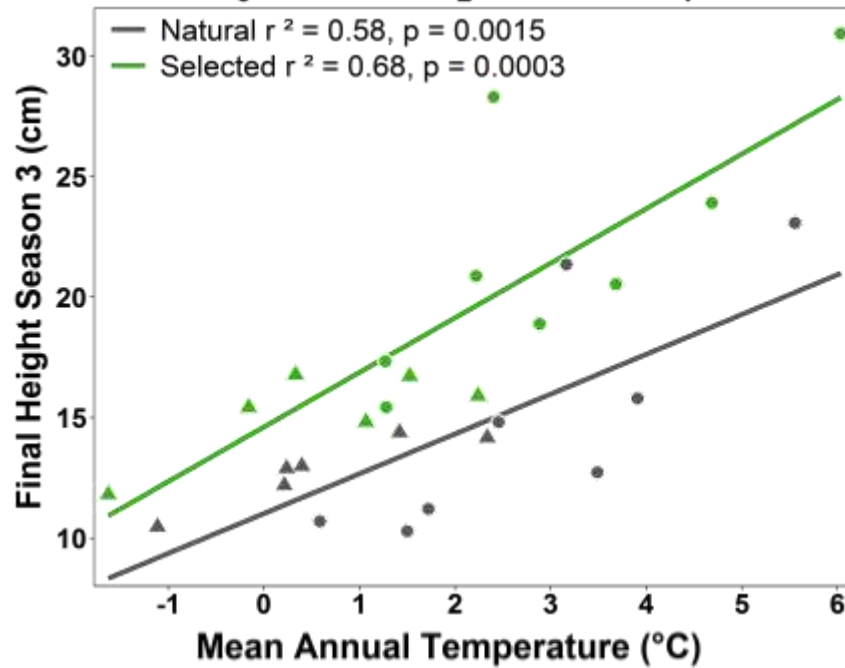
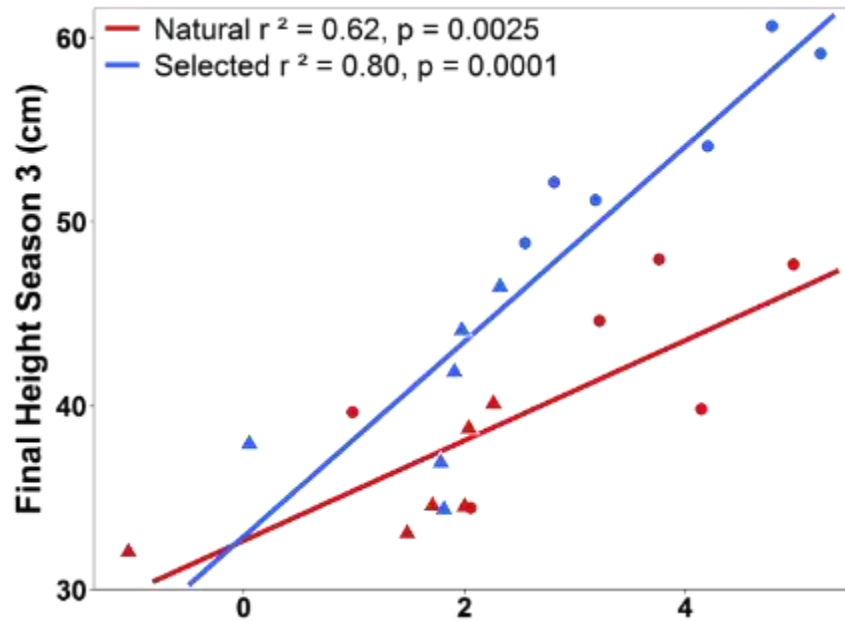
## Interior spruce:

2424 seedlings from 14 breeding zones



# Gains in growth from breeding

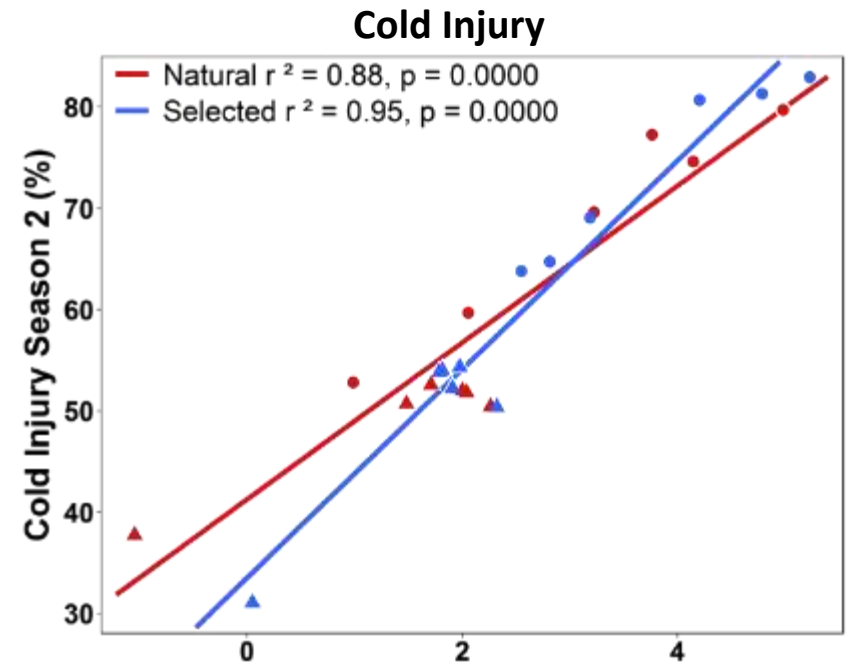
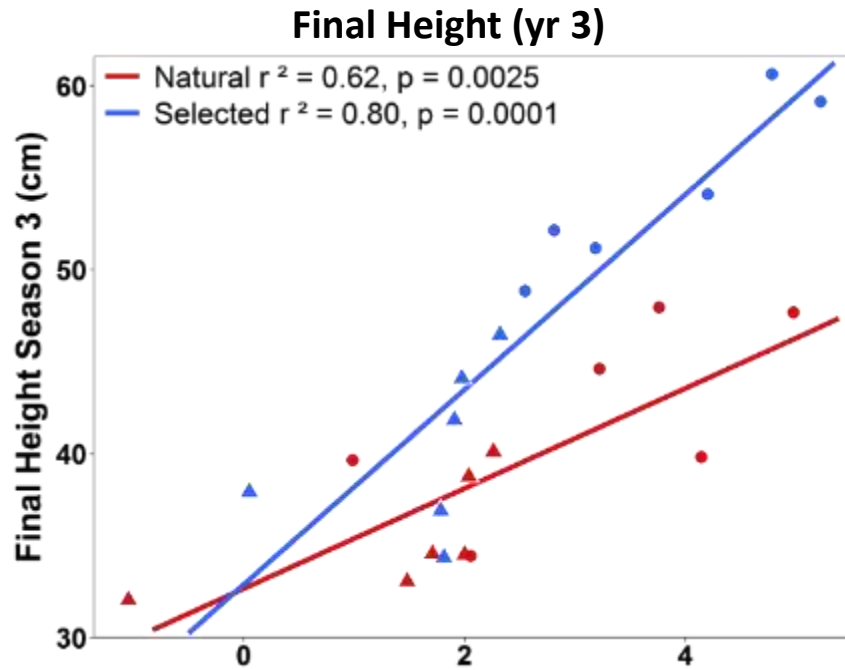
Final Height (yr 3)



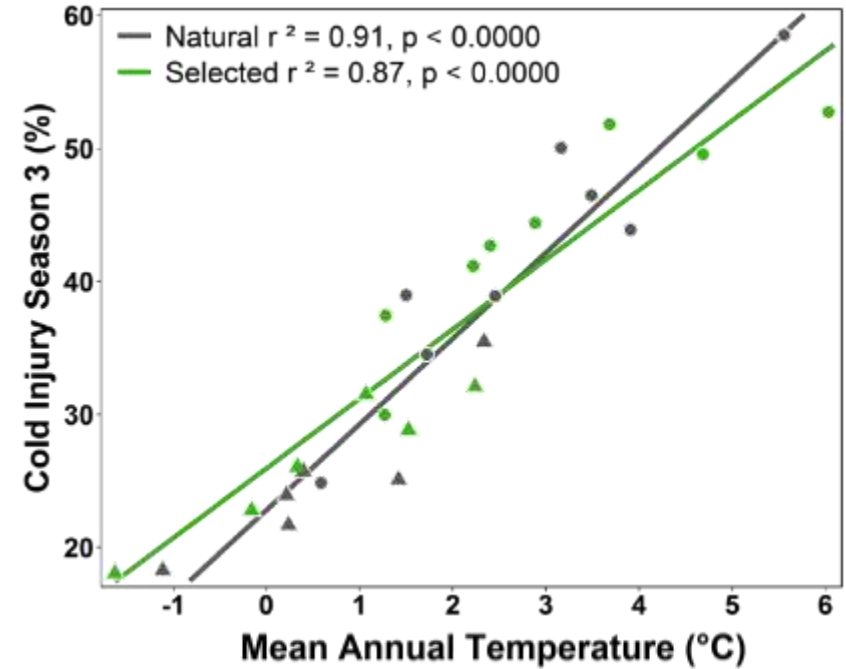
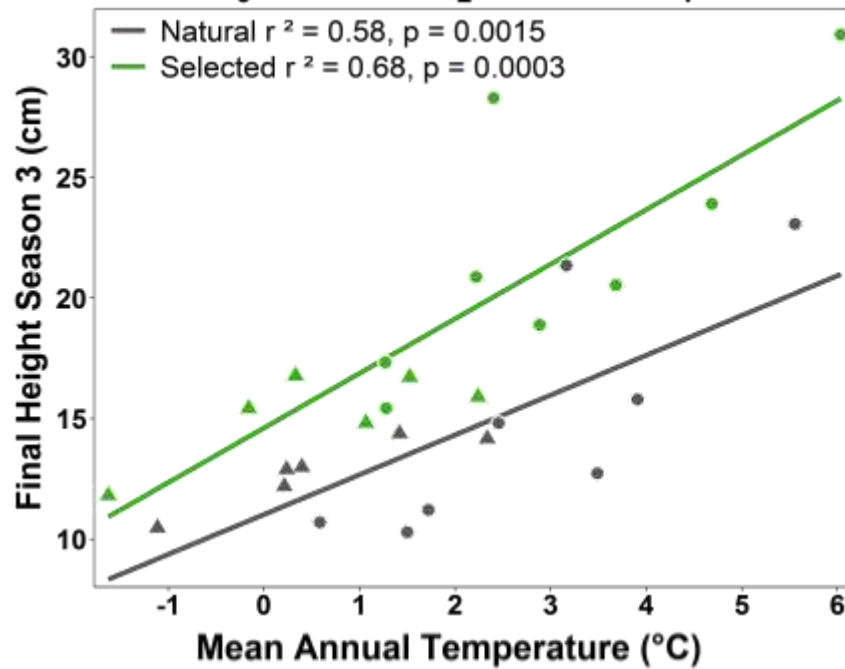


# Gains in growth from breeding with little impact on cold injury

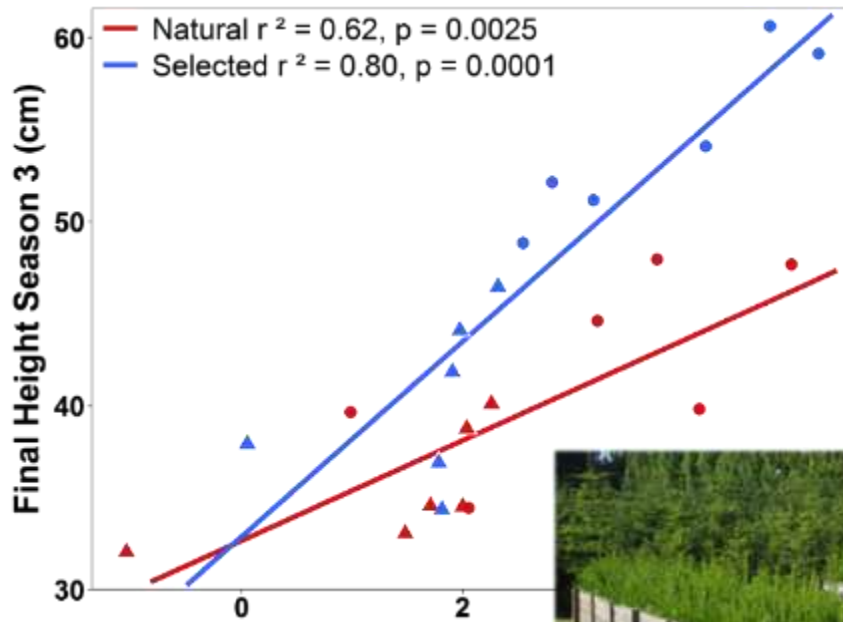
Pine



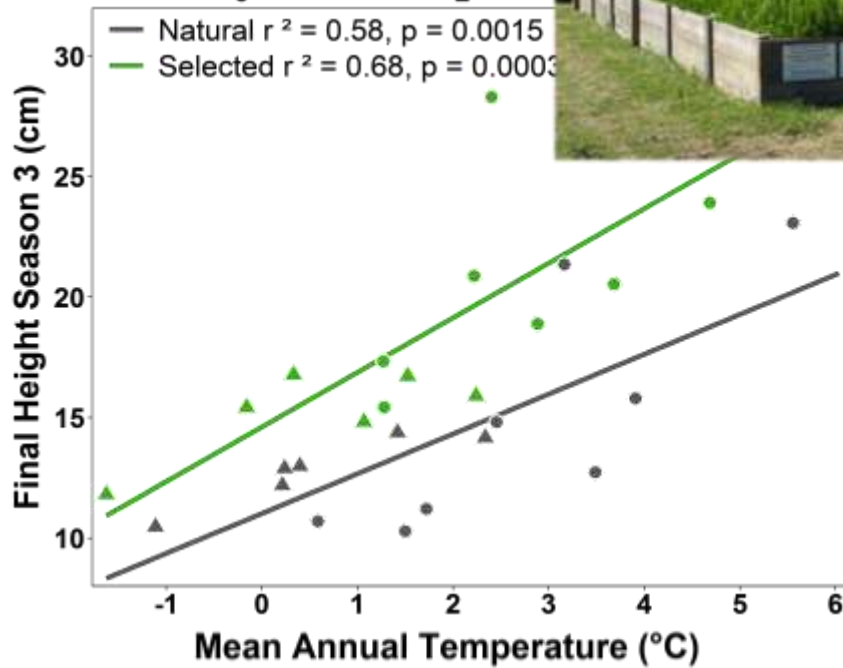
Spruce



### Final Height (yr 3)



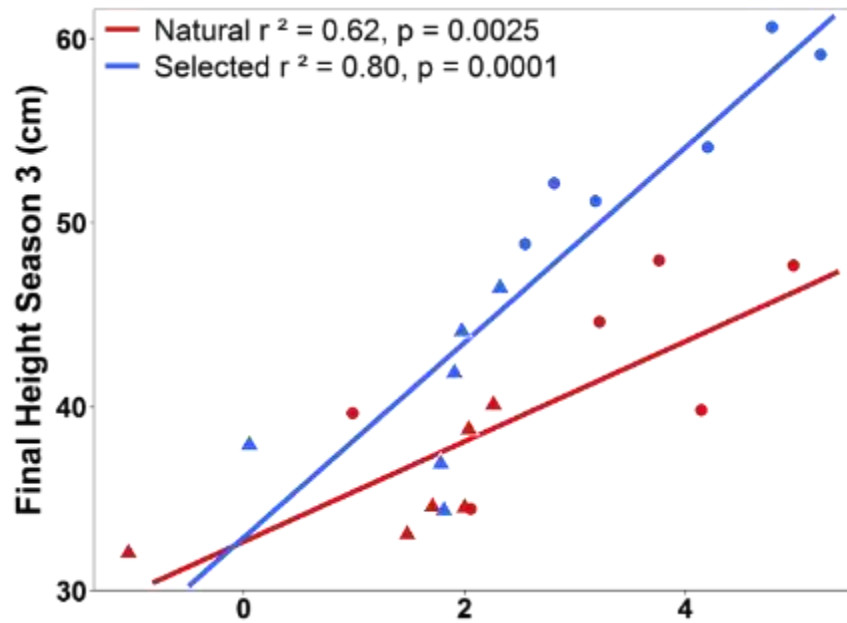
Are our growth phenotypes  
from Vancouver relevant?



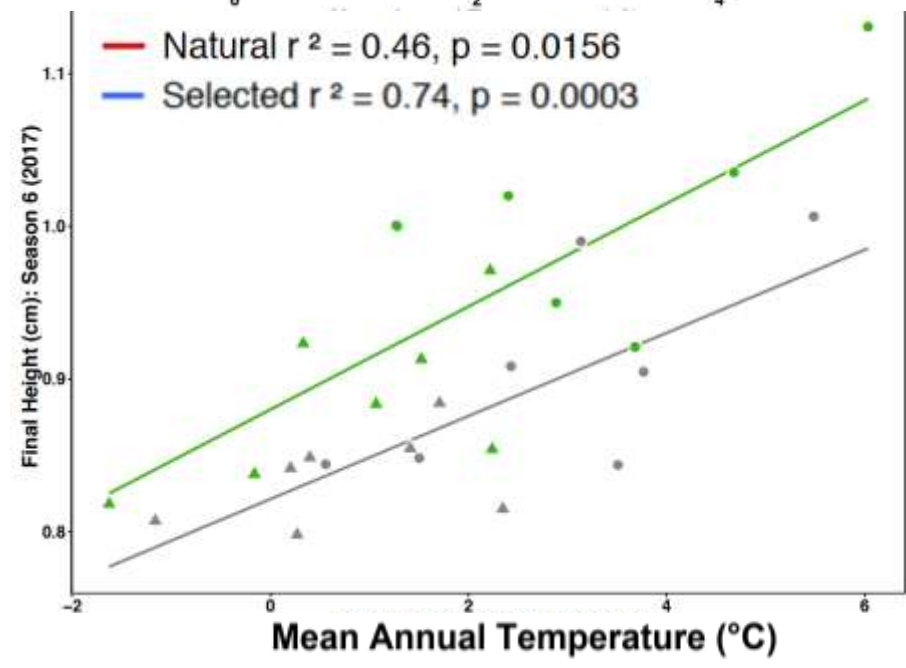
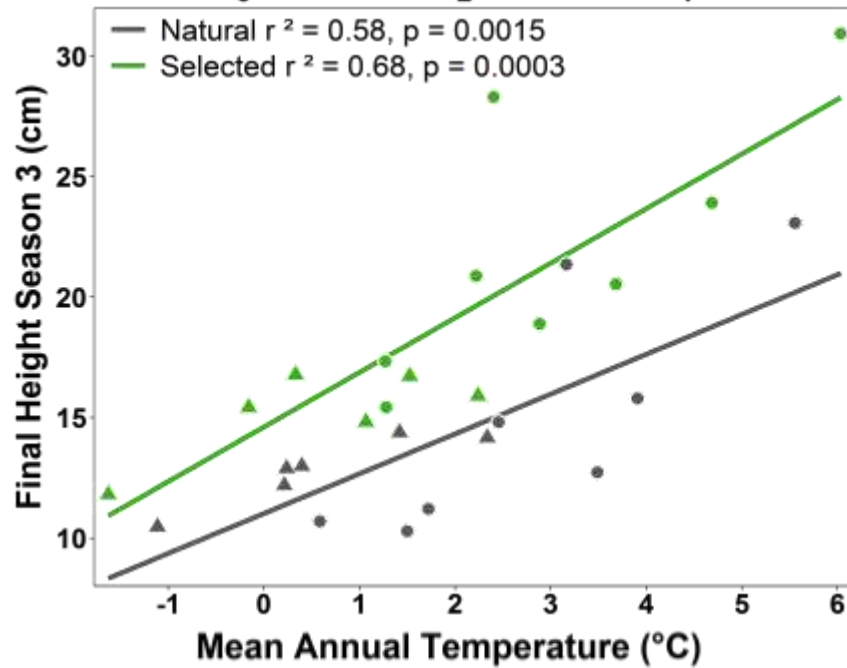
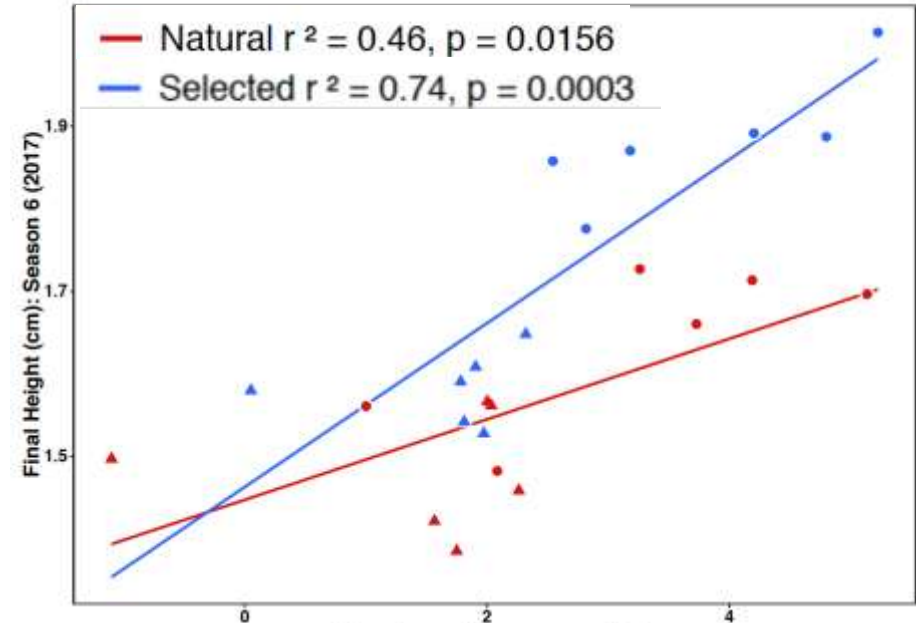


# Results similar between UBC and Alex Fraser RF

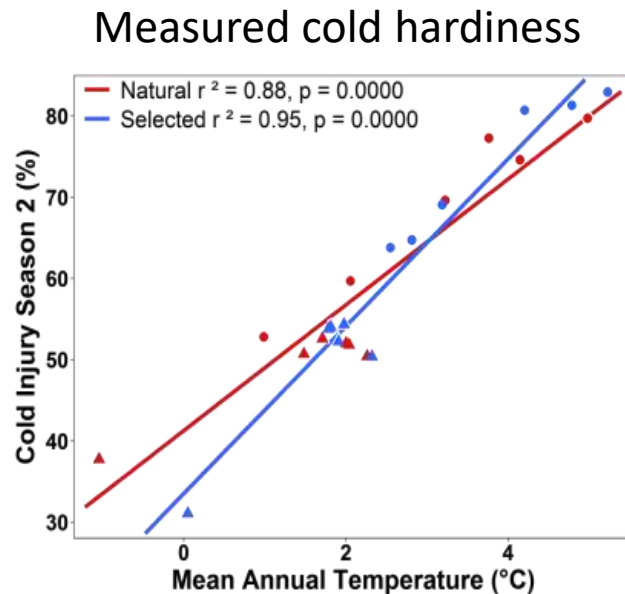
## Final Height (yr 3)



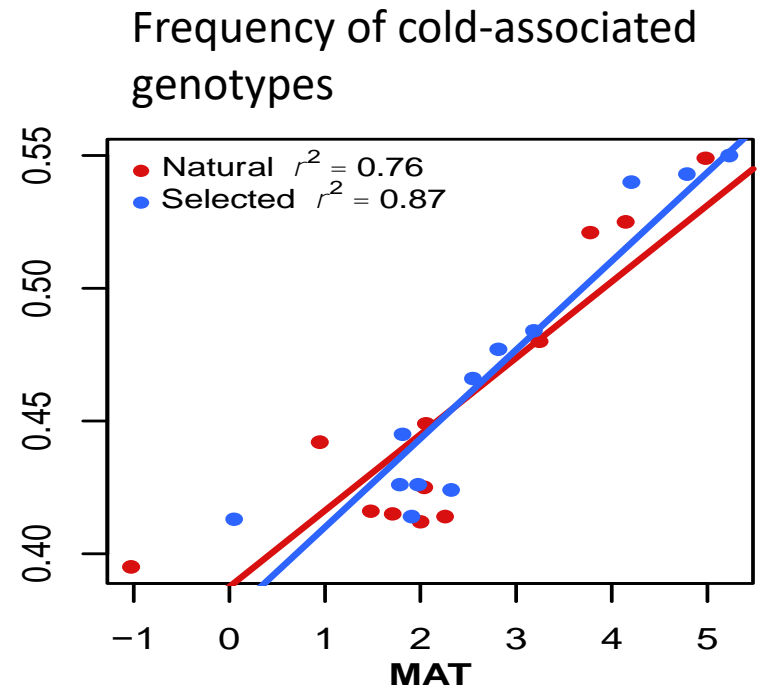
## Field height Age 6 – Alex Fraser RF



We can rapidly characterize climate adaptation using genomic analyses, e.g., for cold hardiness



Frequency of Positive Effect Alleles

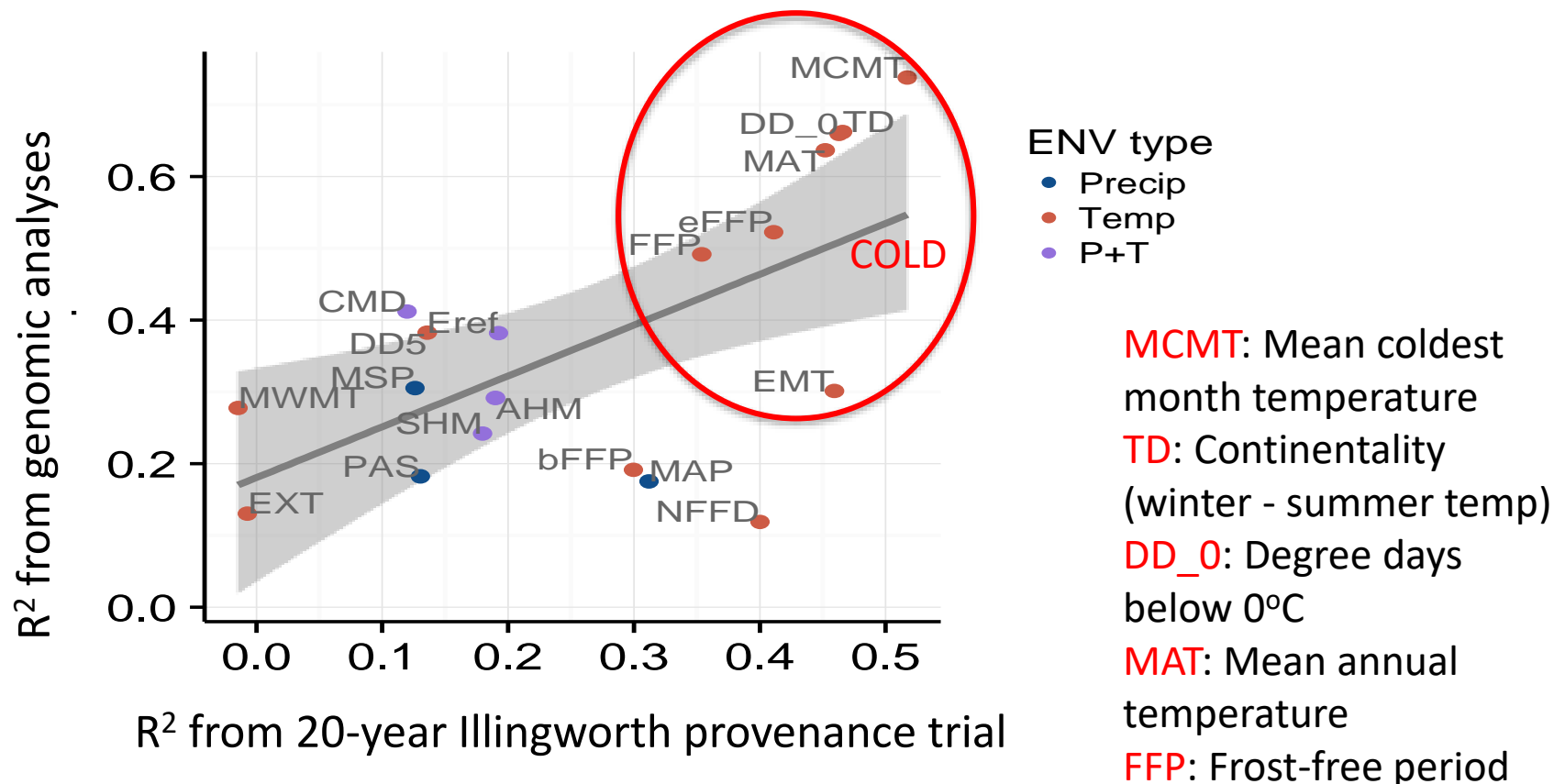


MacLachlan et al. 2017. Tree Genetics and Genomes

Ian MacLachlan. PhD Dissertation. Manuscript in prep.

# Genomic analyses identify the same importance of climate factors as provenance trials

## Lodgepole pine

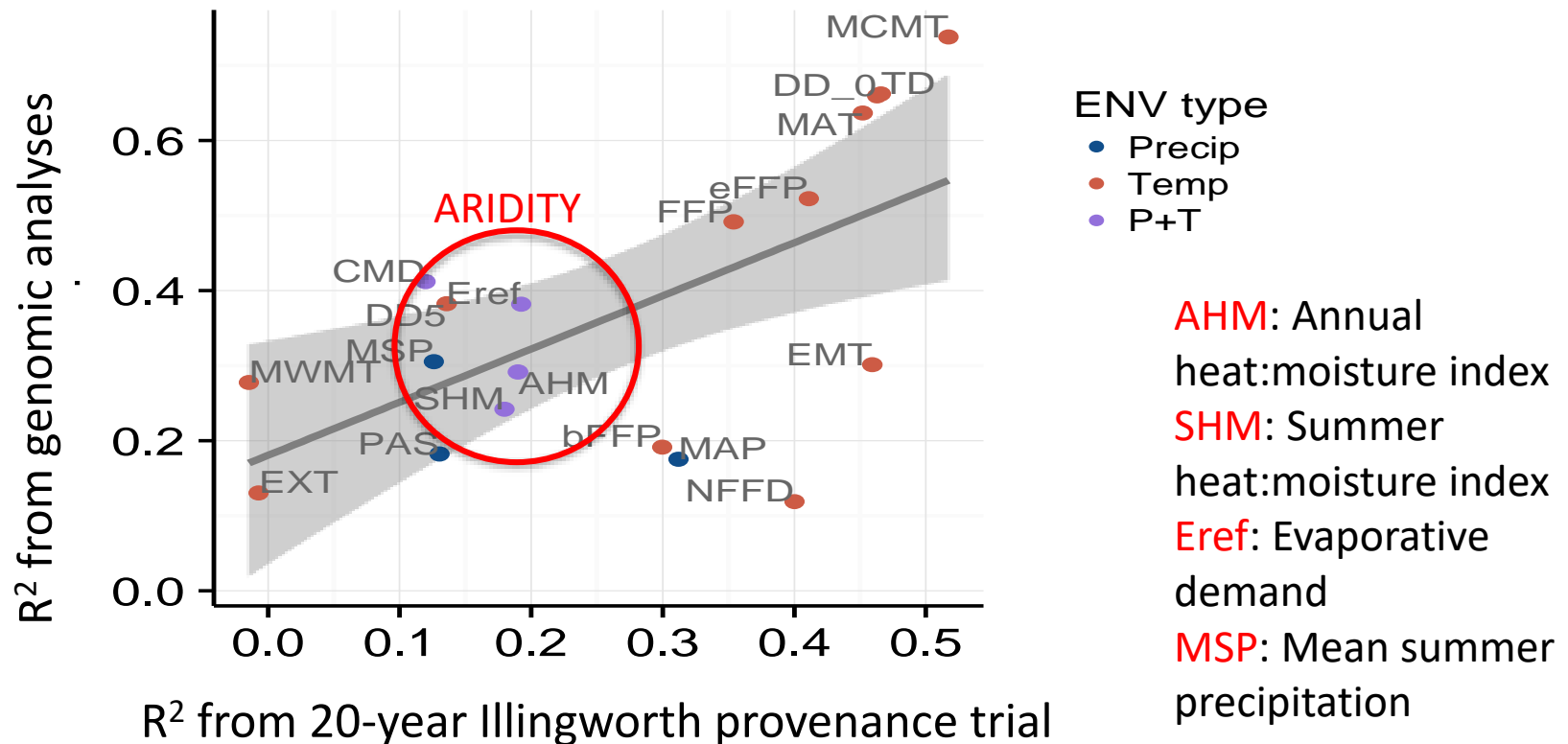


Analysis by Jeremy Yoder, Tongli Wang. Provenance data from FLNRORD.



# Genomic analyses identify the same importance of climate factors as provenance trials

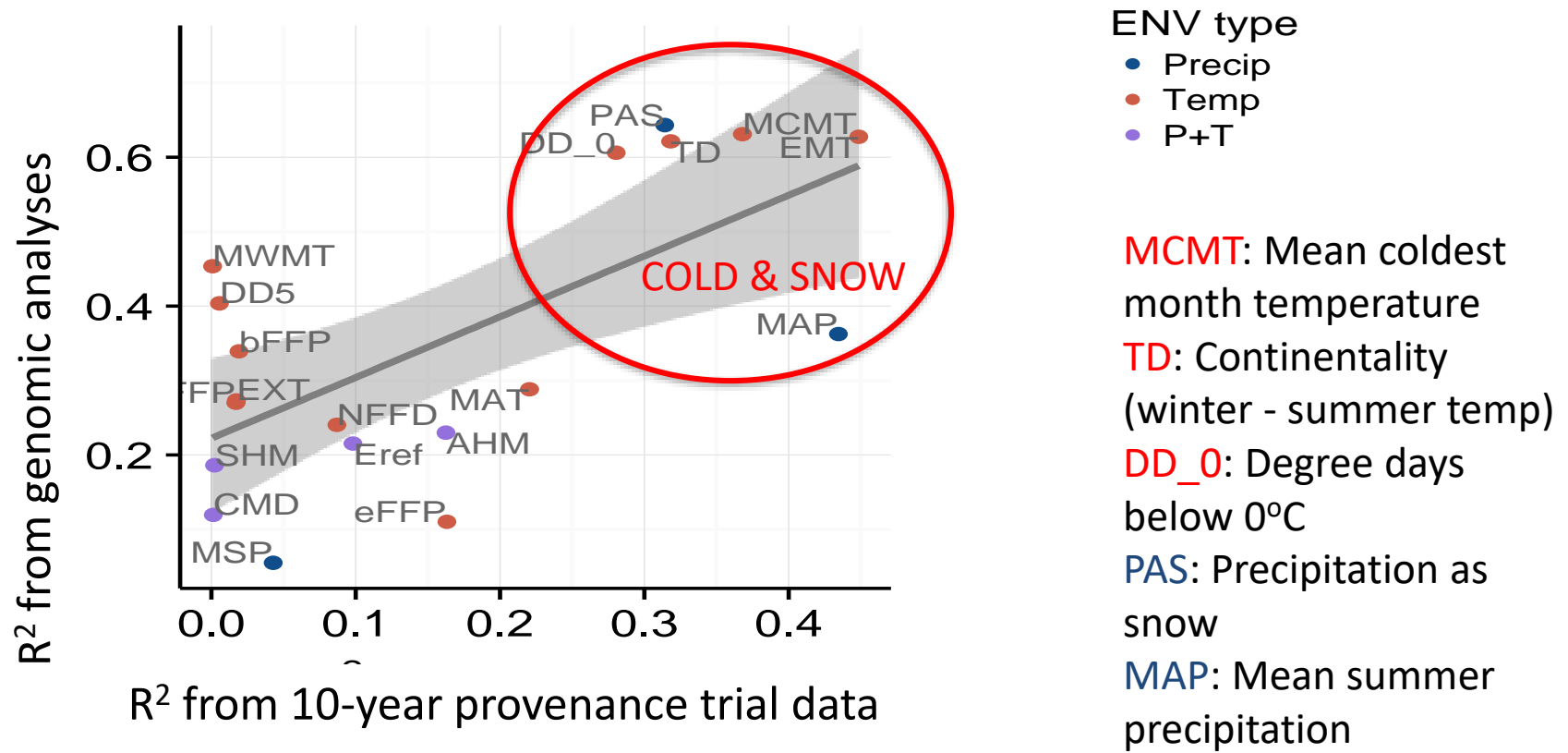
## Lodgepole pine



Analysis by Jeremy Yoder, Tongli Wang. Provenance data from FLNRORD.

# Genomic analyses identify the same importance of climate factors as provenance trials

## Interior spruce



Analysis by Jeremy Yoder, Jon Degner.. Provenance data from FLNRORD.

# CoAdapTree: Targeting four species



**Douglas-fir:**  
Climate  
adaptation  
& Swiss  
needle cast  
resistance



Western  
larch:  
Climate  
adaptation



**Lodgepole  
pine:** (Climate  
adaptation) &  
Dothistroma  
resistance/tolerance



Jack pine:  
Climate  
adaptation

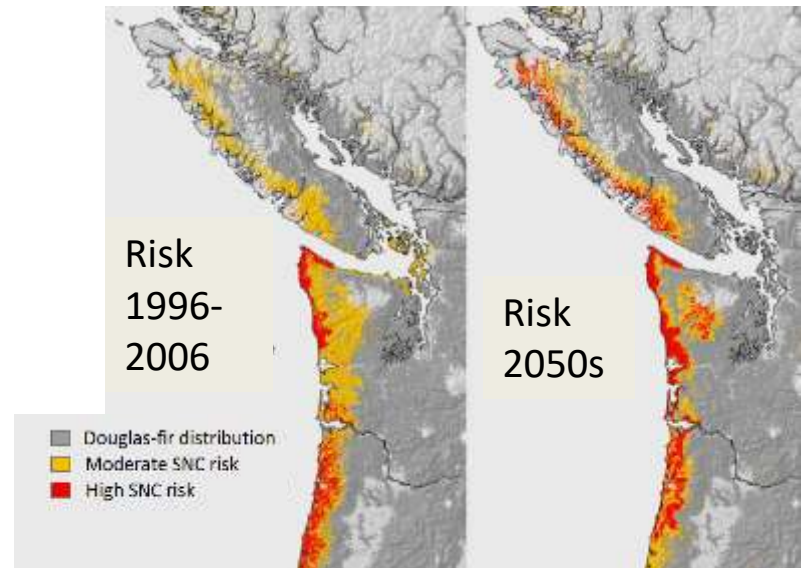


# Pathogen resistance/tolerance:

Genetics of pathogens causing *Dothistroma* needle blight and Swiss needle cast as well as hosts

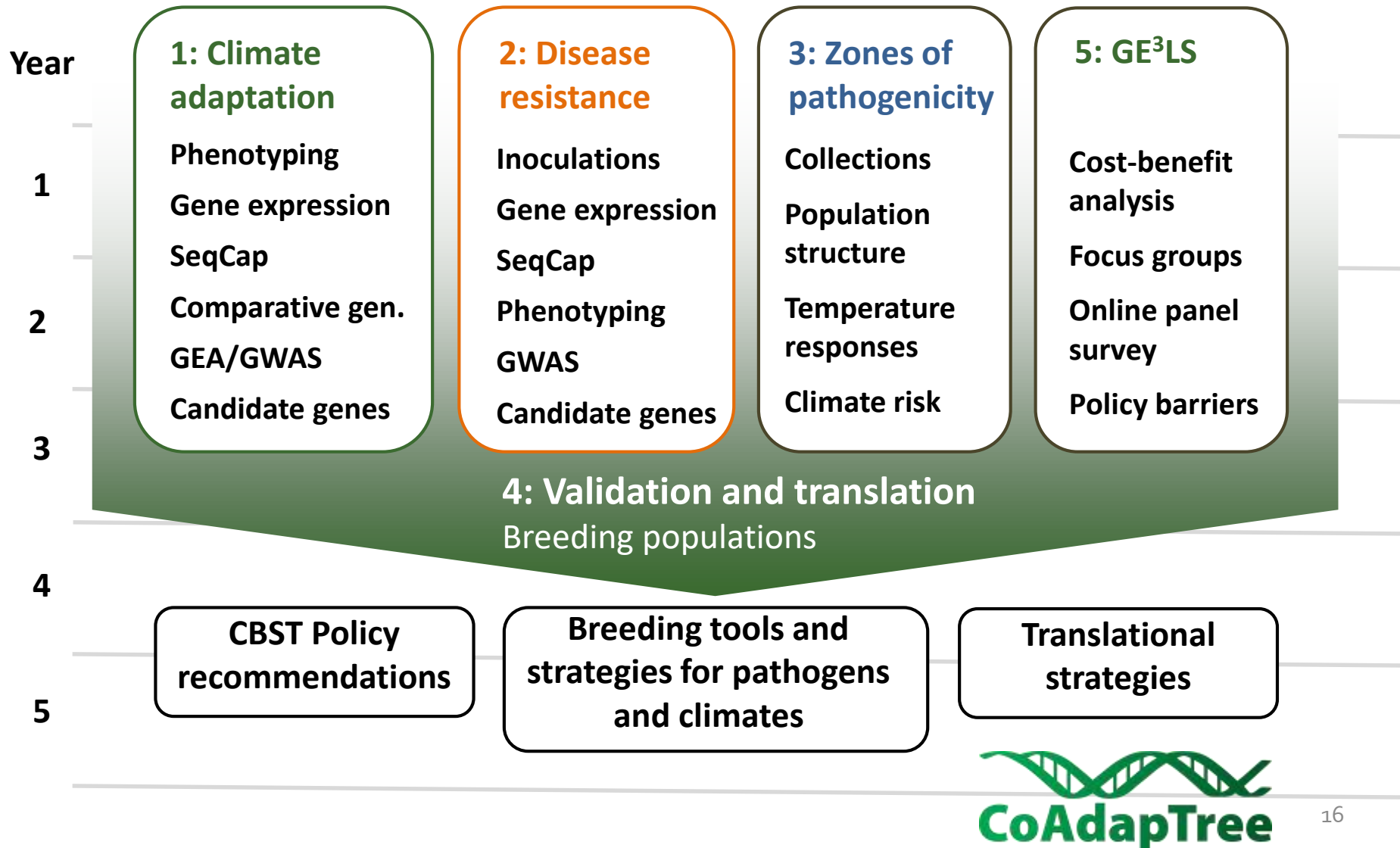


Identify candidate genes and population variation for disease resistance or tolerance.

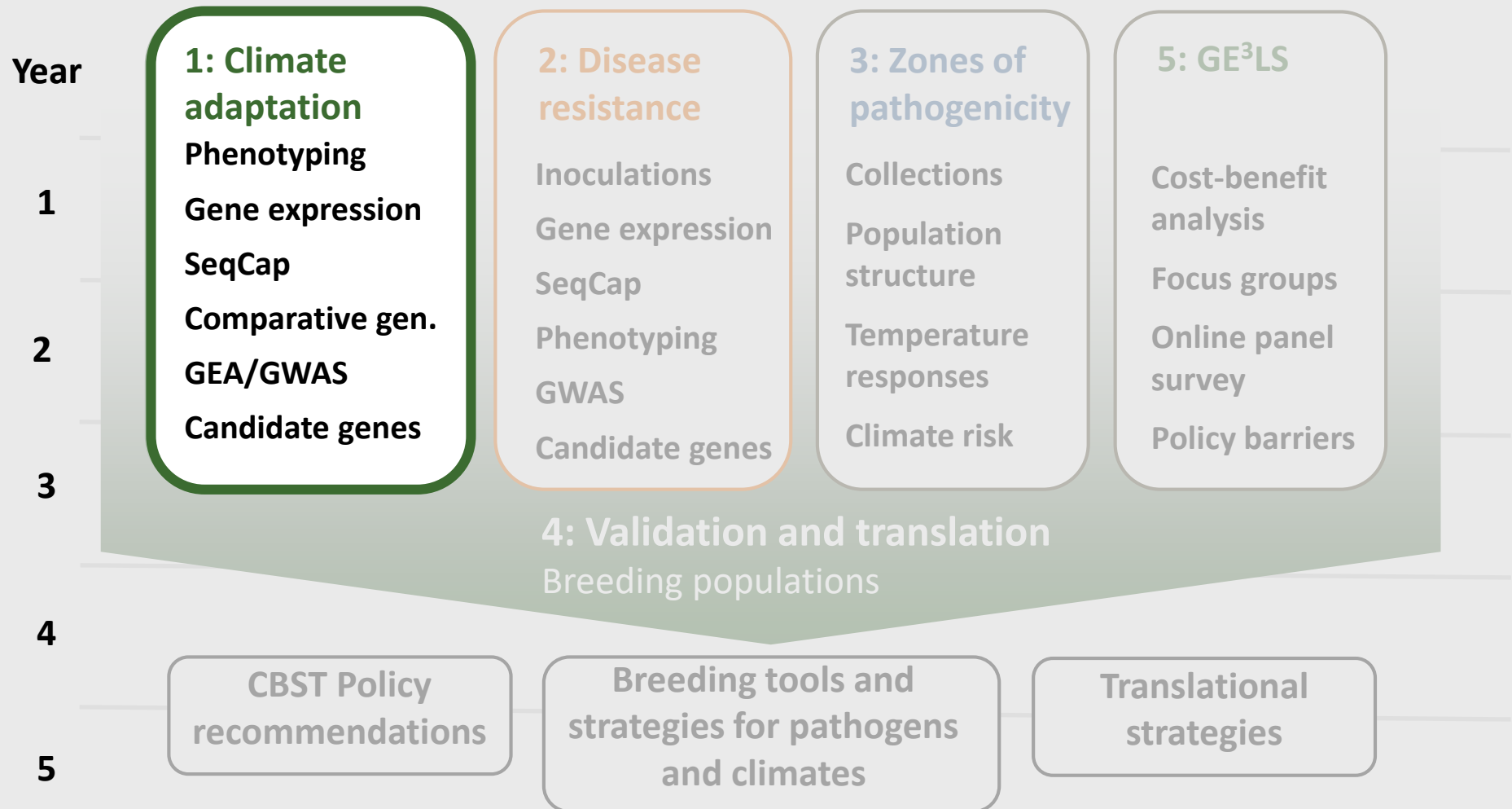


Define pathogenicity zones and predict disease response to climate change

# Activities and timeline - Oct. 2016-Sept.'20



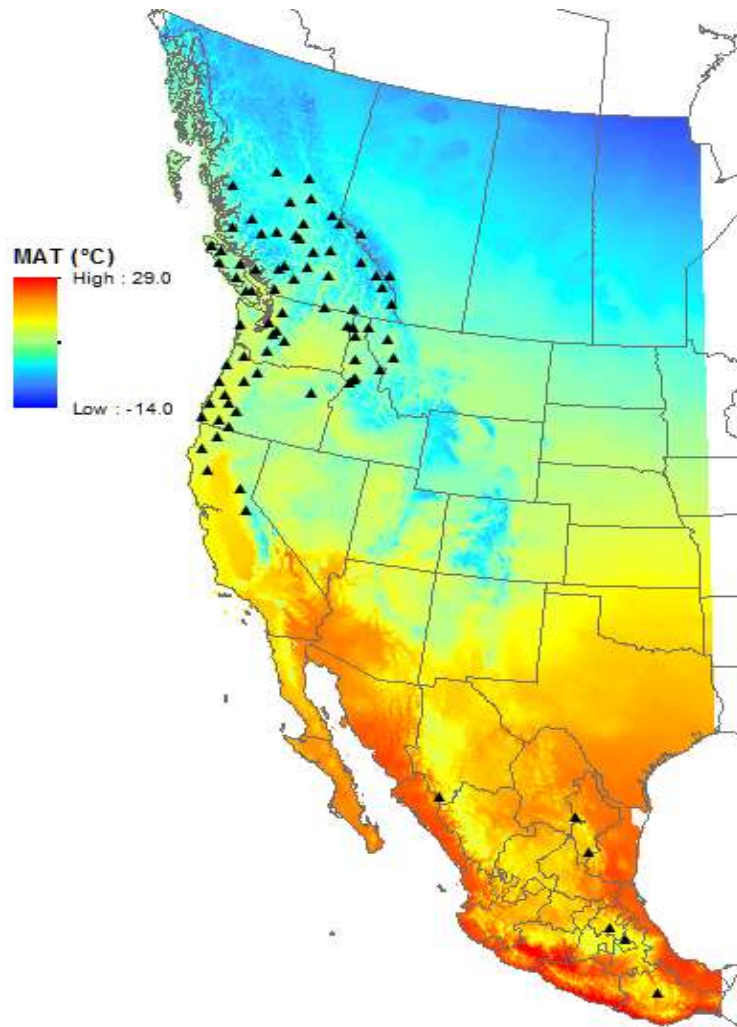
# Activity 1: Genetics of local adaptation to climate in Douglas-fir, western larch (and jack pine)



S. Aitken, S. Yeaman, I. Ensminger,  
M. Whitlock, L. Rieseberg



# Activity 1.1 – Populations sampled for climate adaptation in Douglas-fir @UBC



- ~80 natural population bulk seedlots
- 11 selectively bred seedlots from BC, OR and WA
- 40-50 Mb sequence capture probes being designed to sequence 20,000 to 30,000 genes

# Activity 1.1 – Sowing, growing and sampling Douglas-fir populations



Sowing



Greenhouse



Growing

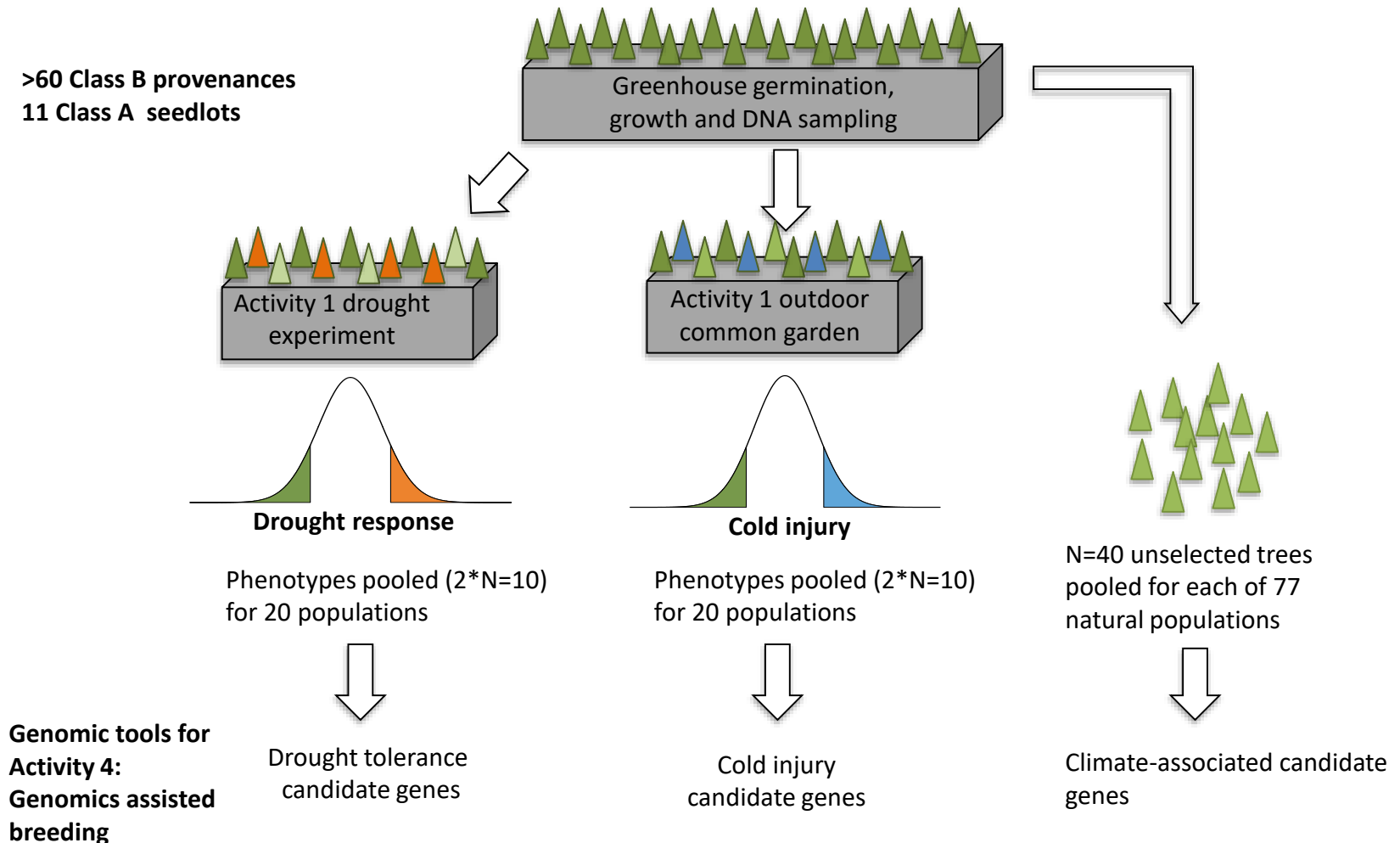


Sampling



Ready for transplanting

# Activity 1.1: Douglas-fir @UBC



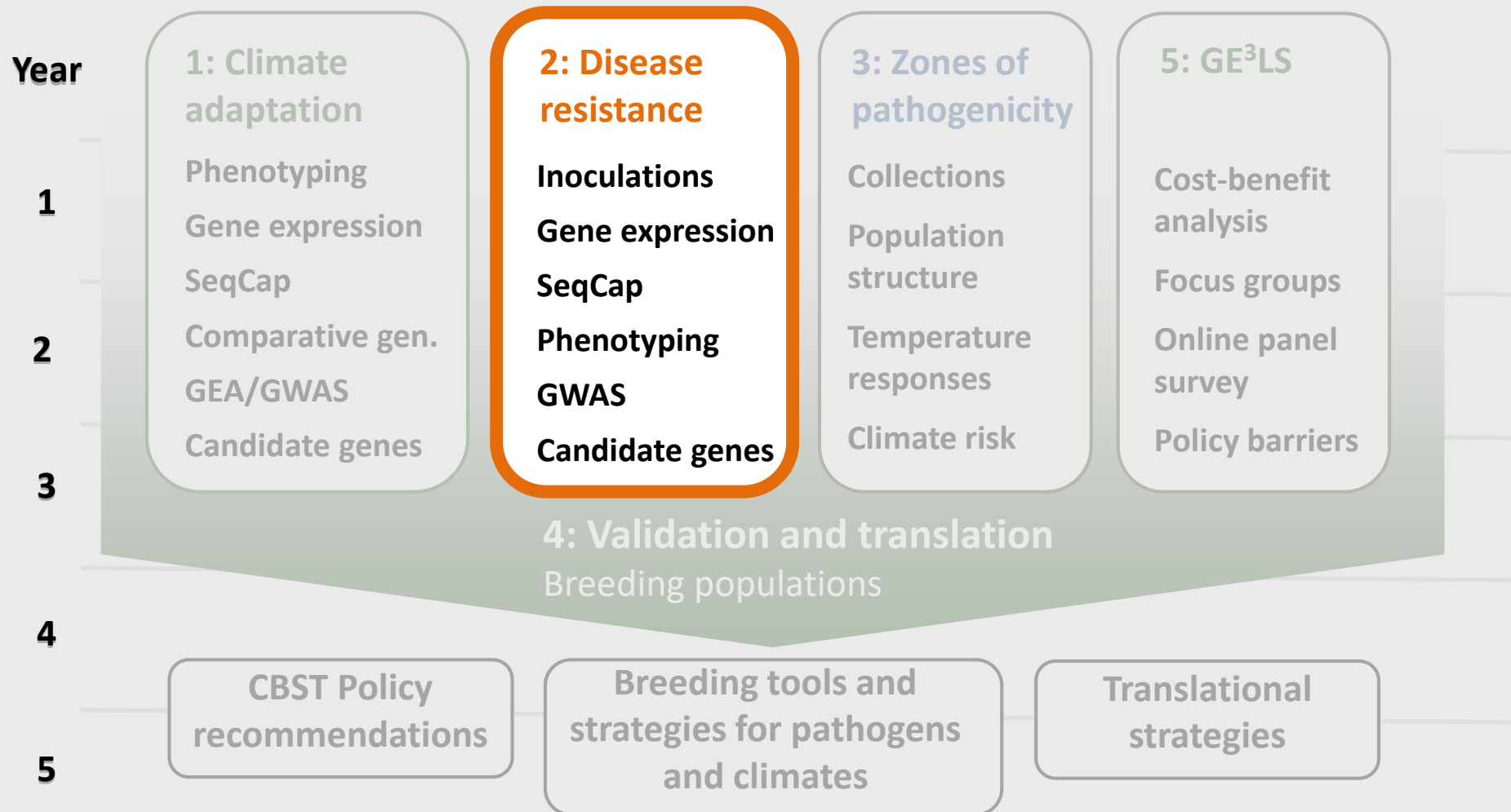
# Activity 1.2 – Climate adaptation candidate genes in western larch

- Sampled 40 populations from existing western larch field provenance trial in July; DNA extraction underway
- 40-50 Mb sequence capture probes being designed (20-30,000 genes)
- Phenotypic data on growth; additional traits difficult to phenotype due to tree size in provenance trial
- Propose establishing seedling common garden (resources permitting; B. Roskilly, incoming PhD student)





## Activity 2: Genomic basis of resistance to disease-causing fungi in lodgepole pine and Douglas-fir



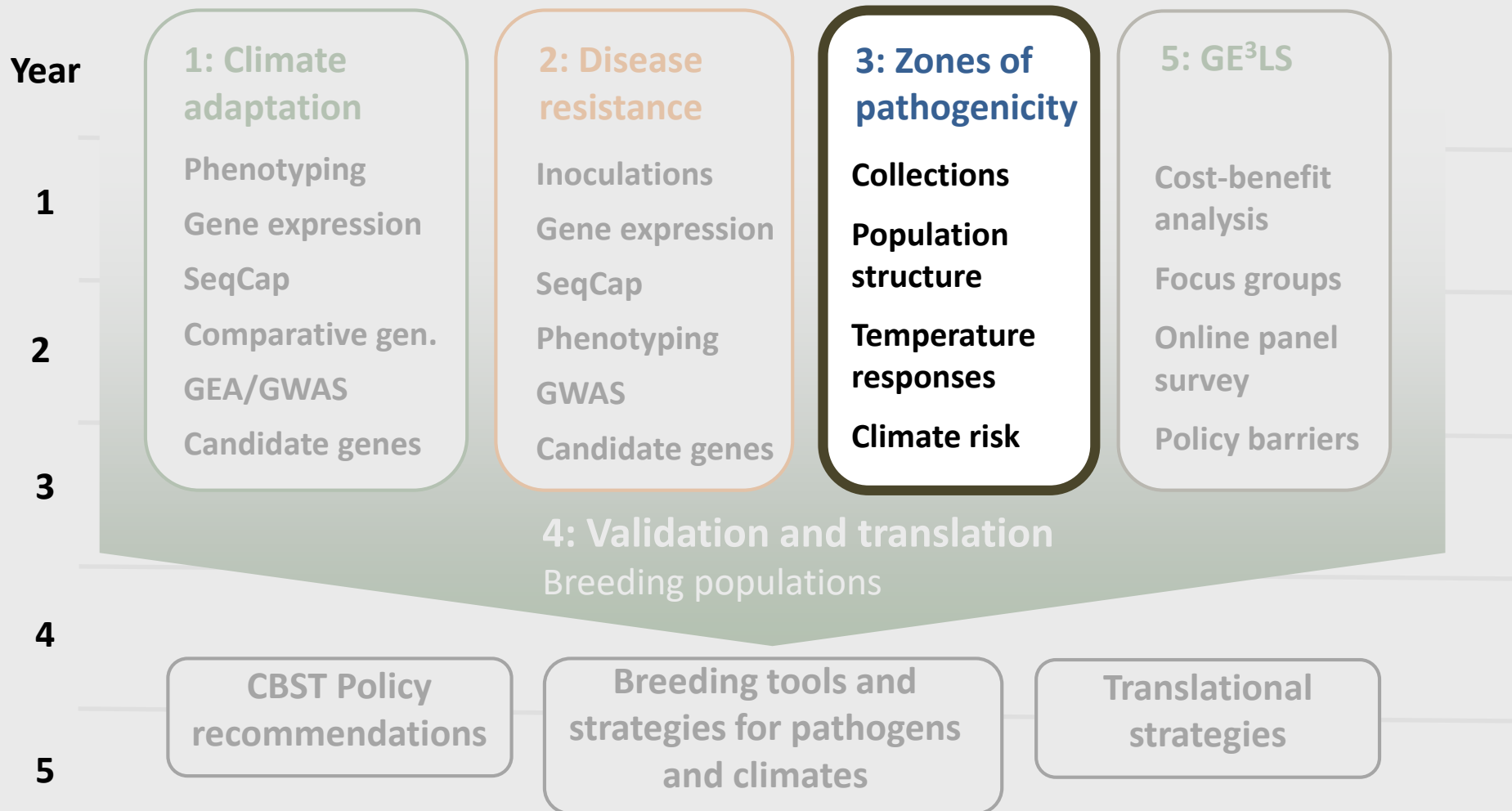
S. Yeaman, N. Ukrainetz, J. Ehlting, R. Hamelin

# Act. 2 Genetic basis of resistance to Dothistroma Needle Blight

- Artificial inoculation methods developed and gene expression characterized (N. Feau, R. Hamelin)
- 40 class B populations inoculated; will do pooled sequencing of most and least resistant in each population
- Candidate genes will be validated in breeding populations



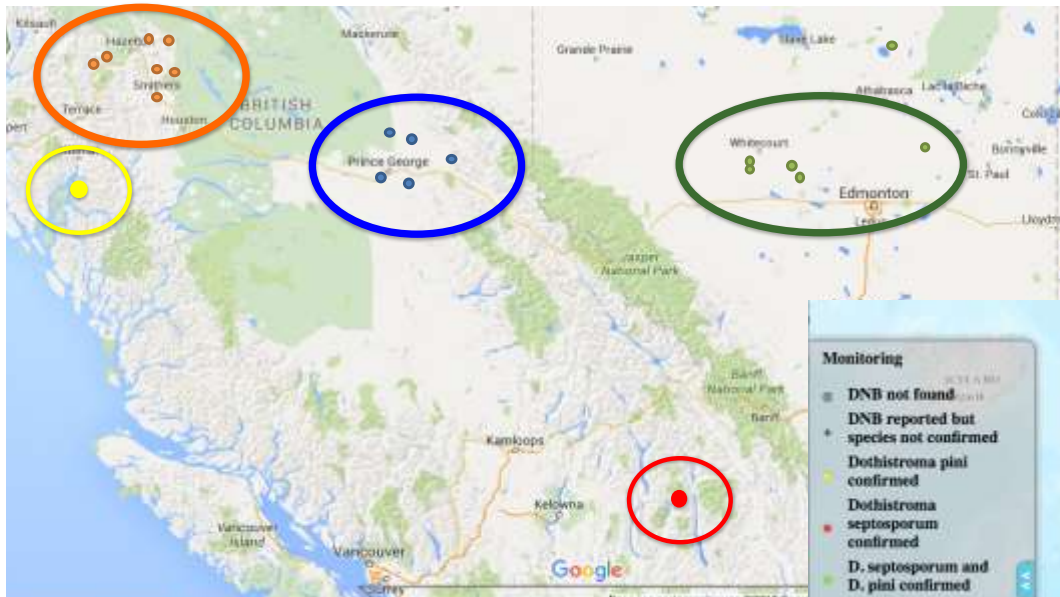
# Activity 3: Population genomics and climate responses of fungal pathogens



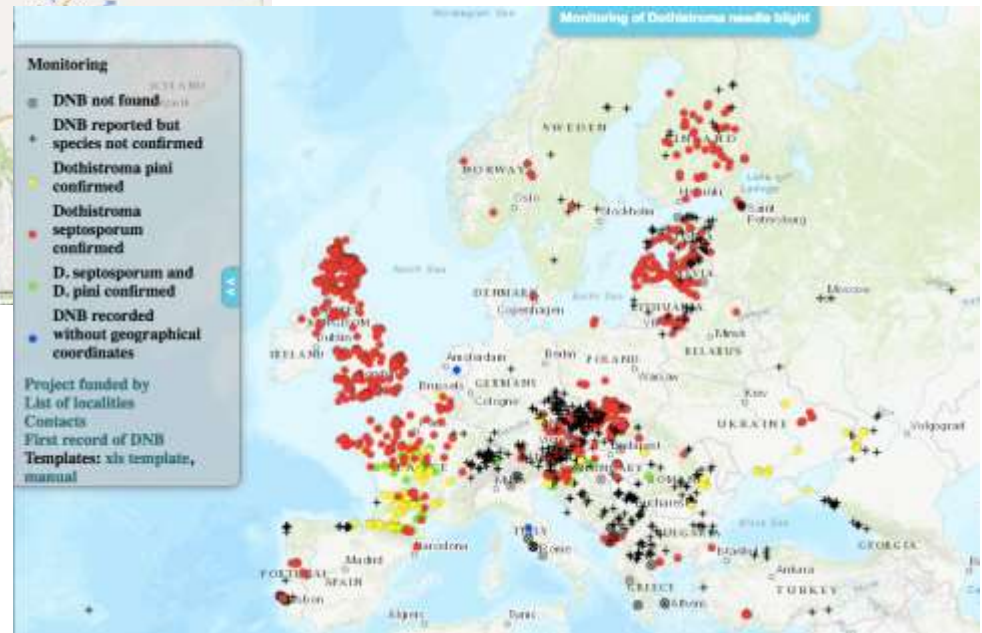
R. Hamelin, S. Yeaman, M. Whitlock,  
T. Wang, A. Hamann,

# 3.1 Reference collections of fungi, e.g., Dothistroma Needle Blight

BC and Alberta



Europe



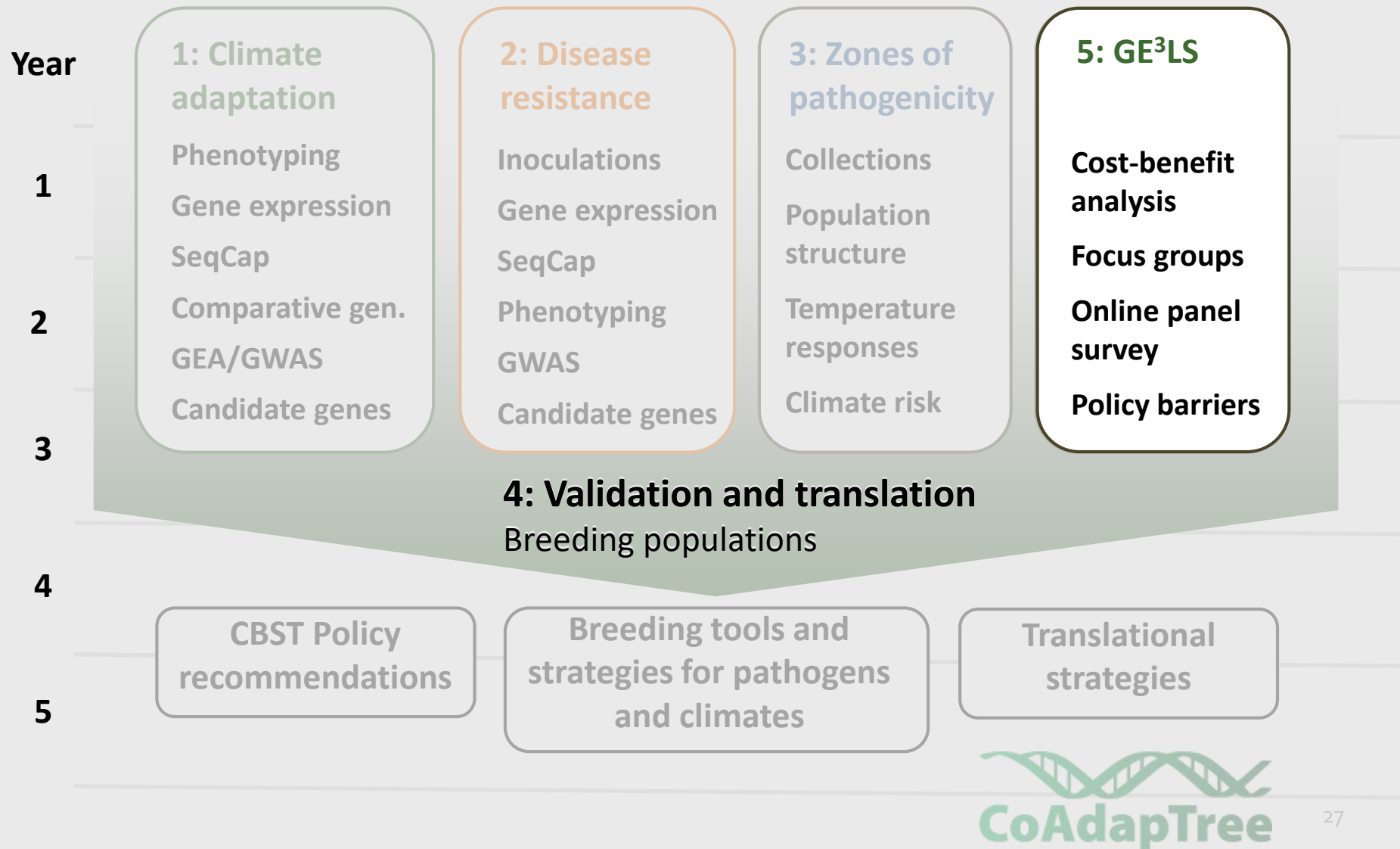


## 3.3: Climate models of outbreak risks

- Dothistroma: collection of occurrence points around the world in progress;
- 389 *D. septosporum* records 22 *D. pini* records in North America
- 2205 *D. septosporum* records 170 *D. pini* records worldwide
- SNC: collection of occurrence points in North America (mostly in western North America)
- Collaboration with Kishan Simbaraju (CFS), Tongli Wang, Andreas Hamann

# Activity 5: GE<sup>3</sup>LS

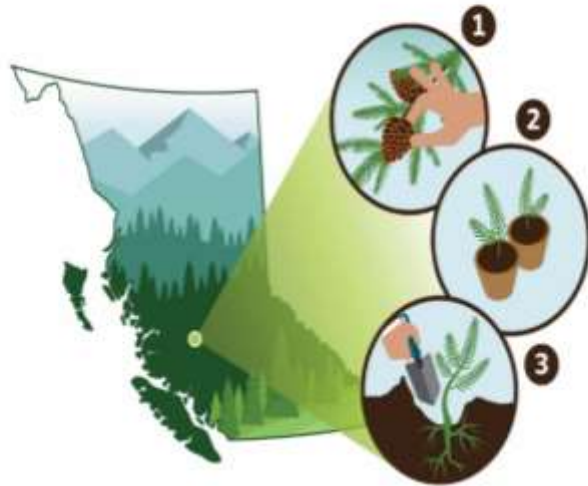
S. Hagerman, R. Kozak



# Survey of public acceptability of tree breeding, CBST and other adaptation strategies (N=1926): Broad acceptance of breeding and CBST

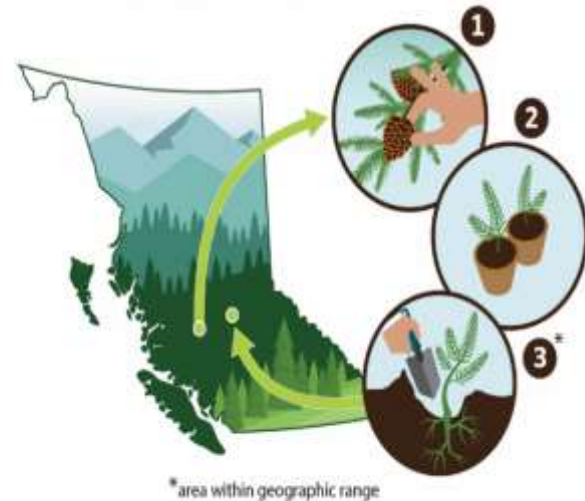
## Tree breeding, no seed transfer

(1) Forests are re-grown by collecting seeds thought to produce the healthiest and fastest growing trees. (2) These seeds are used to grow seedlings that are then (3) planted in close proximity to where the seeds originated, within the species' natural geographic range.



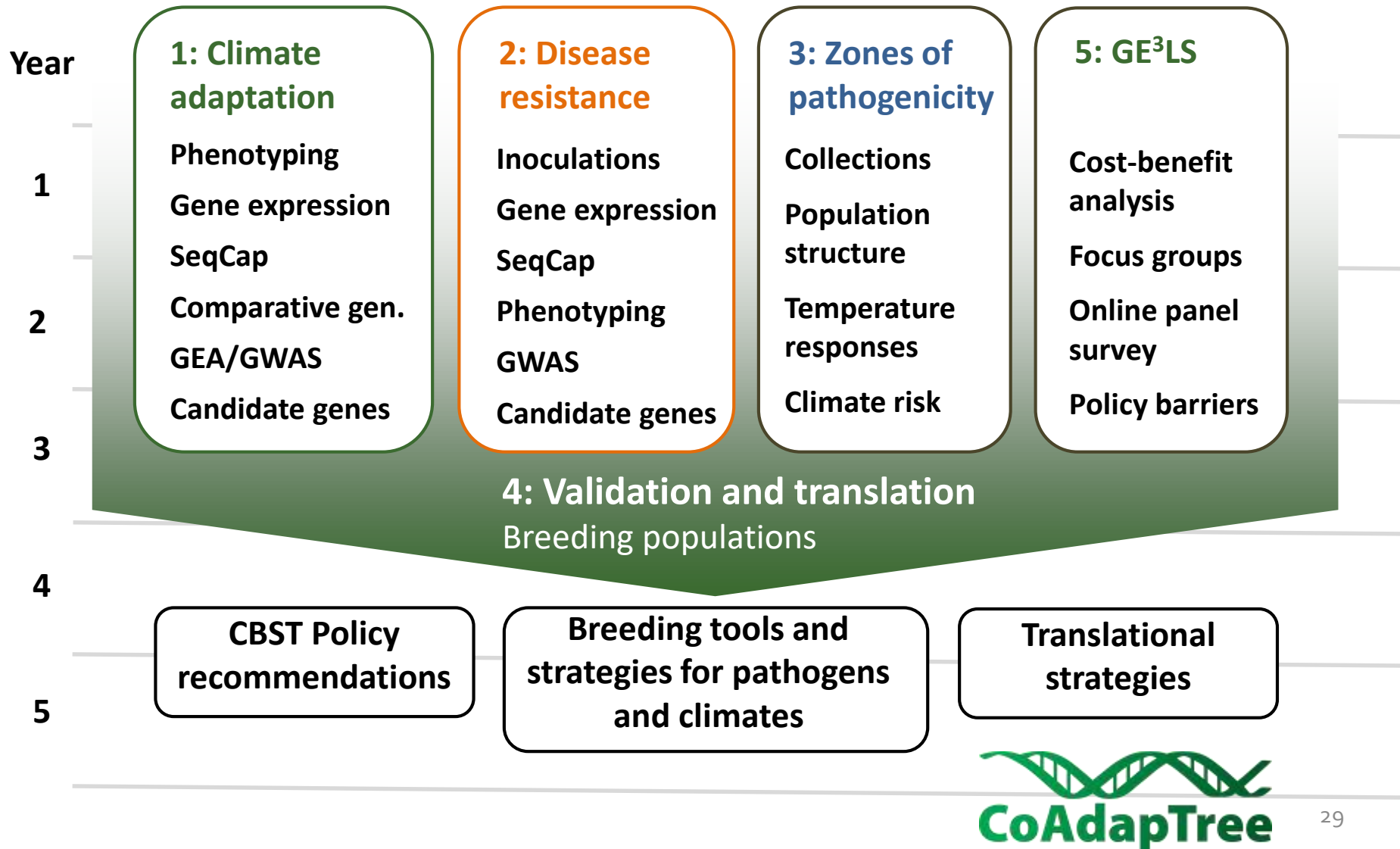
## Climate based seed transfer

(1) Forests would be re-grown by collecting seeds from trees that are genetically adapted to anticipated future climatic conditions. (2) These seeds would be used to grow seedlings that are then (3) planted at longer distances from where the seeds originated, but still within the species' natural geographic range, in that area at that time.



K. Findlater, S. Hagerman, R. Kozak. Stay tuned for results.

# Activities and timeline





# Plans for 2018/19

1. Establish two Douglas-fir seedling common gardens for drought, cold hardiness, phenology and growth phenotyping (Rafael Candido Ribeiro)
2. Sequence >20,000 genes in all populations of Douglas-fir (77) and larch (40)
3. Sequence pools of high and low drought hardiness, cold hardiness and disease resistance
4. Establish material from breeding populations for validation of climate and disease-related markers
5. Establish western larch seedling common garden for phenotyping cold and drought

**AdapTree Team:**

**Andreas Hamann** (Co-PL) – Geospatial anal. (U of A)  
**Jason Holliday** -- Re-sequencing (Virginia Tech)  
**Loren Rieseberg** -- Bioinformatics (UBC)  
**Michael Whitlock** -- Population structure (UBC)  
**Tongli Wang** -- Climatology (UBC)  
**Sam Yeaman** – Bioinformatics (UBC)  
**Kay Hodgins** – Bioinformatics (Monash U)  
**Katie Lotterhos** – Pop. structure (Wake Forest U)  
**Simon Nadeau** – Population genetics (UBC)  
**Haktan Suren** – Association gen. (Virginia Tech)  
**Jon Degner** – Hybrid analysis (UBC)

**CoAdapTree Team (partial list):**

**Sam Yeaman** – Genomics (U of Calgary)  
**Richard Hamelin** – Pathology (UBC and Laval)  
**Juergen Ehling, Ingo Ensminger, Shannon Hagerman,**  
**Rob Kozak, Loren Rieseberg, Mike Whitlock, Andreas**  
**Hamann**



**Ian MacLachlan** – Effects of breeding (UBC)  
**Katharina Liepe** – Geospatial analysis (U of A)  
**Kristin Nurkowski** – Genomics (UBC/Monash)  
**Laura Gray** – Phenotypic analysis (U of A)  
**David Roberts** – Geospatial analy. (U of A)  
**Gina Conte** – Bioinformatics (UBC)  
**Jon Degner** – Hybrid analysis & EEMS (UBC)  
**Rafael Candido Ribeiro** – Douglas-fir (UBC)  
**Pia Smets** – Project management (UBC)

**Collaborators (partial list):**

**FLNRO:** Greg O'Neill, Nick Ukrainetz, Barry Jaquish, Trevor Doerksen, Michael Stoehr  
**FGC:** Jack Woods, Brian Barber  
**USFS:** Brad St. Clair, Richard Cronn  
**UC Davis:** David Neale (PineRefSeq)  
**UBC:** Joerg Bohlmann (white spruce genome)

Thanks to the FGC, ITAC, FLNRORD and VSOC for co-funding



GenomeCanada



Genome  
British Columbia



GenomeQuébec



GenomeAlberta



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Lands & Natural  
Resource Operations



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Solutions



Vernon Seed Orchard  
Company



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of British Columbia



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