

Genomics is a tool, not an outcome, for developing reforestation strategies for new climates

Sally Aitken

Department of Forest and Conservation Sciences
University of British Columbia



Forestry
University of British Columbia

AdapTree 



Assessing the adaptive portfolio of reforestation stocks for future climates



Genomic data analysis:

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)

Principal investigators:

Andreas Hamann (Co-PI) – Geospatial anal. (U of A)

Jason Holliday -- Re-sequencing (Virginia Tech)

Loren Rieseberg -- Bioinformatics (UBC)

Michael Whitlock -- Population structure (UBC)

Tongli Wang -- Climatology (UBC)

Rob Kozak – Socioeconomics (UBC)

Team members:

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)

Jon Degner – Hybrid analysis (UBC)

David Roberts – Geospatial analy. (U of A)

Jon Degner – Hybrid analysis (UBC)

Pia Smets – Project management (UBC)

Reem Hajjar - Socioeconomics UBC

Erin McGuigan - Socioeconomics UBC

Molly Moshofsky - Socioeconomics UBC

Old knowledge (19th century): Growth of trees in common gardens reflects differences in “home” climate



- Most variation continuous, not discrete
- Variation physiological rather than morphological
- Common gardens needed to study variation
- Local seed should be used for reforestation

*Aitken and Bemmels. 2016.
Evolutionary Applications.*

Local geographic zones used to manage
local adaptation across heterogeneous areas
but local seed use is becoming inadequate

Lodgepole pine



Pinus contorta ssp. latifolia

'Interior' spruce complex



Picea glauca



hybrid



P. engelmannii

SCIENCE

The New York Times

For Trees Under Threat, Flight May Be Best Response

SEPT. 18, 2014



Trees setting sail in Croatia.



518

CATEGORIES SECTIONS LIVE

E-News

TIME FOR TREES TO PACK THEIR TRUNKS?

As climate changes, forest ecosystems will need to shift to more suitable sites. Should humans lend a helping hand?

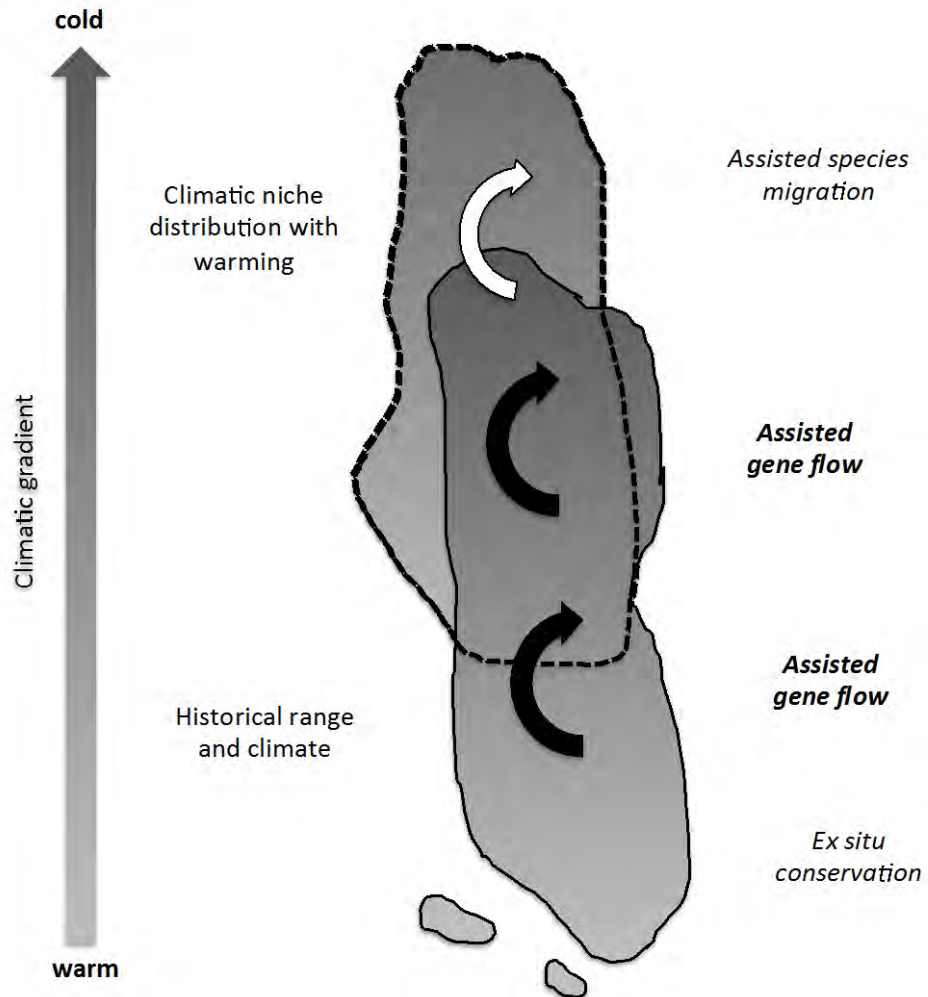


Assisted gene flow strategies informed by patterns of local adaptation to climate

Assisted gene flow:

Intentional translocation of individuals within a species range to facilitate adaptation to anticipated local conditions.

(Aitken and Whitlock 2013 Ann Rev Ecol Evol Syst)

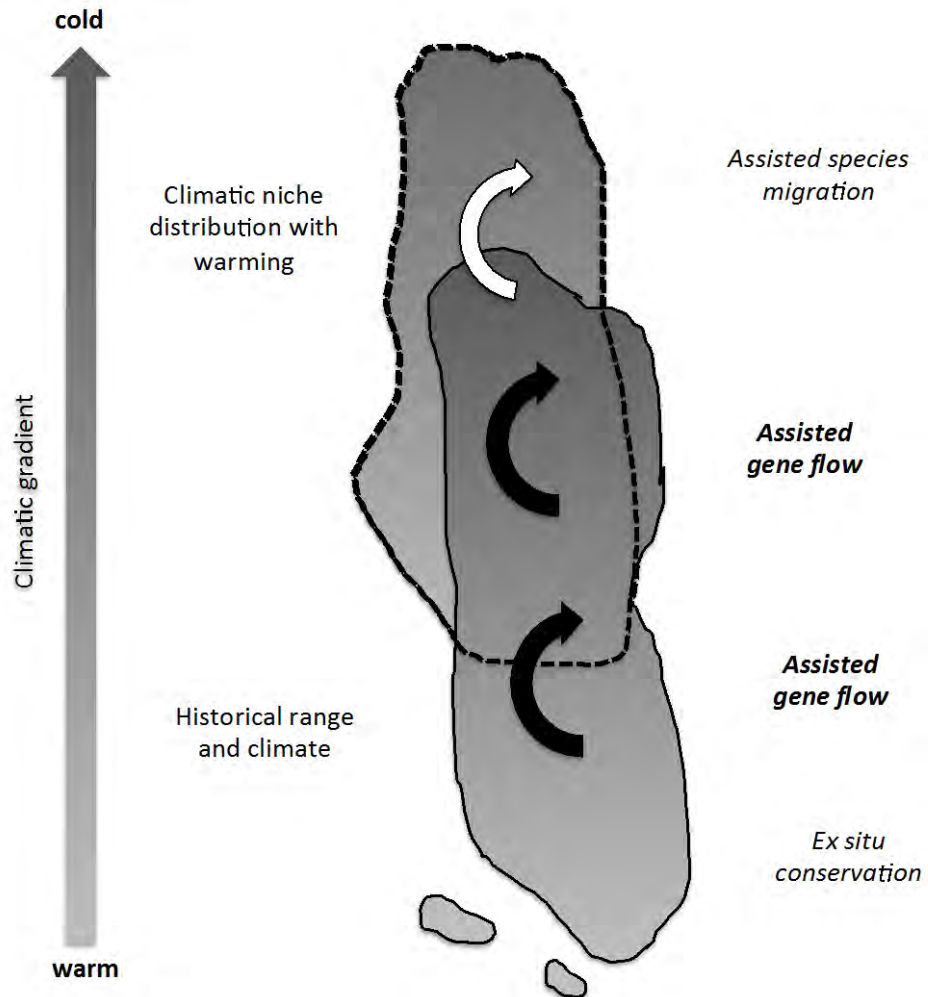


(Aitken and Bemmels. 2016. Evolutionary Applications)

Assisted gene flow strategies informed by patterns of local adaptation to climate

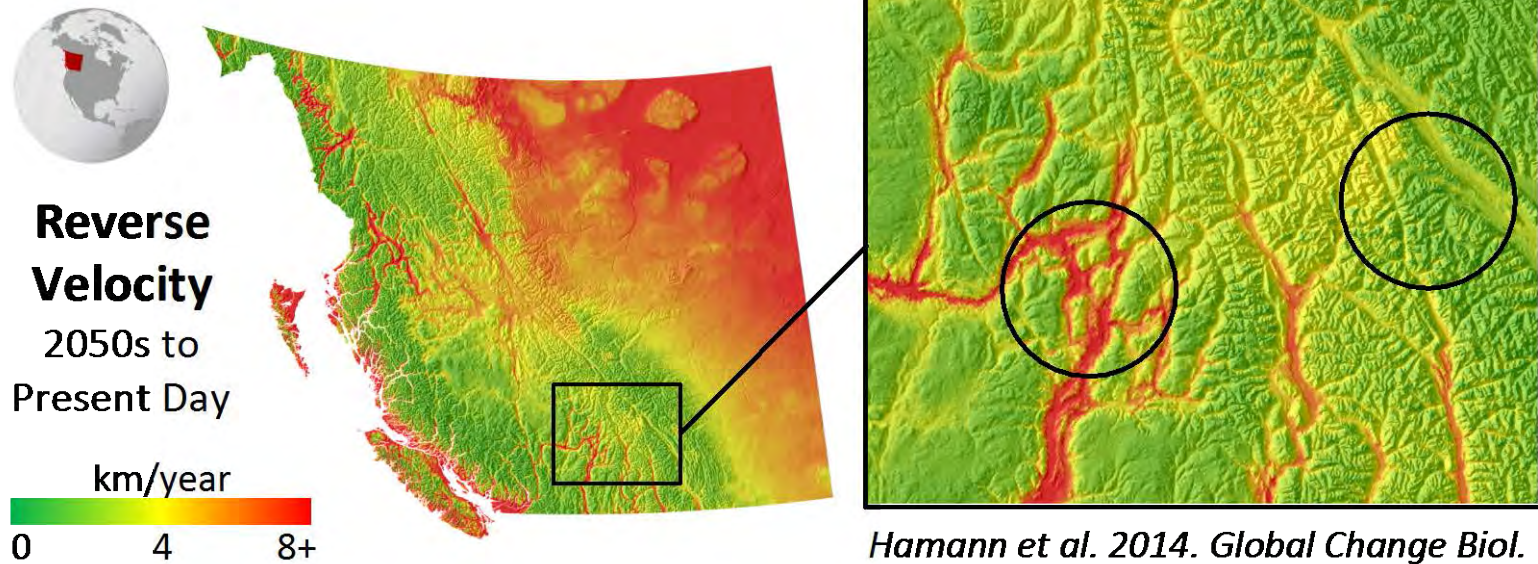
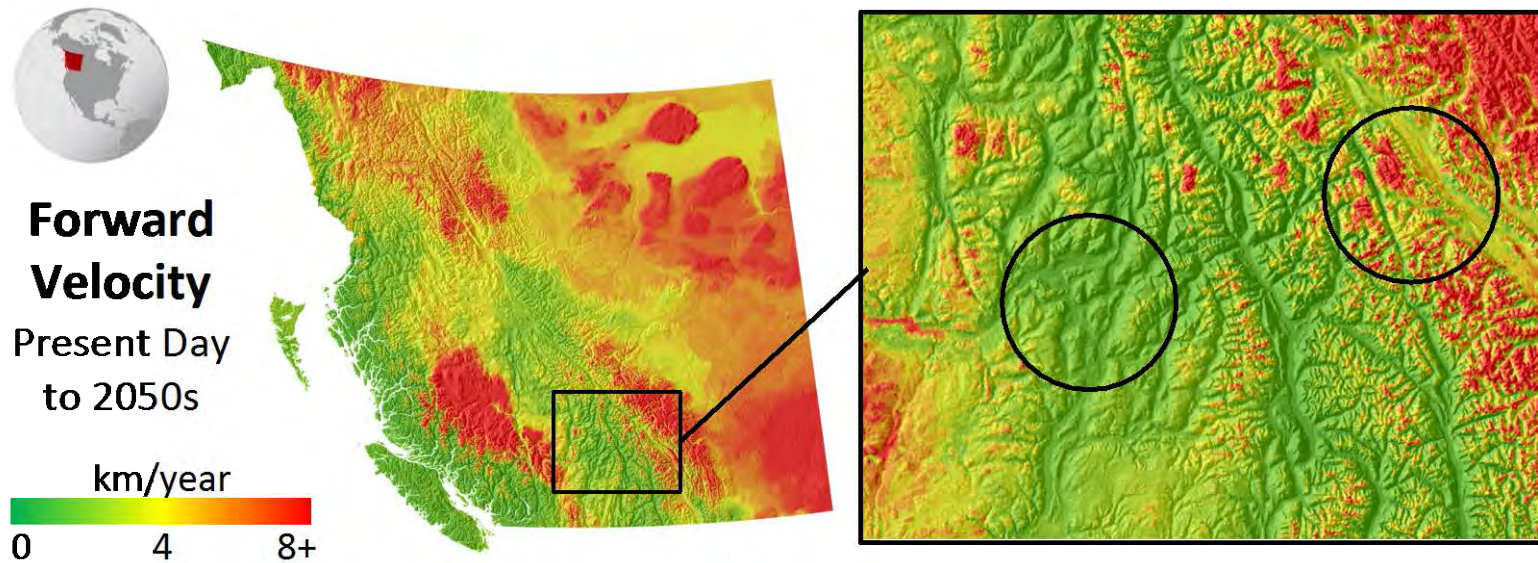
Assisted gene flow strategies can be based on:

- 1) *Climate models*
- 2) *Field or seedling provenance trial data for focal species*
- 3) *Field or seedling provenance trial data for sympatric species*
- 4) *Genomic data on local adaptation*



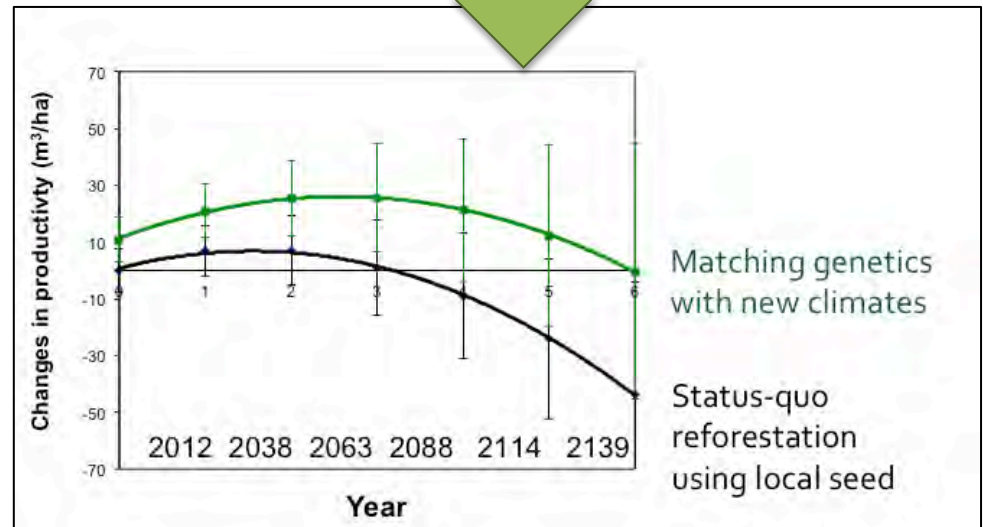
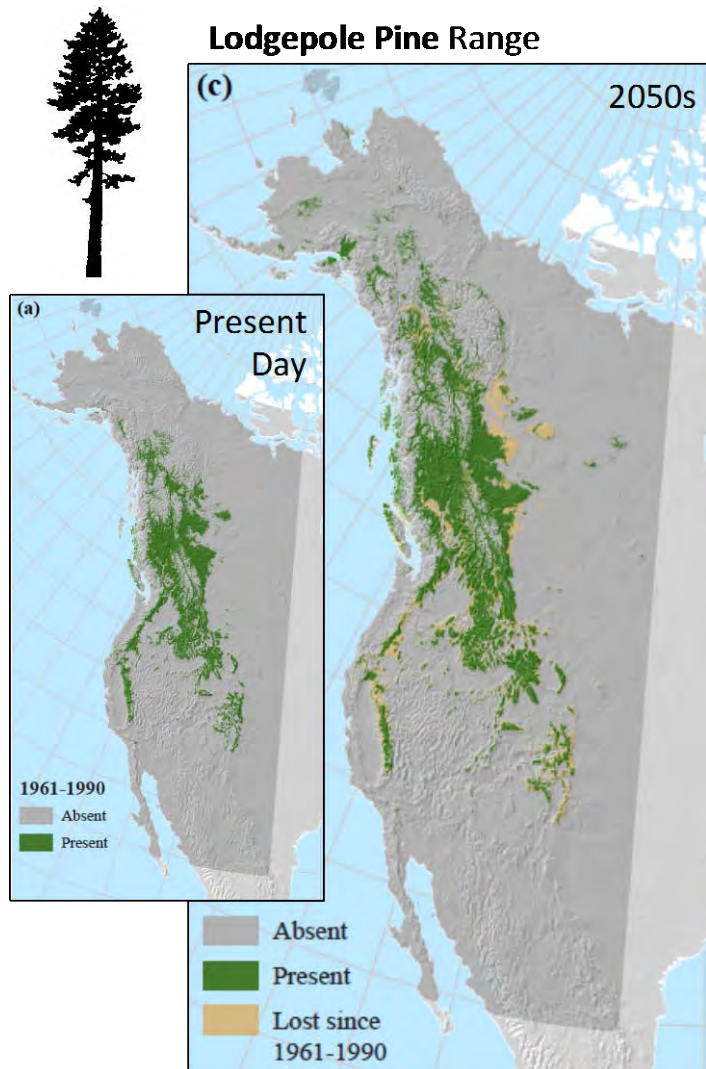
(Aitken and Bemmels. 2016.
Evolutionary Applications)

1) Climate models, e.g., velocity of climate change



Hamann et al. 2014. Global Change Biol.

2) Provenance trials used to predict impacts of climate change and design assisted gene flow



Wang et al. 2006

3) Use generalized patterns from sympatric species along climatic gradients? (primarily temperature driven*)

<i>Abies concolor</i>	Wright et al. 1971
<i>Abies grandis</i>	König 1995 Xie and Ying 1993
<i>Abies lasiocarpa</i>	Hansen et al. 2004
<i>Abies procera</i>	Xie and Ying 1994
<i>Cornus nuttallii</i>	Keir et al. 2011
<i>Picea engelmannii</i>	Rehfeldt 1994
<i>Picea pungens</i>	Bongarten 1978
<i>Picea sitchensis</i>	Mimura and Aitken 2007 Ying 1997
<i>Pinus albicaulis</i>	Bower and Aitken 2008
<i>Pinus attenuata</i>	Brown and Doran 1985
<i>Pinus contorta</i>	Dow et al. 1998 Illingworth 1978
<i>Pinus monticola</i>	Rehfeldt et al. 1984
<i>Pinus ponderosa</i>	Enrico et al. 2000 Read 1980
<i>Populus trichocarpa</i>	McKown et al. 2013
<i>Pseudotsuga menziesii</i>	Sweet 1965 White and Ching 1985
<i>Quercus garryana</i>	Huebert 2009
<i>Thuja plicata</i>	Cherry 1995
<i>Tsuga heterophylla</i>	Kuser and Ching 1981

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*Alberto et al. 2013. *Global Change Biology*

Aitken and Bemmels. 2016.
Evolutionary Applications

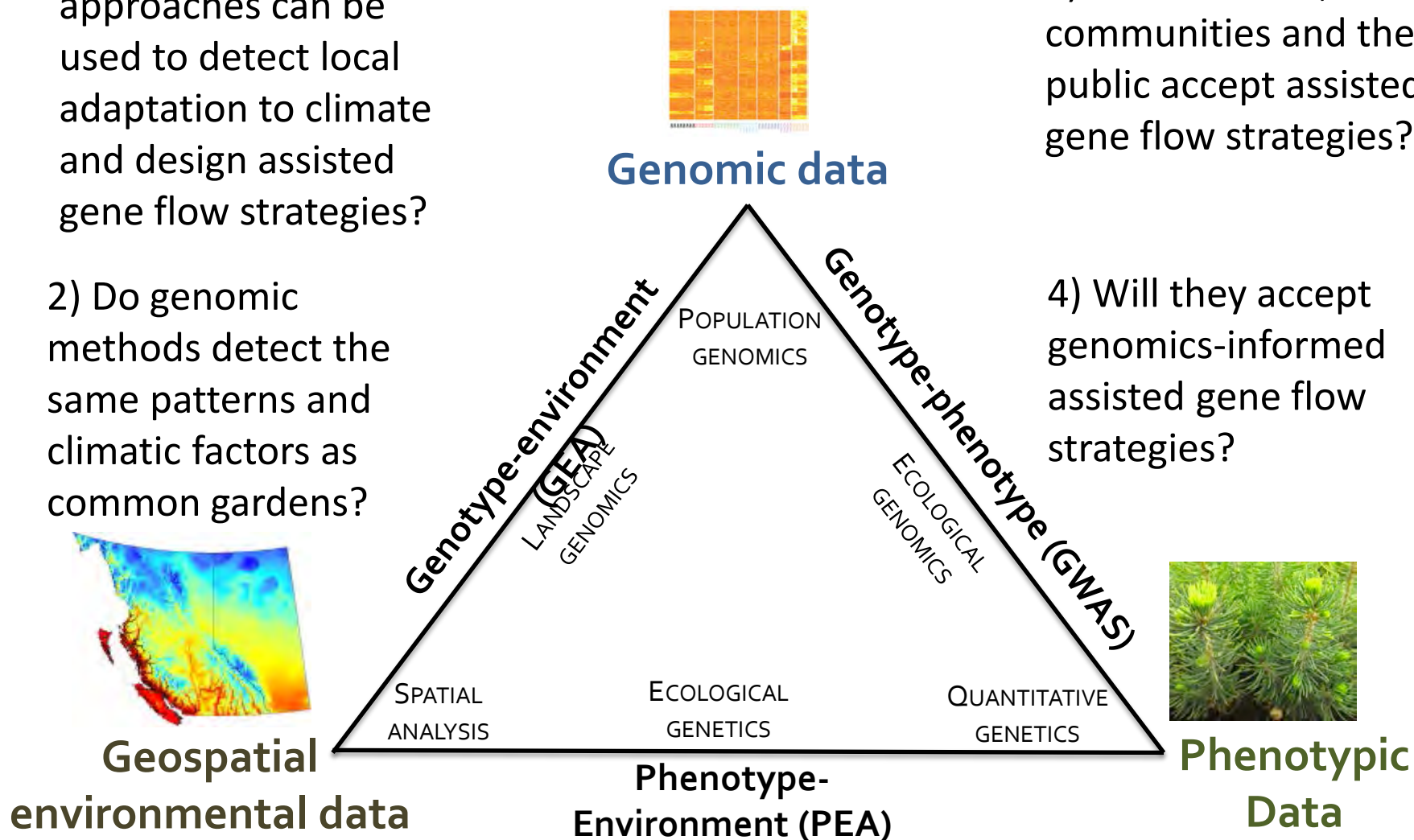
Can genomic data be used to design assisted gene flow?

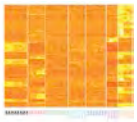
1) What genomic approaches can be used to detect local adaptation to climate and design assisted gene flow strategies?

2) Do genomic methods detect the same patterns and climatic factors as common gardens?

3) Will foresters, communities and the public accept assisted gene flow strategies?

4) Will they accept genomics-informed assisted gene flow strategies?





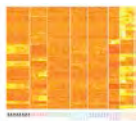
Genomic approaches

RNAseq experiment:

- temperature, moisture, photoperiod treatments



- Pine transcriptome aligned to loblolly PineRefSeq genome;
- Spruce aligned to SMarTForests interior spruce genome for probe design



Genomic approaches

RNA seq experiment:

- temperature, moisture, photoperiod treatments



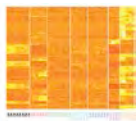
- Pine transcriptome aligned to loblolly ref. genome;
- Spruce to interior spruce genome for probe design

Sequence capture:

- ~25K genes
- 4,500 non-coding regions
- ~600 trees/sp



- Pine: 10.9 million SNPs;
1.25 million after filters
- Spruce: 8.3 million SNPs;
1.1 million after filters



Genomic approaches

RNA seq experiment:

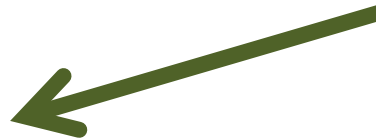
- temperature, moisture, photoperiod treatments



- Pine transcriptome aligned to loblolly ref. genome;
- Spruce to white spruce genome for probe design

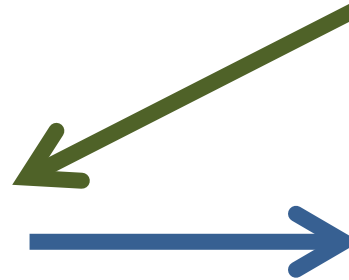
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- **Genotype-environment associations (GEA)**
- **Genotype-phenotype associations (GWAS)**



- 50K lodgepole pine SNP array**
- 50K interior spruce SNP array**
- GEA, GWAS candidates
- Functional candidates
- Control loci

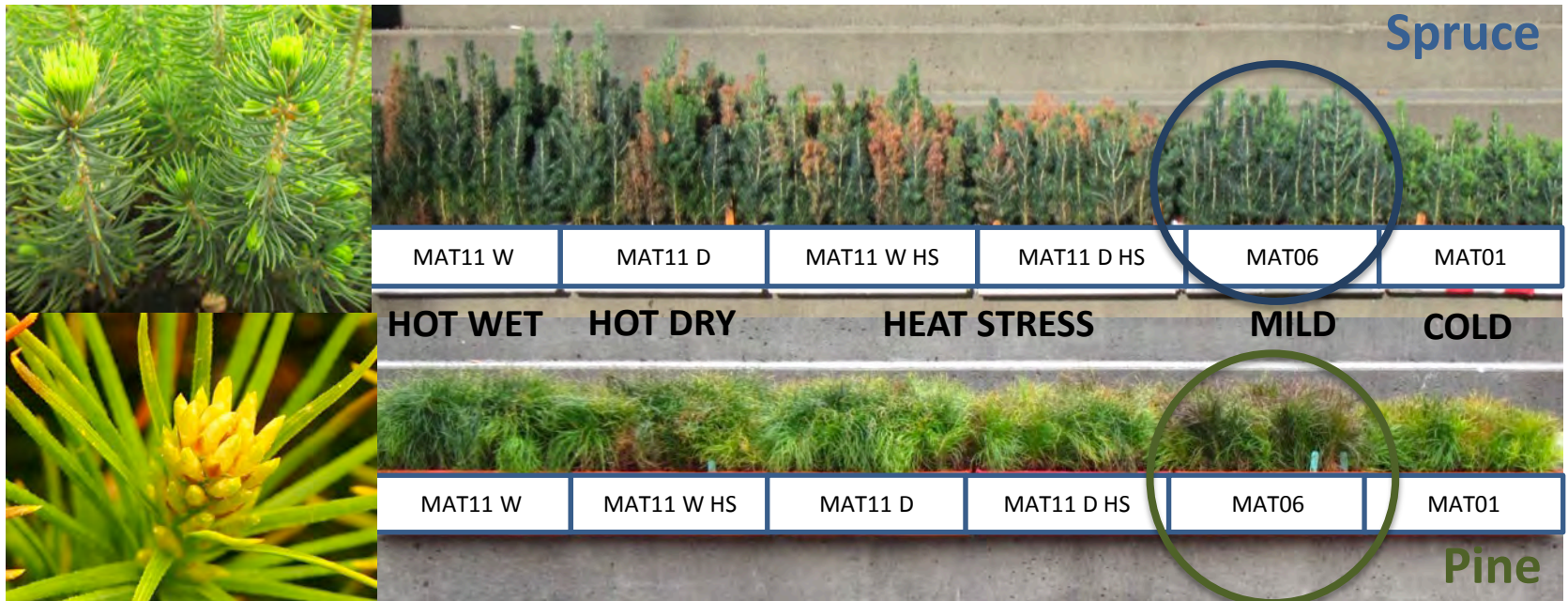
Intensive phenotyping effort

- 4 treatments x 2 species in controlled climate chambers
- 1 outdoor experiment per species comparing natural & breeding pops

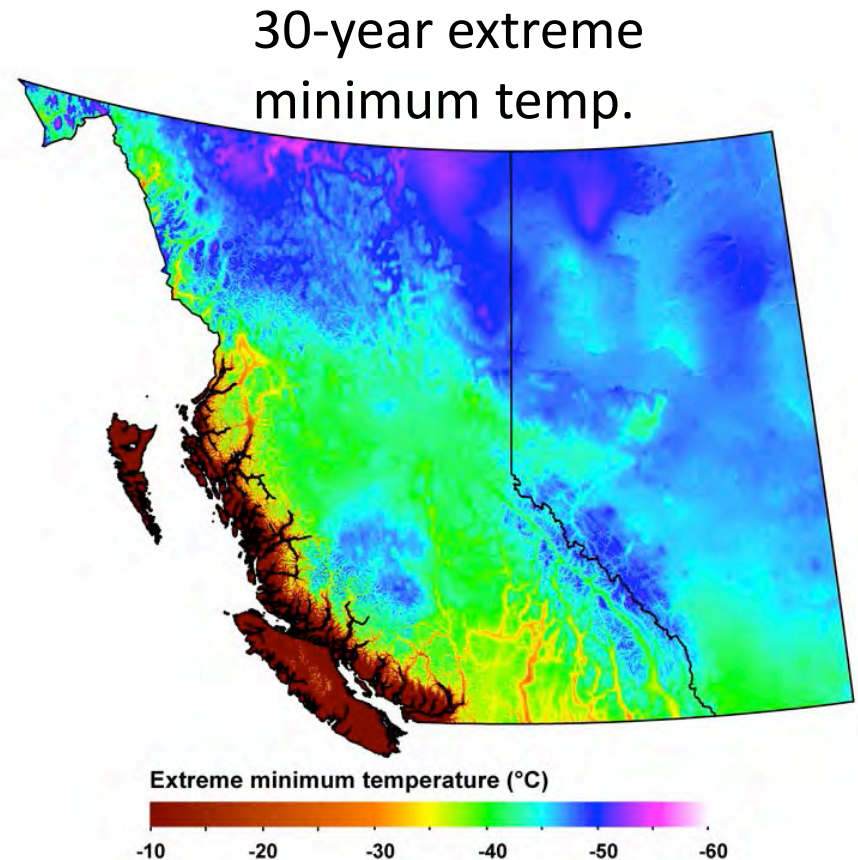
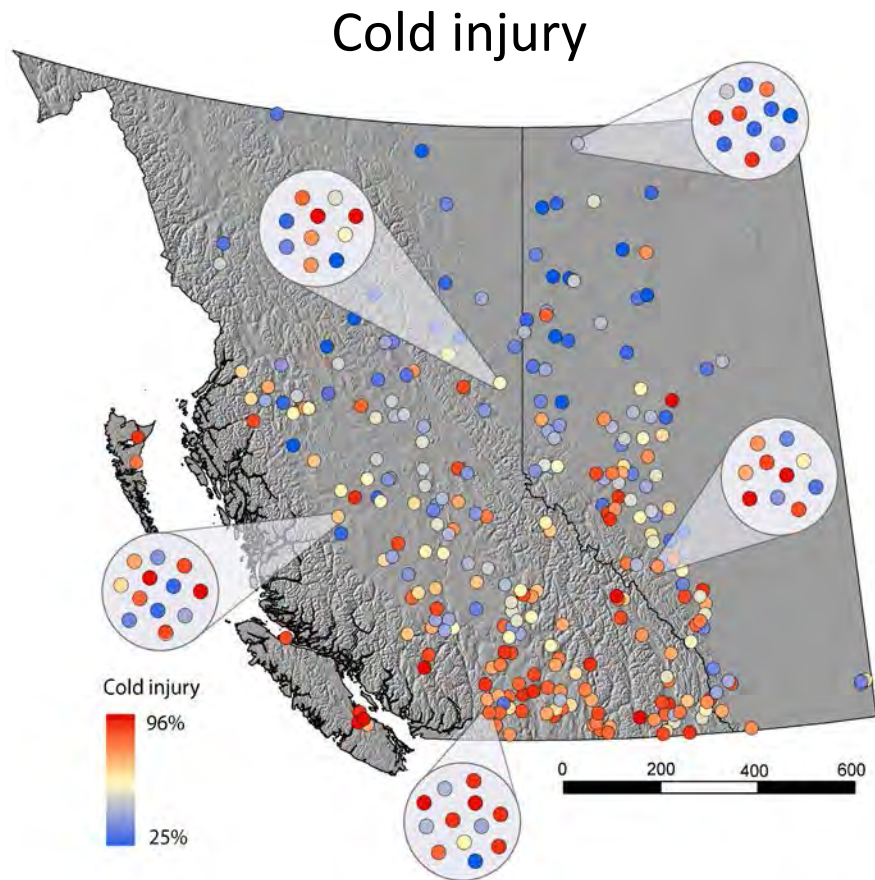
Plant size: Height, diameter, and root, shoot and total biomass

Phenology: Bud break, bud set, growing season length, growth curve

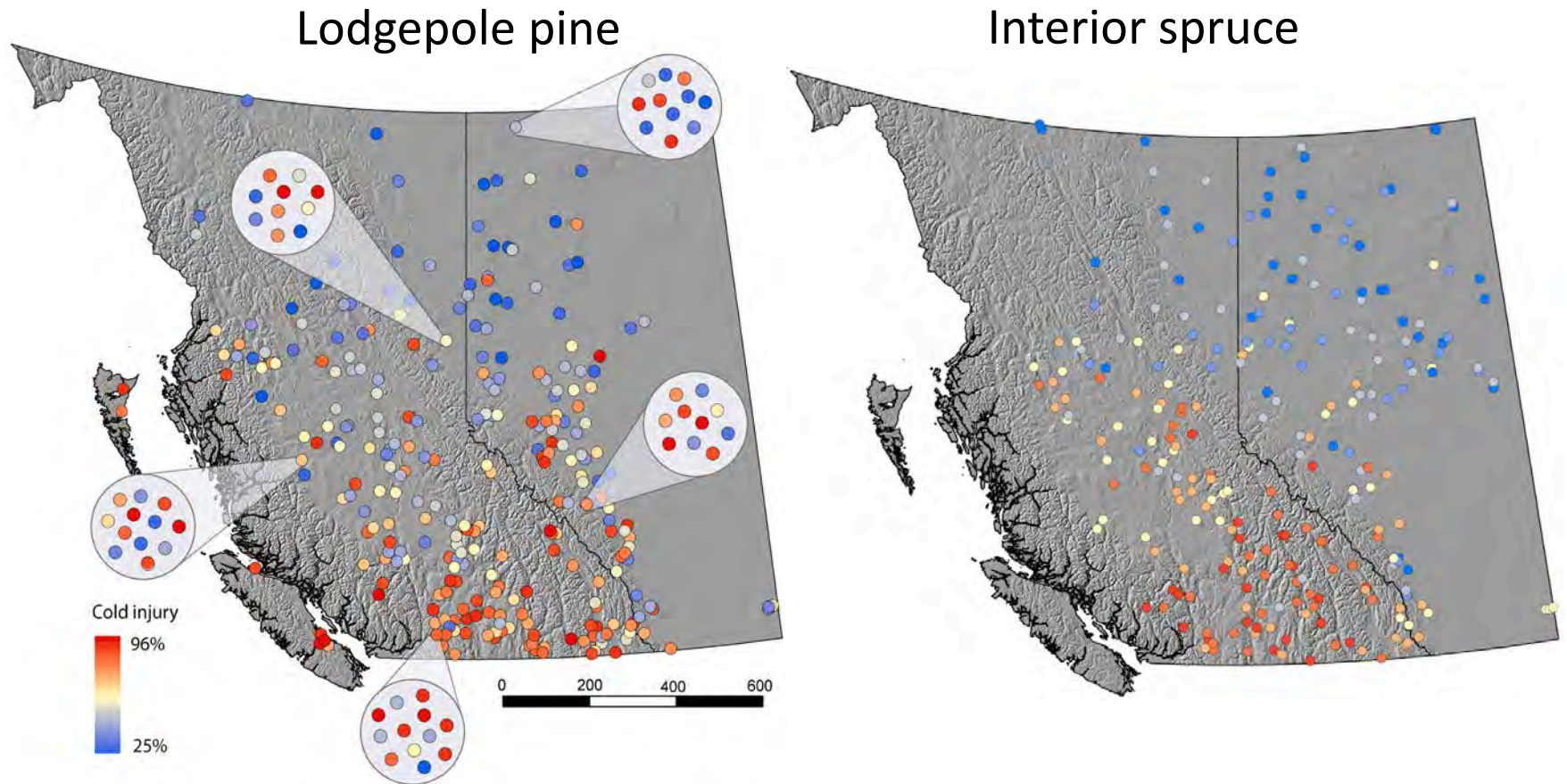
Cold hardiness: Fall, winter and spring cold injury in artificial freeze tests



Cold hardiness in artificial freeze tests showed strongest local adaptation in lodgepole pine

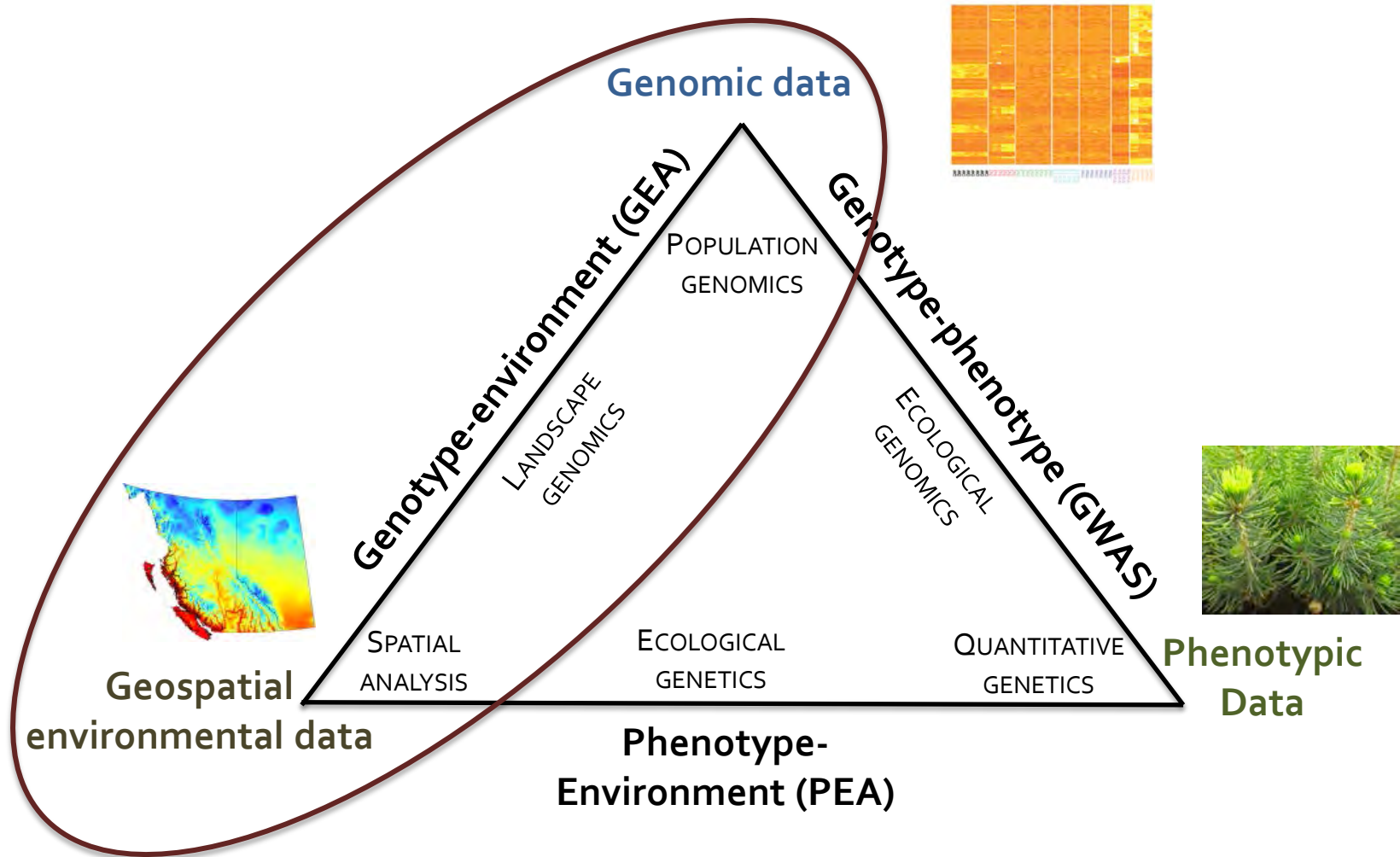


Lodgepole pine and interior spruce showed very similar geographic patterns of cold hardness



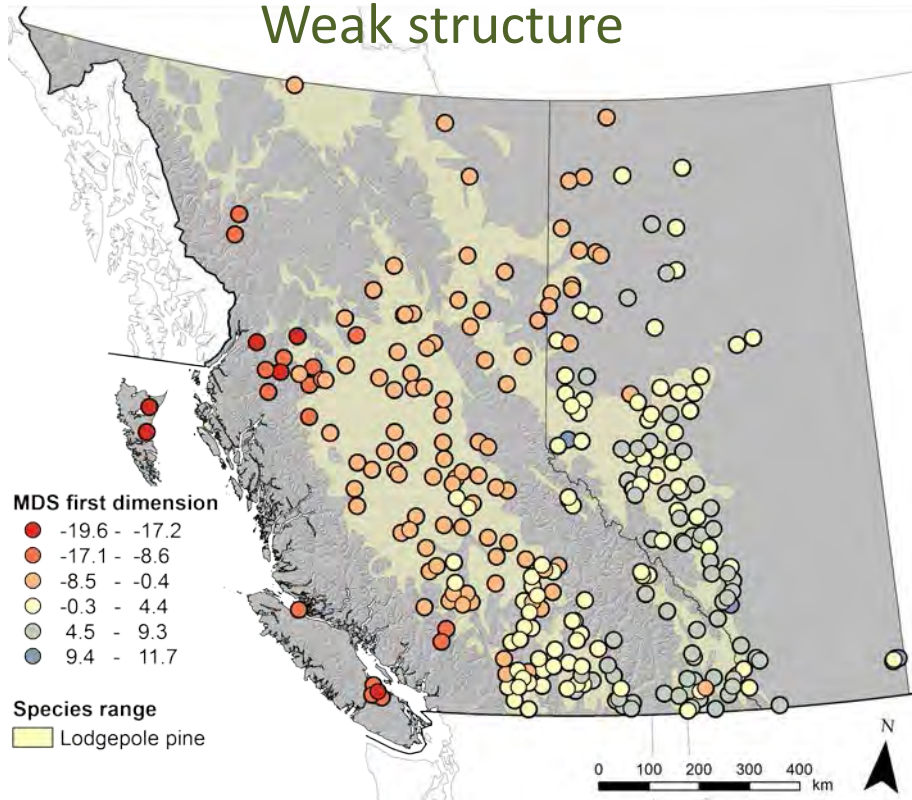
Phenotypic variation among
populations (V_{pop}) 22 to 50% of total

Can we detect patterns of local adaptation from genomic data?

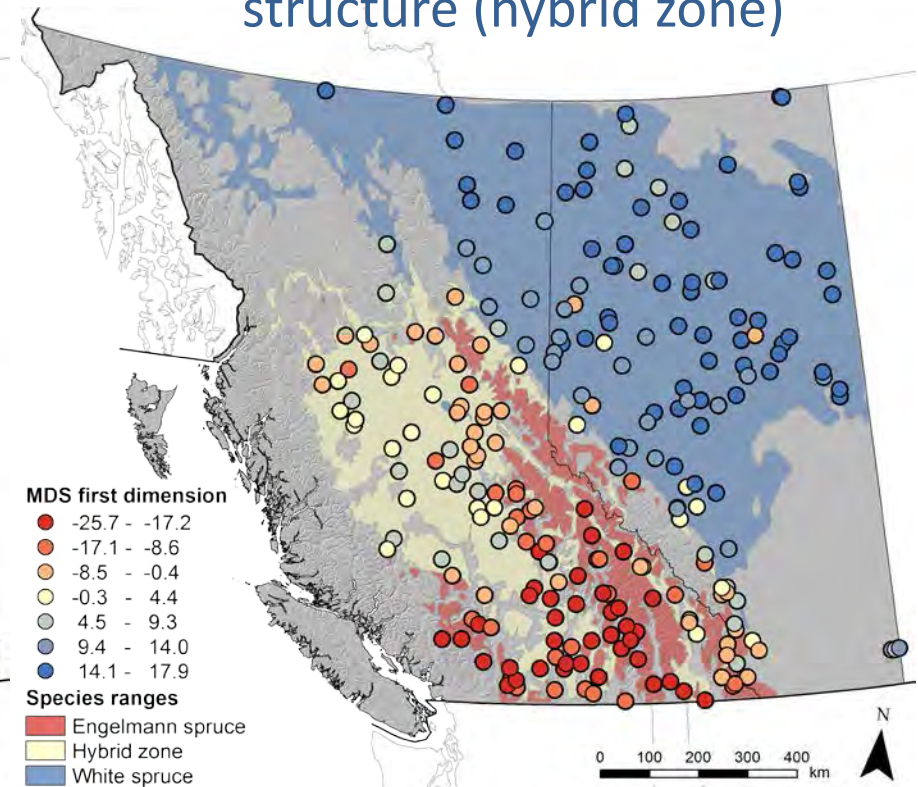


Adjust for neutral population structure in genomic analyses (multi-dimensional scaling using independent set of ~10K non-coding SNPs)

Lodgepole pine:
Weak structure

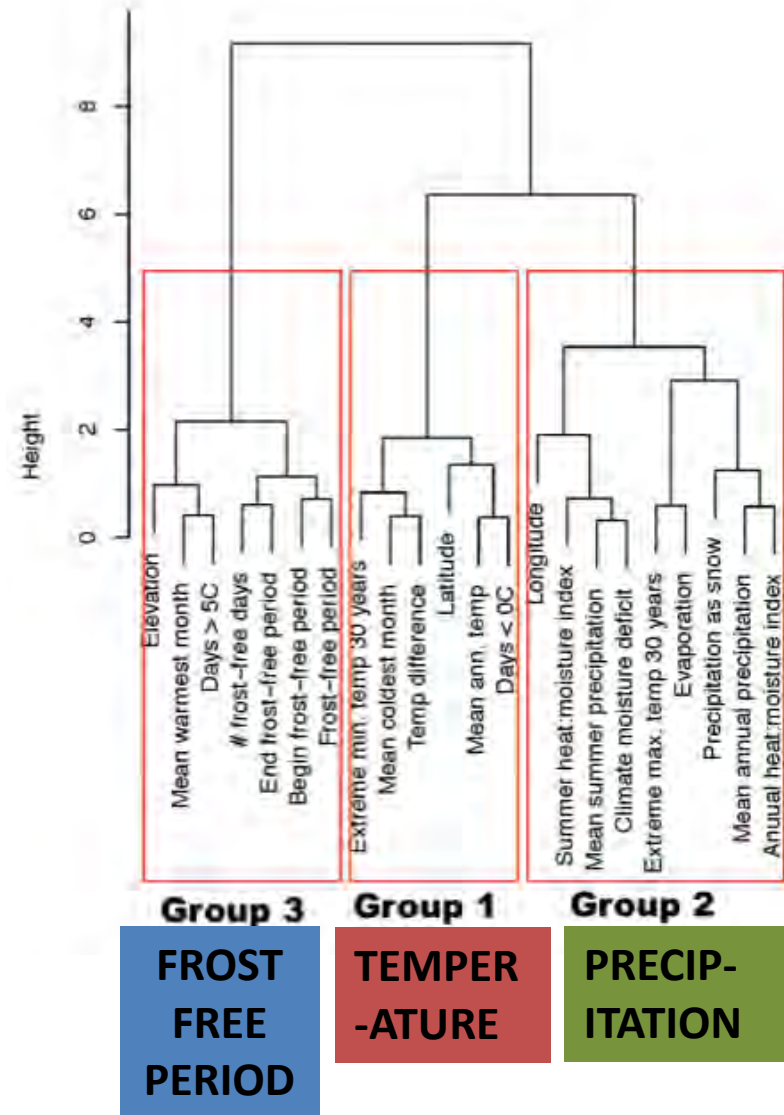


Interior spruce: Strong
structure (hybrid zone)

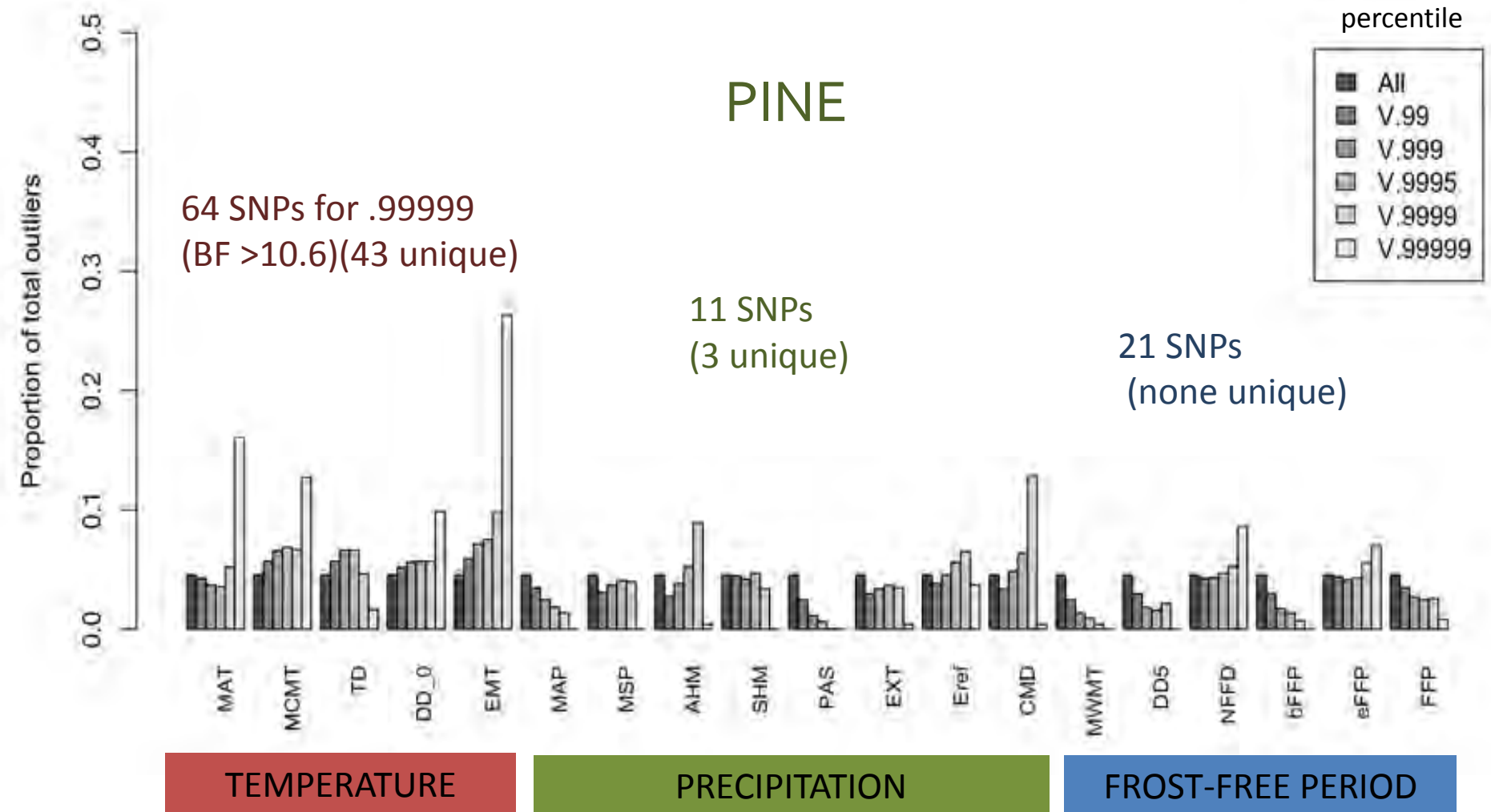


See Lotterhos and Whitlock 2014, 2015 Molecular Ecology on population structure and false positives in outlier tests.

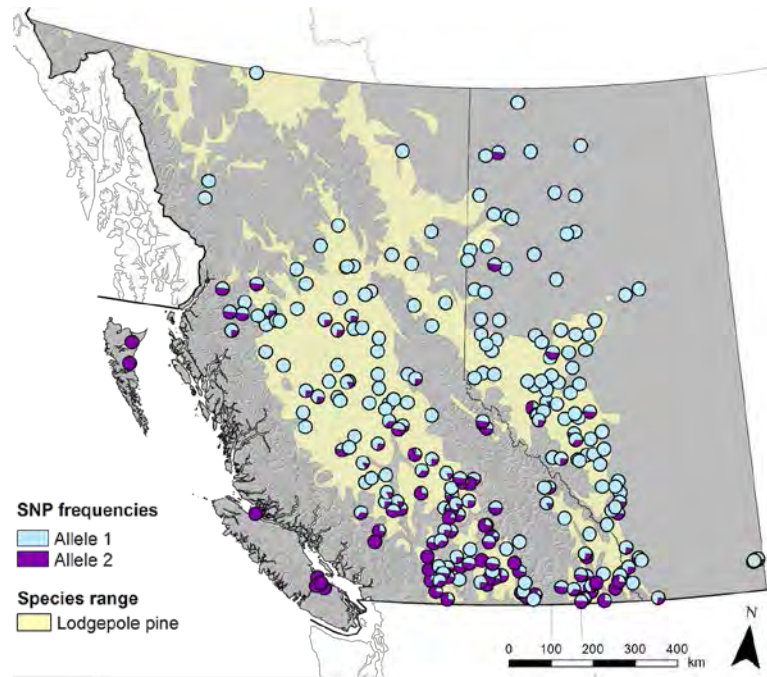
GEA: 19 climatic variables from ClimateWNA and 3 geographic variables form 3 clusters



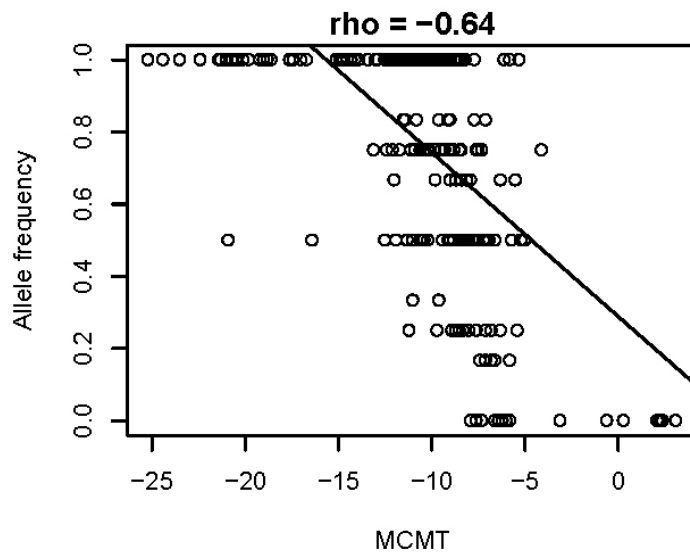
Relative importance of climatic variables in Bayenv2 (Gunther and Coop 2013) depends on threshold; enrichment for temperature variables



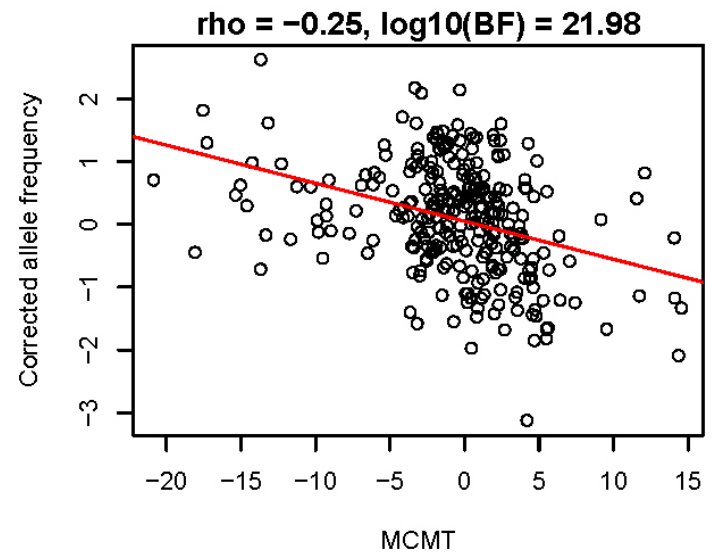
SNP with strongest GEA – PINE



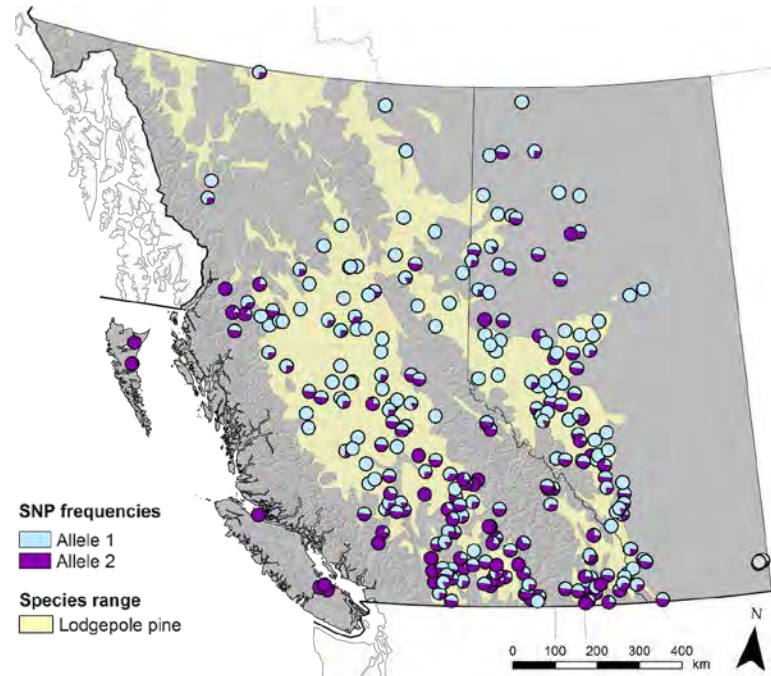
No population structure adj.



Population structure adj. (Bayenv2)

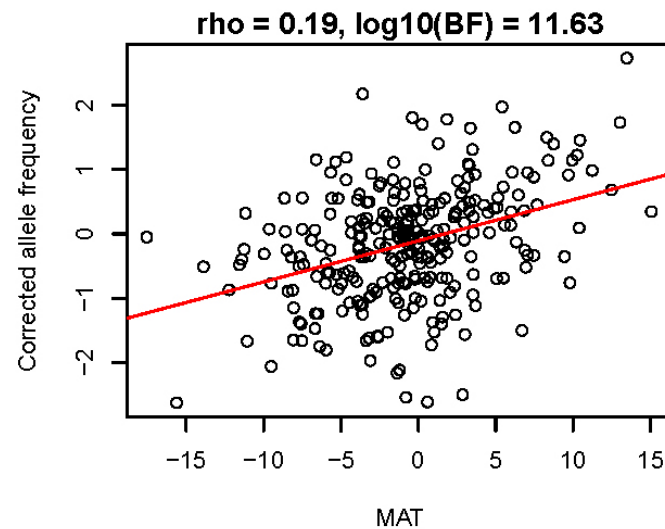
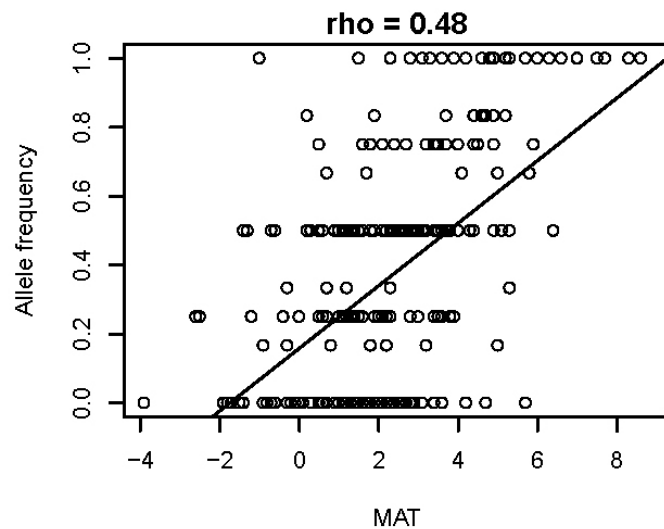


SNP with 34th strongest GEA – PINE

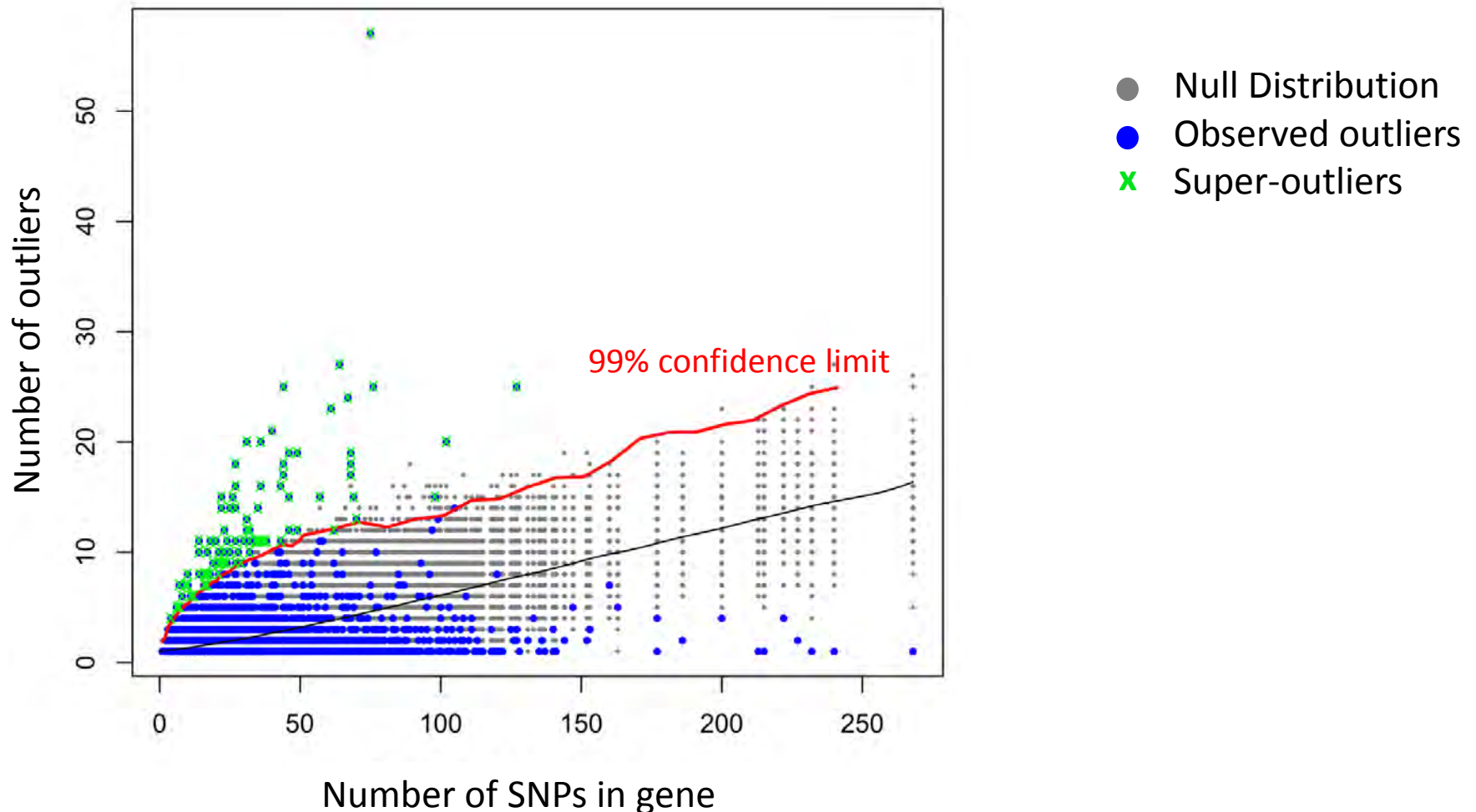


No population structure adj.

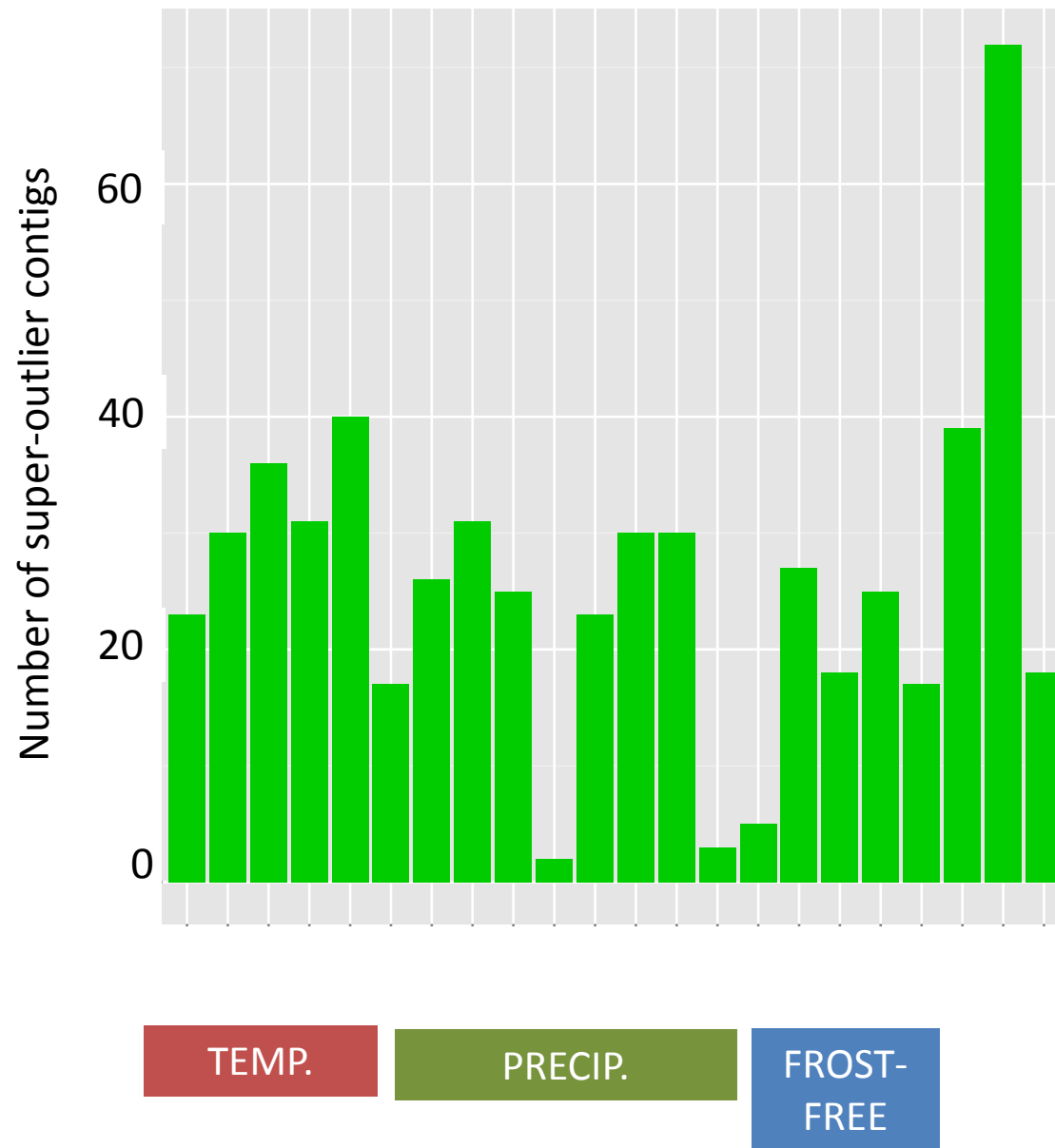
Population structure adj. (Bayenv2)



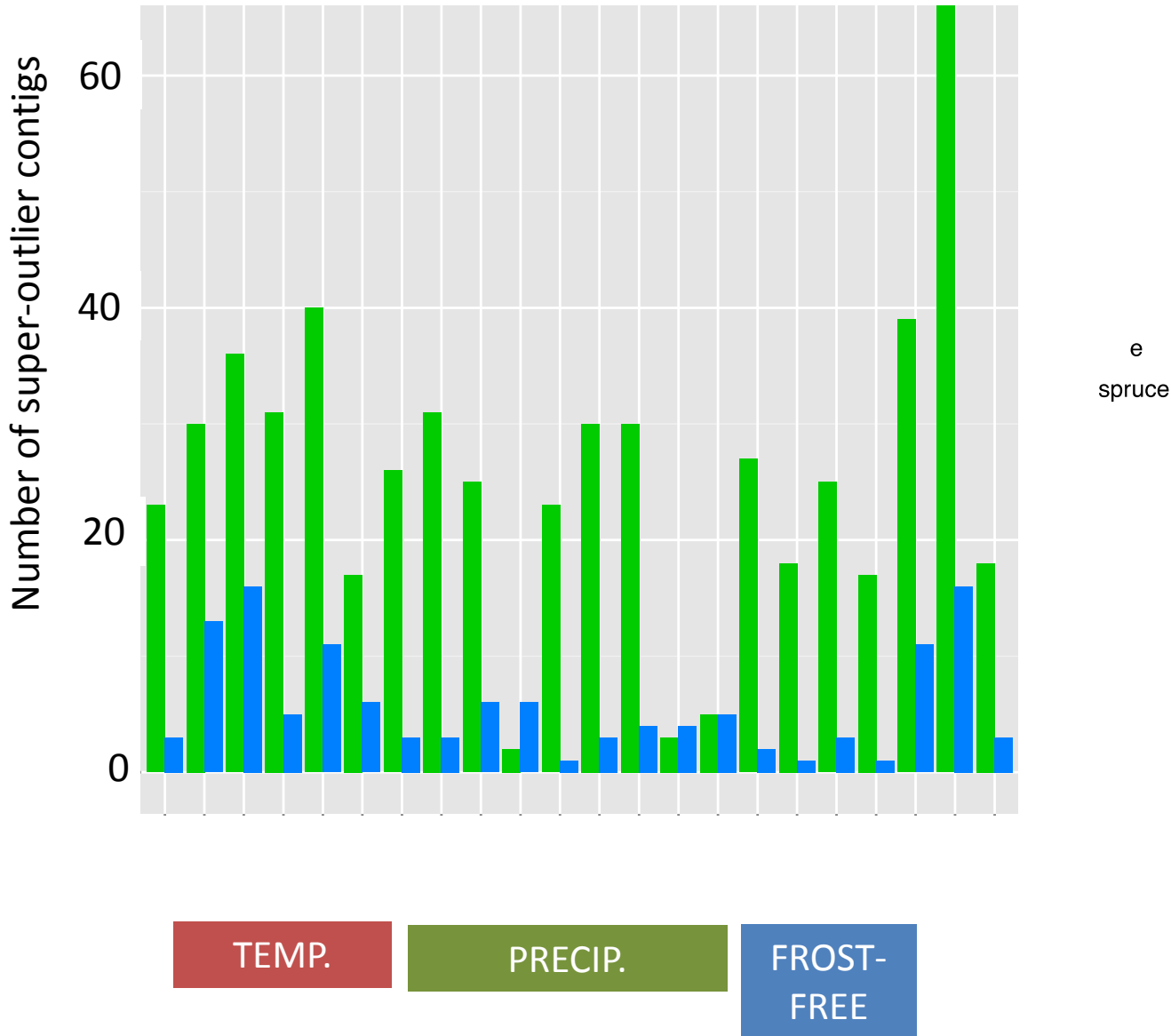
Identify **super-outlier genes** based on high number of outlier SNPs relative to random expectation



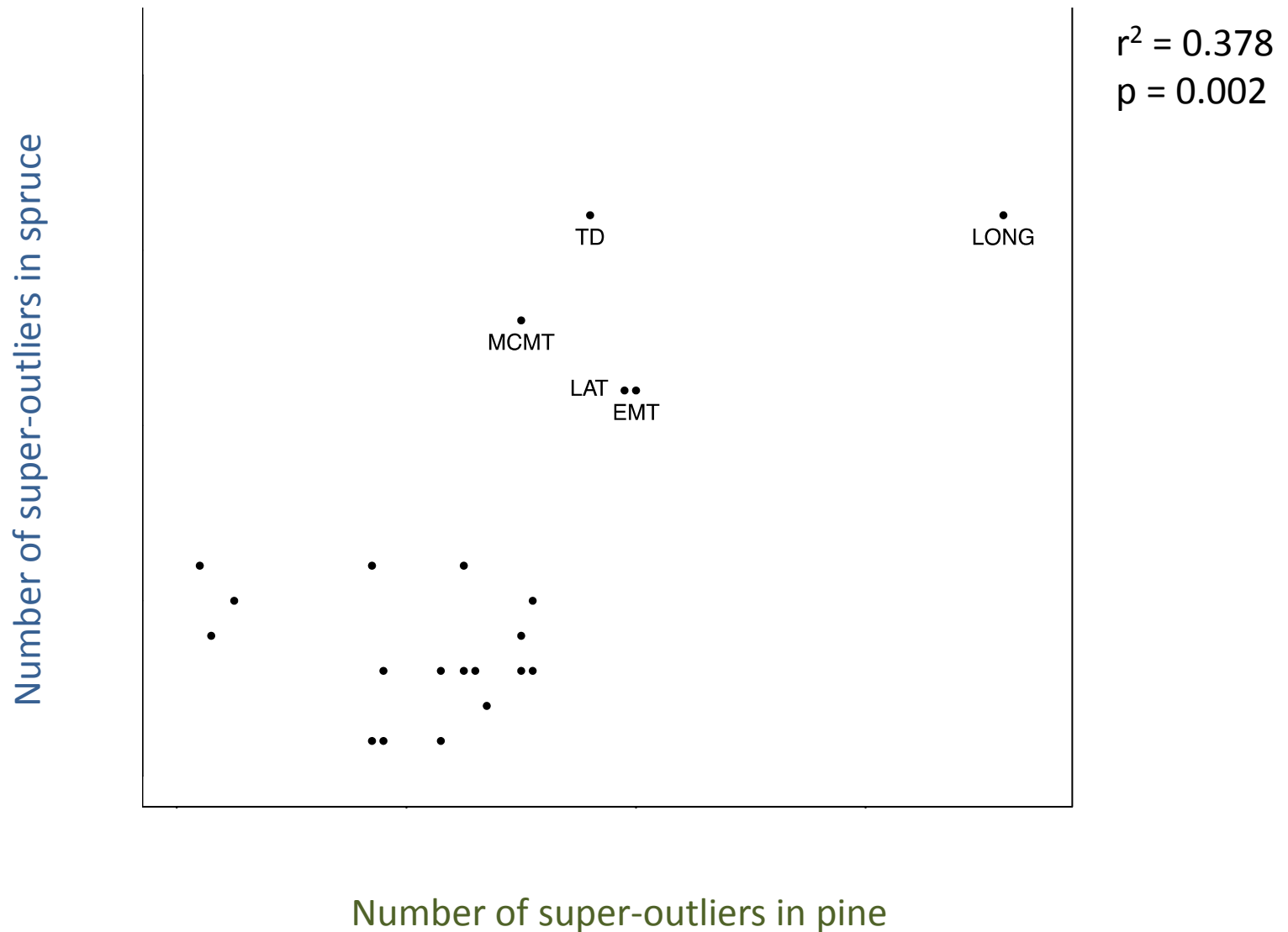
GEA Super-outliers (Bayenv2; pine)



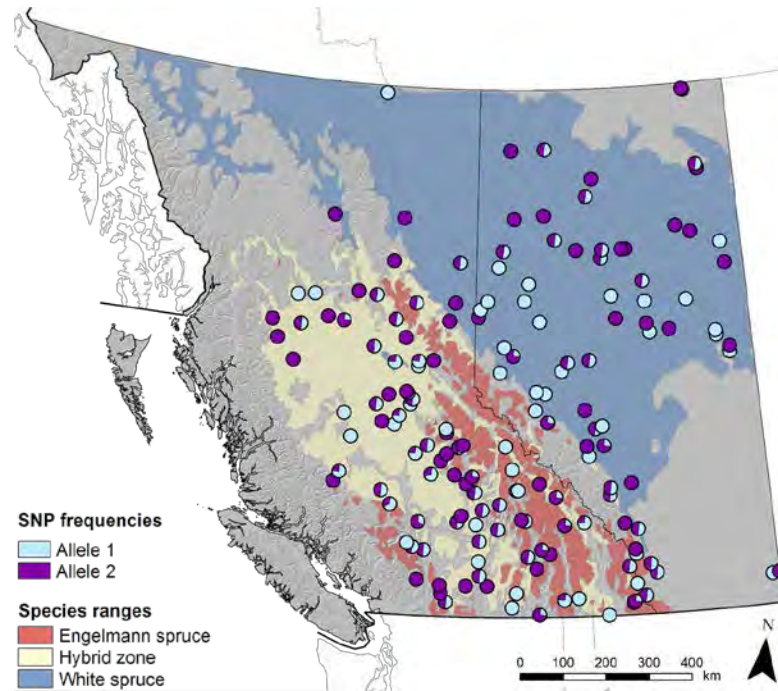
Spruce has far fewer GEA super-outliers than pine but similar climatic drivers



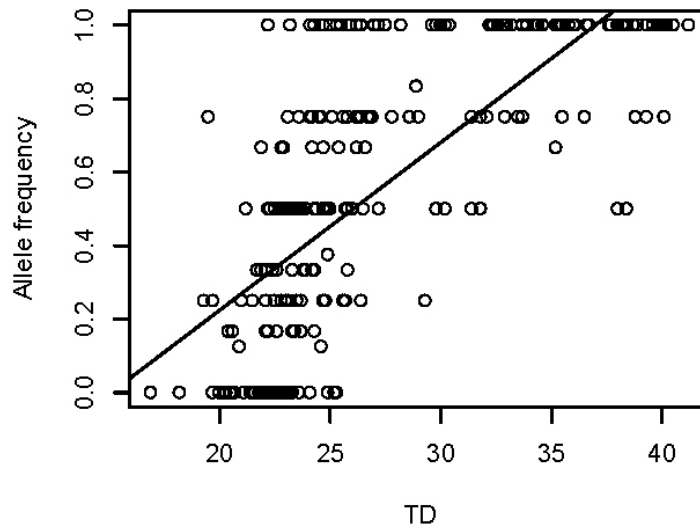
Similar environmental drivers of GEA in pine and spruce (Bayenv2)



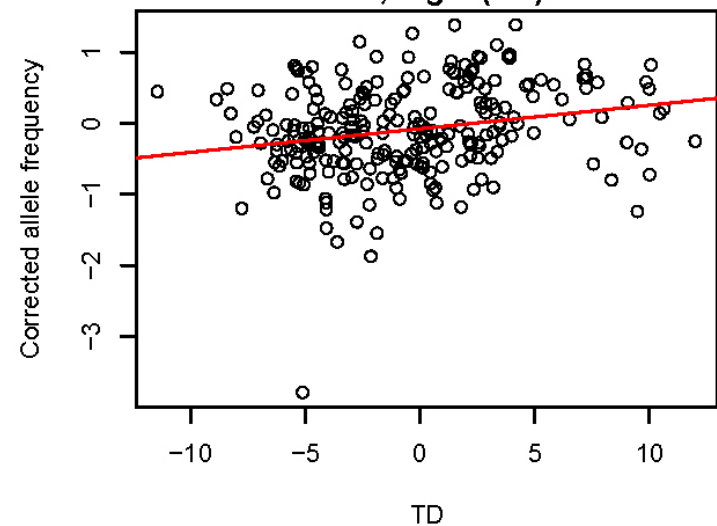
SNP with strongest GEA – **SPRUCE**



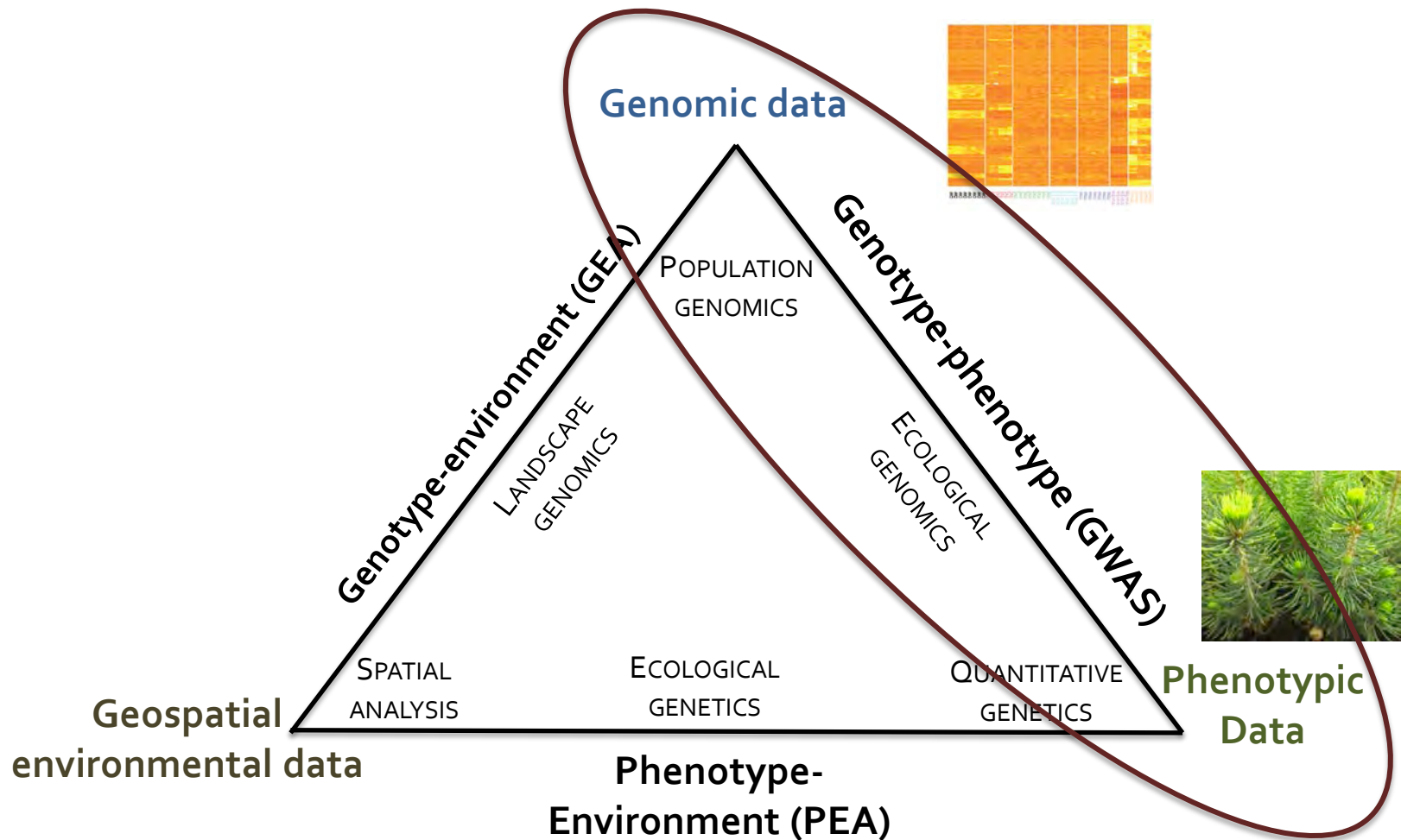
No population structure adj.
 $\rho = 0.77$



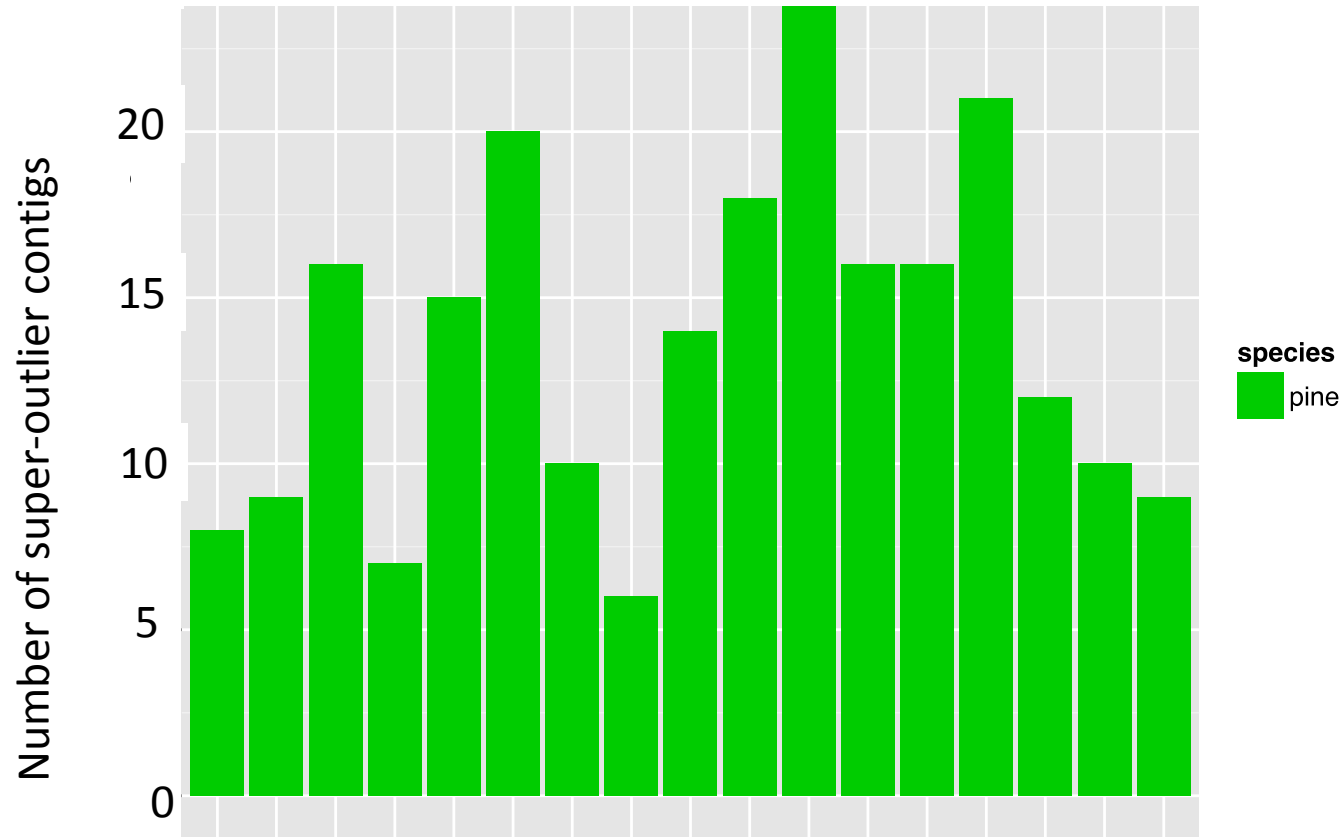
Population structure adj. (Bayenv2)
 $\rho = 0.16$, $\log_{10}(\text{BF}) = 8.1$



Can we identify SNPs involved in adaptation to climate through GWAS approaches?



Many genes associated with phenotypes
(GCTA; **PINE** – similar results for spruce)

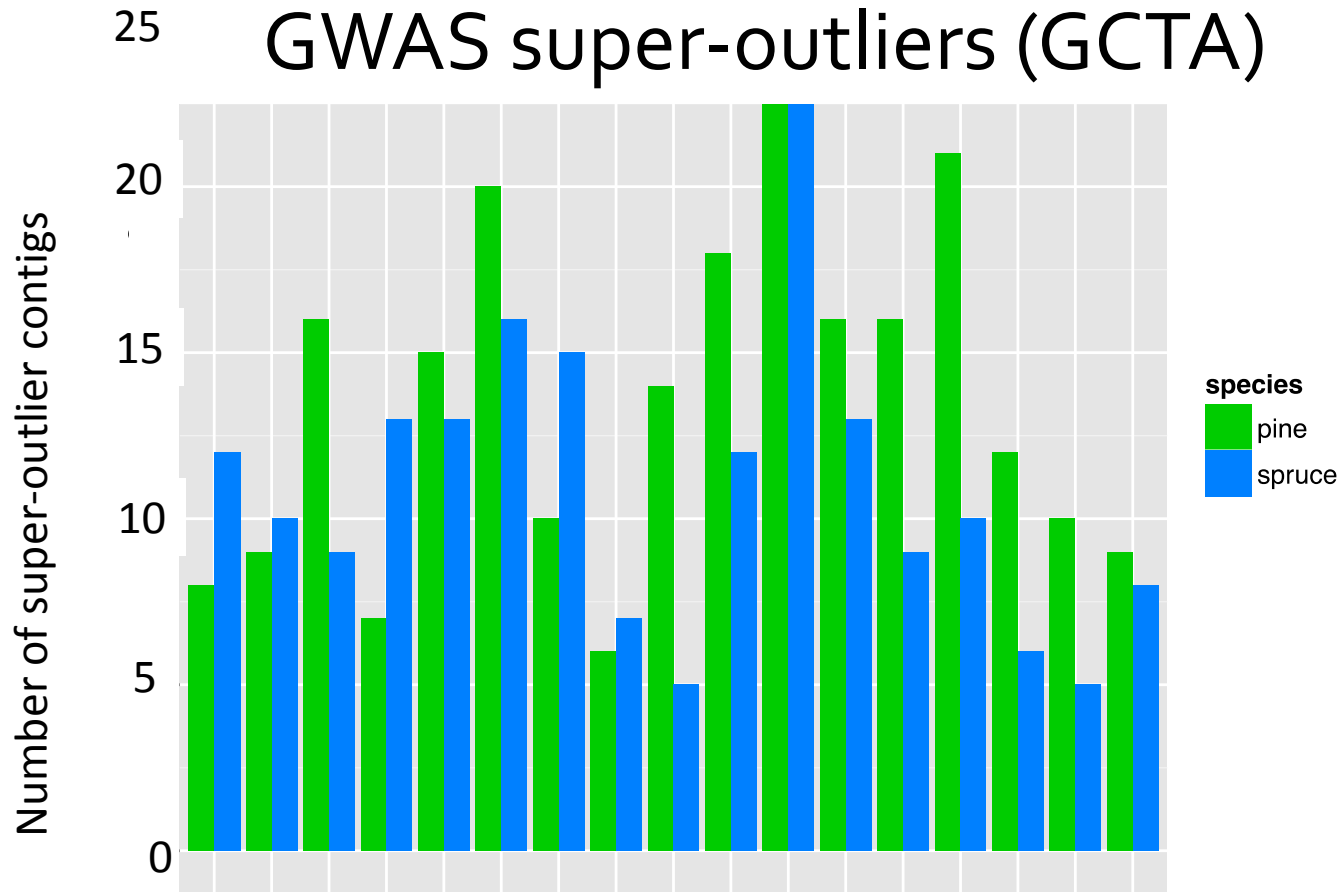


Plant size

Phenology

Cold injury

Pine and spruce have similar patterns of GWAS super-outliers (GCTA)



Plant size

Phenology

Cold injury

Can we detect patterns of local adaptation from genomic data? **YES**

1) Do GEA, PEA and GWAS detect the same environmental drivers of local adaptation?

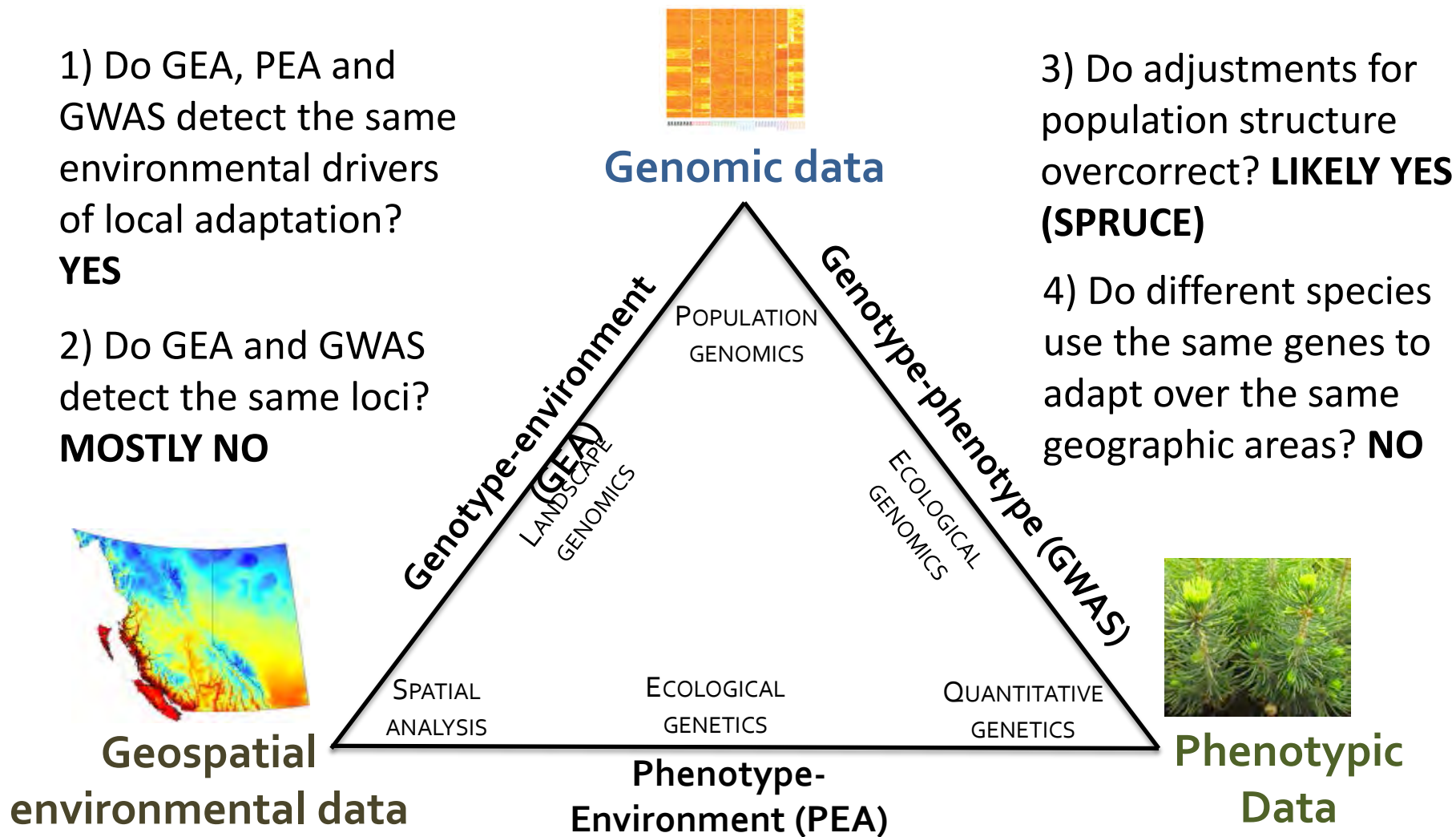
YES

2) Do GEA and GWAS detect the same loci?

MOSTLY NO

3) Do adjustments for population structure overcorrect? **LIKELY YES (SPRUCE)**

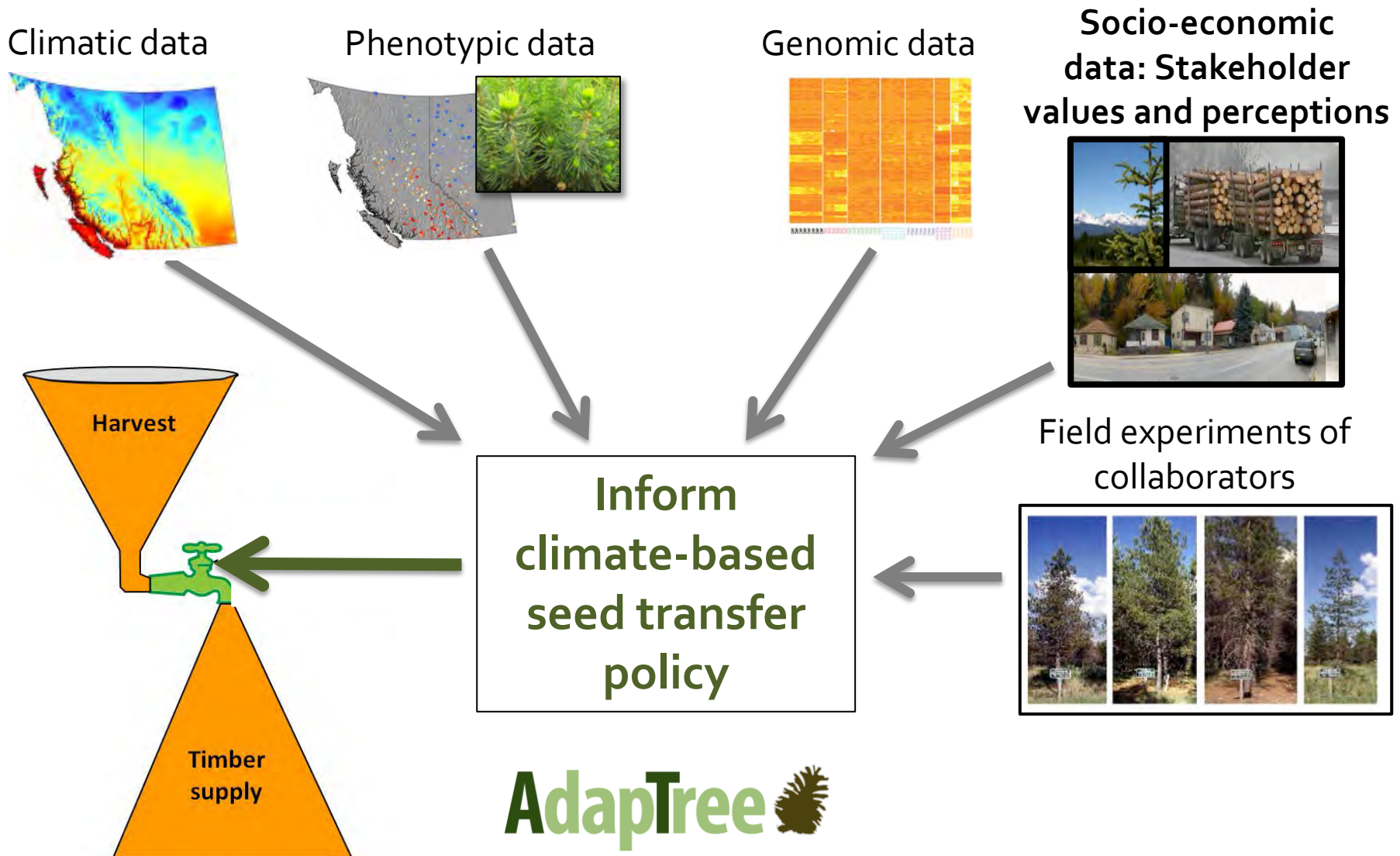
4) Do different species use the same genes to adapt over the same geographic areas? **NO**



Next Steps in Analyses

- Validate candidate genes with ~6,000 trees per species including field trials, 50K Affymetrix SNP arrays
- Evaluate genomic and phenotypic differences in adaptation between natural populations and orchard seedlots (Ian MacLachlan's talk today)
- Evaluate alternative assisted gene flow strategies for managing, maintaining and deploying adaptive variation for new climates including composite provenancing
- Evaluate capacity for adaptation to new climates in unmanaged populations

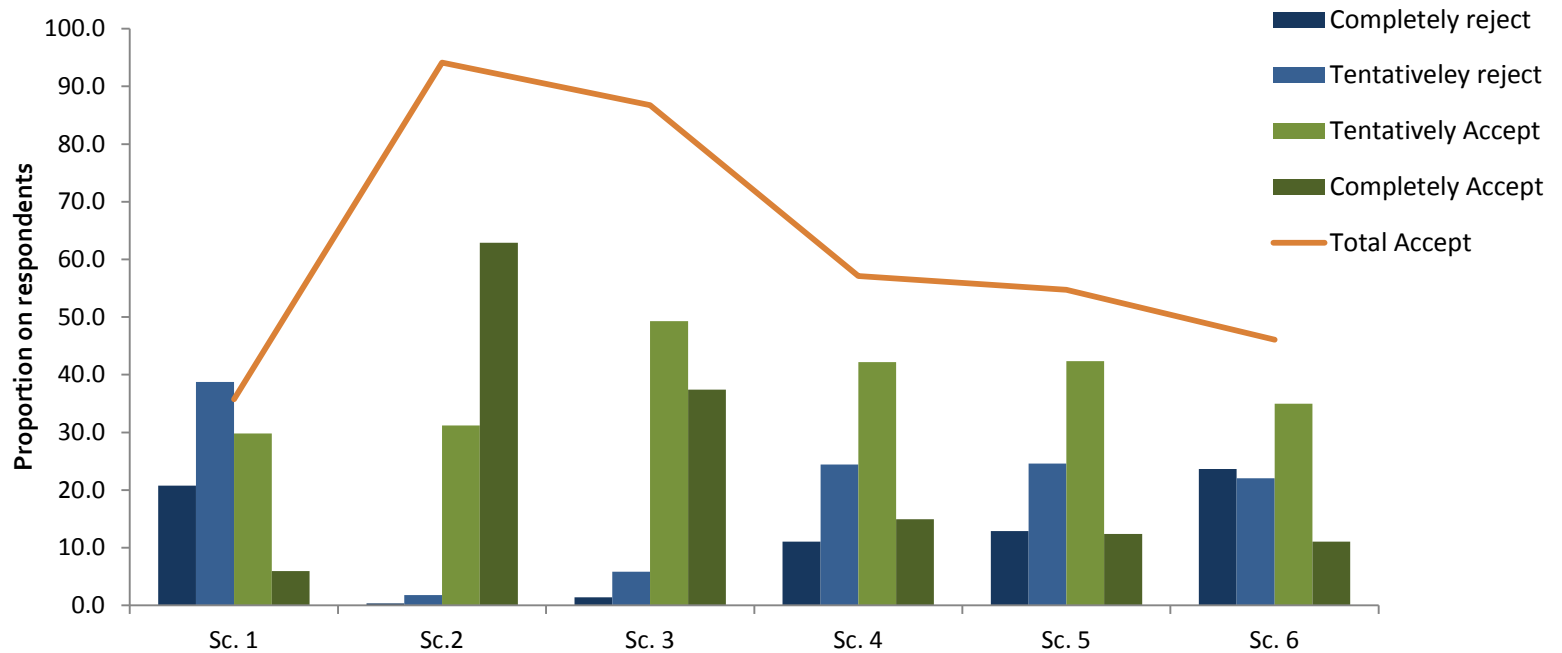
Integrating genomic, phenotypic, climatic and socio-economic data to inform climate-based seed transfer policy for long-term timber supply



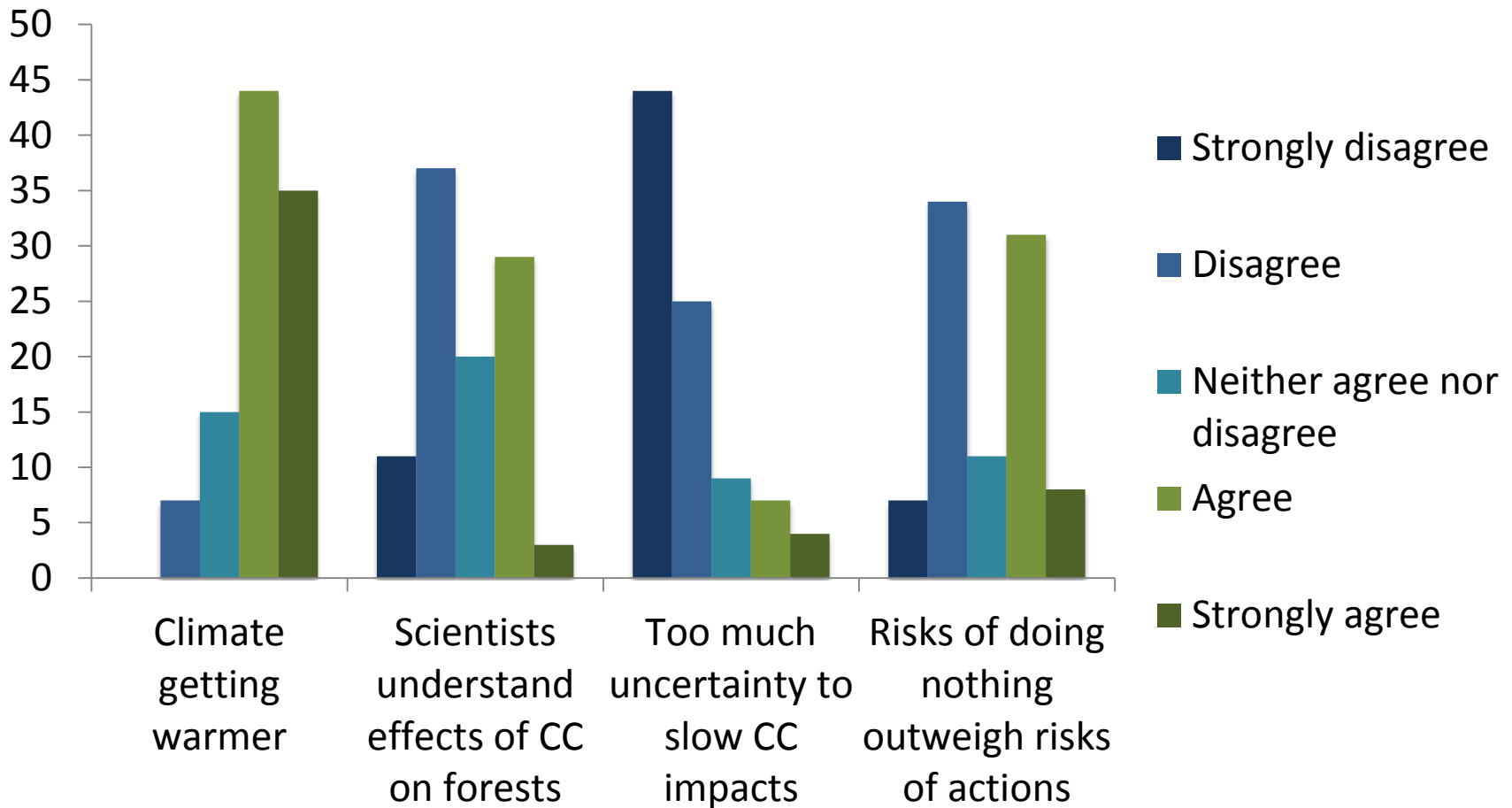
Acceptance of forest management interventions

Sc. 1	Sc. 2	Sc. 3	Sc. 4	Sc. 5	Sc. 6
Do nothing, natural regen.	Local seeds, no breeding	Local seeds, with breeding	Assisted gene flow	Assisted species migration	GMOs

Public Survey
N=1544
(similar results for community leaders)

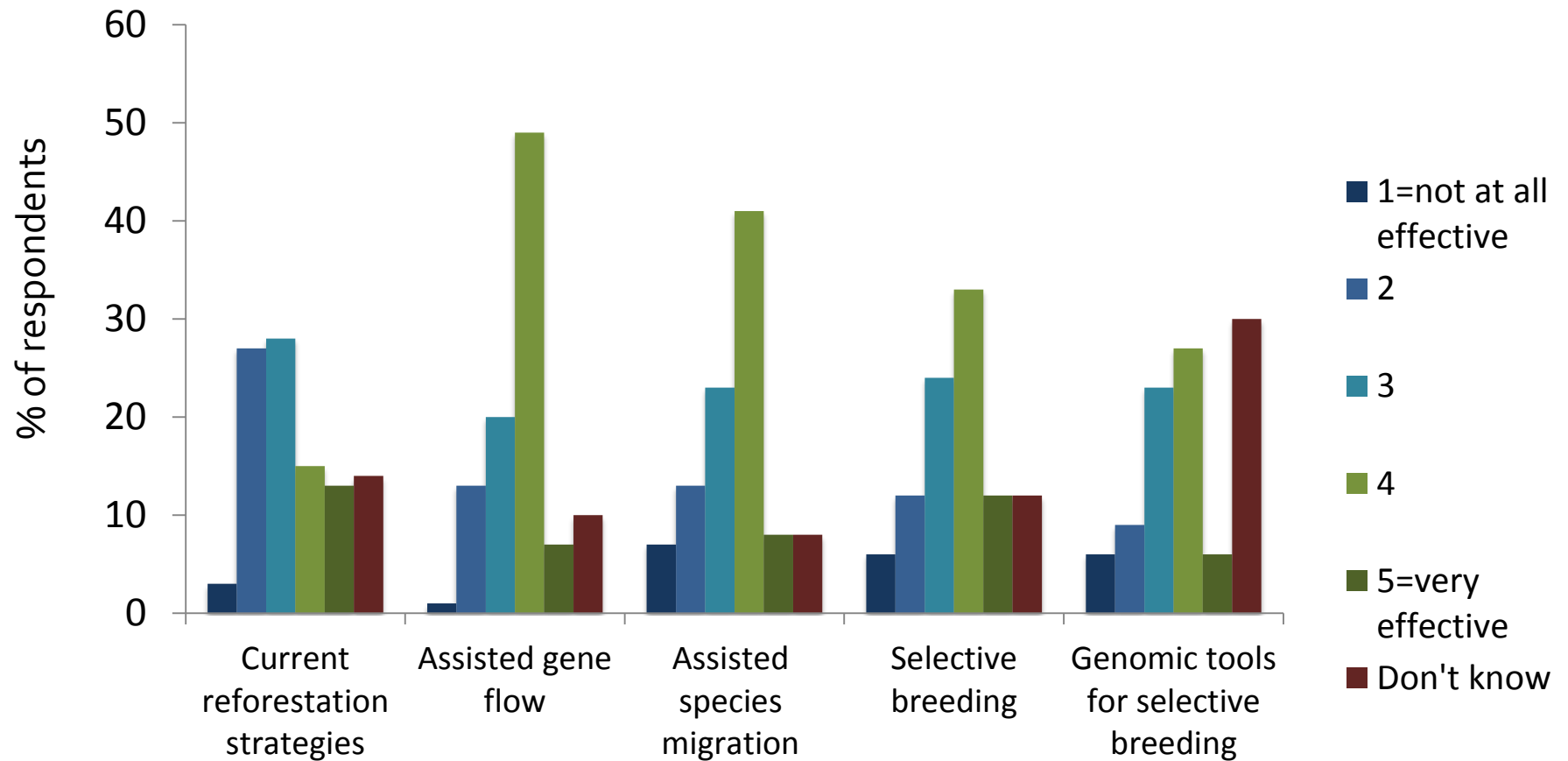


Climate change perspectives of professional foresters: 79% think climate is getting warmer but disagree about uncertainty and risk



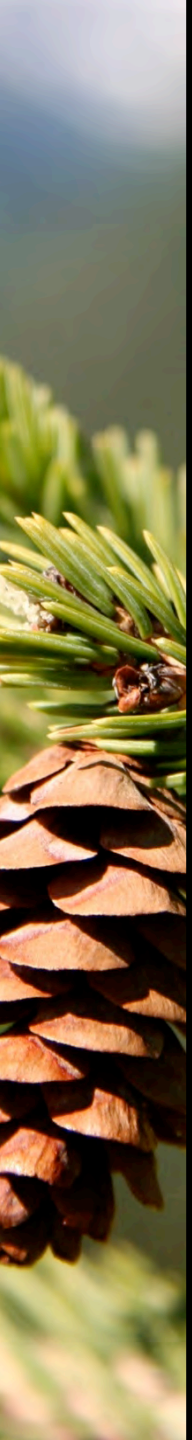
Climate change perspectives of professional foresters:

Some support for assisted migration and breeding; lack of knowledge about genomics



Key Points

- Lowest acceptance among public is for “do nothing” reforestation strategy, and highest for replanting using local seed
- While acceptance of more manipulative strategies was low, a high proportion of respondents changed answers when provided with more information about outcomes
- Foresters feel current strategies inadequate but are cautious and uncertain about using new technologies to inform seed sources
- Translation of knowledge is needed for meaningful participatory dialogue with stakeholders in climate adaptation strategies
- Management practice, not tool for understanding variation, should be the primary focus of discussion



Acknowledgements

IUFRO Tree Biotechnology 2015 conference organizers

PineRefSeq for loblolly genome sequence

SMarTForests for spruce genome sequence

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