The Tria Project: Genomics of the Mountain Pine Beetle System

Janice Cooke, Adriana Arango, Catherine Cullingham, David Coltman, Patrick James, Jasmine Janes, Felix Sperling, Brent Murray, and the Tria Consortium

UNIVERSITY OF ALBERTA

Outline

- **Overview of the Tria Project**
- **Genomics 101**
- **Physiology and Genomics:** defining species ranges on the landscape, how species and drought affect pine responses to attack, and how these might affect MPB populations
- **Population Genomics:** analyses of landscape-level genetic variation in MPB and pines, identifying factors that might influence population distributions now and in the future
- **Genomics and Forest Management**
- **Genomics and Risk Assessment**
- **Summary**

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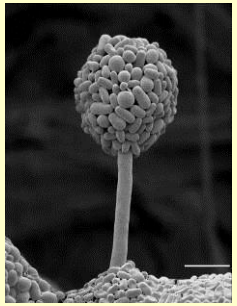
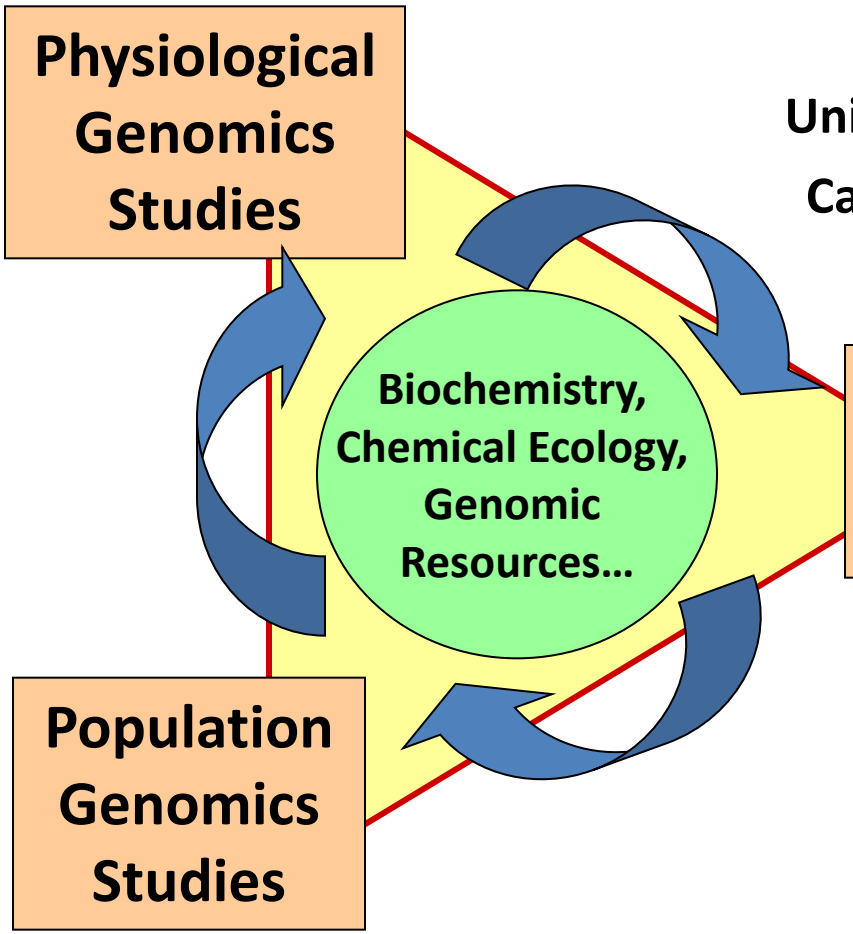
The Tria Project:
A large-scale multidisciplinary collaborative effort


Janice Cooke


Jack Scott


Adrianne Rice



University of Alberta

University of BC

University of Northern BC

Canadian Forest Service

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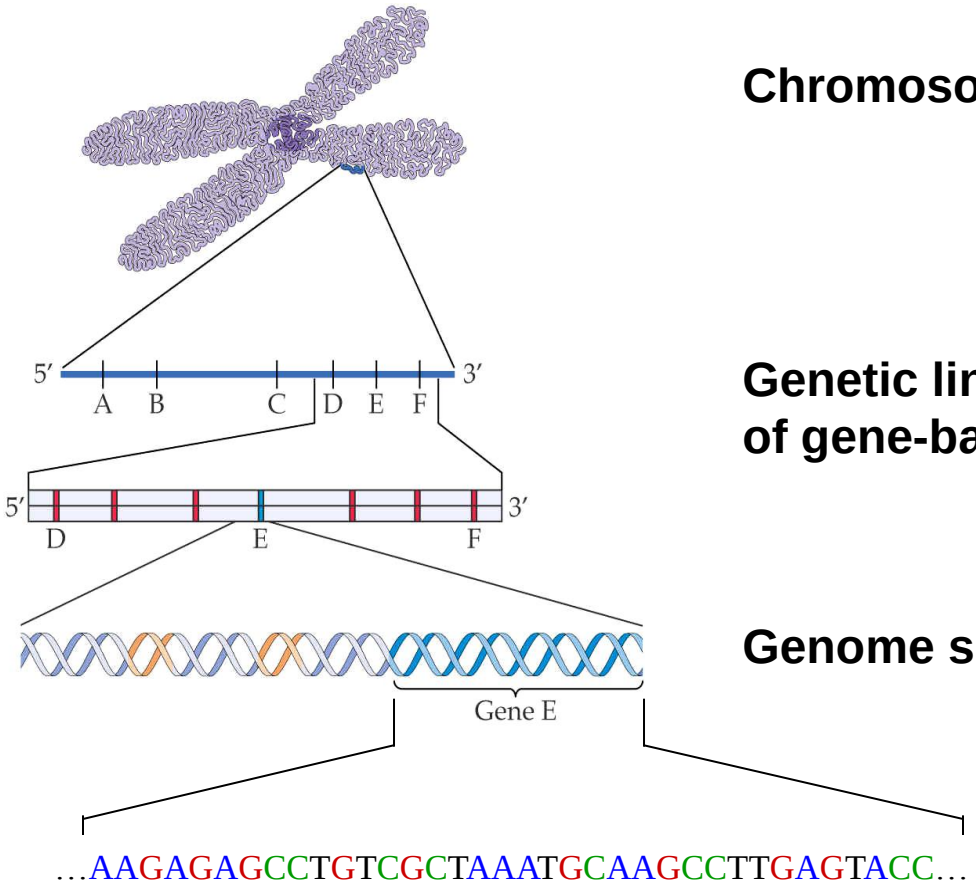
Genomes and Genomic Resources



Chromosomes

Genetic linkage map (relative positions of gene-based or anonymous markers)

Genome sequence

Expressed gene sequences

(Adapted from Paul & Ferl, 2000)

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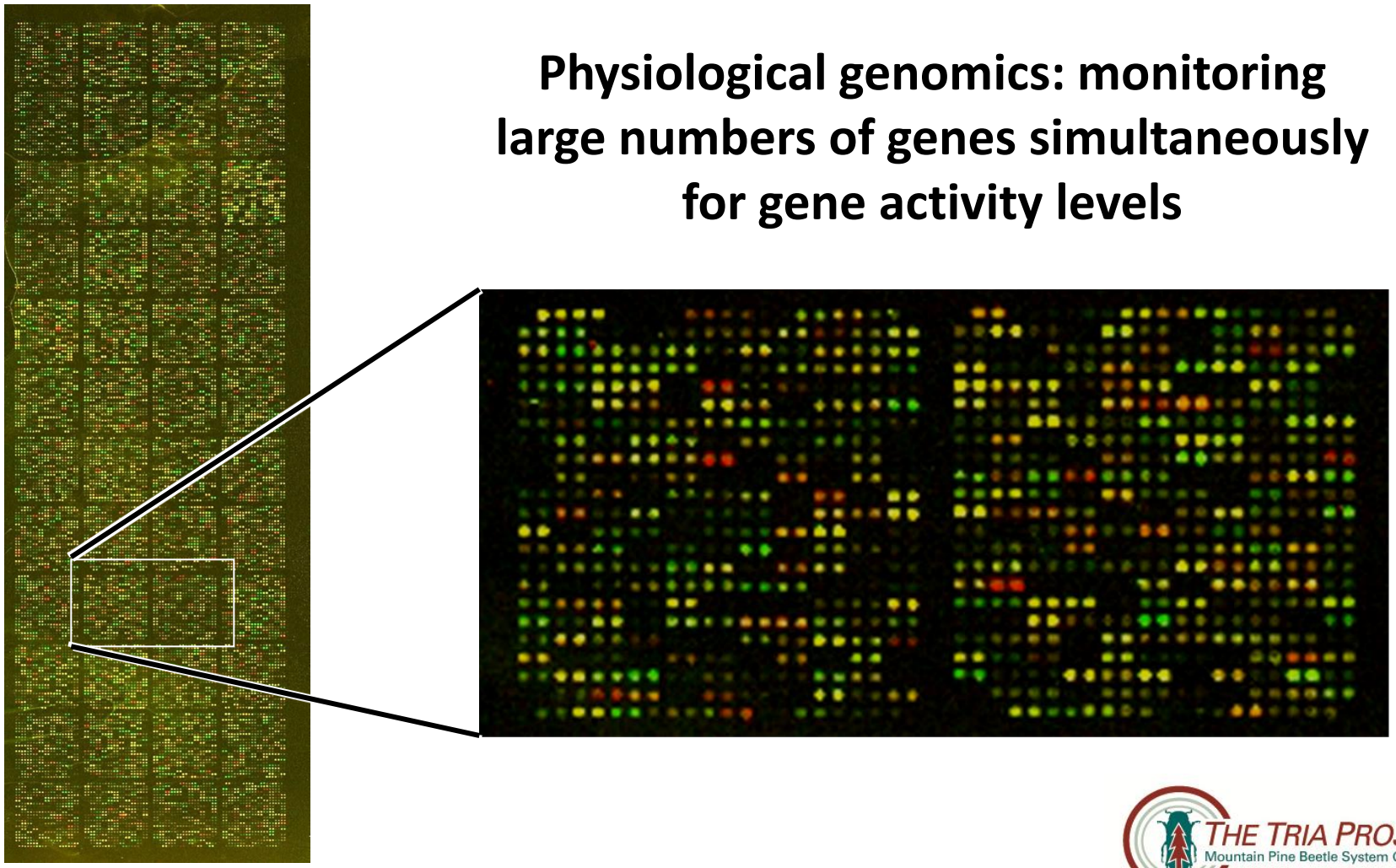
Genomics is the high-throughput analyses of many genes and/or many individuals simultaneously



Physiological genomics: monitoring large numbers of genes simultaneously for gene activity levels

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Genomics is the high-throughput analyses of many genes and/or many individuals simultaneously

Population genomics: assessing genetic variation in large numbers of individuals simultaneously

A/A A/G G/G

Gene Markers

Individuals

	A	B	C	…	*n*
1					
2					
3					
…					
n					

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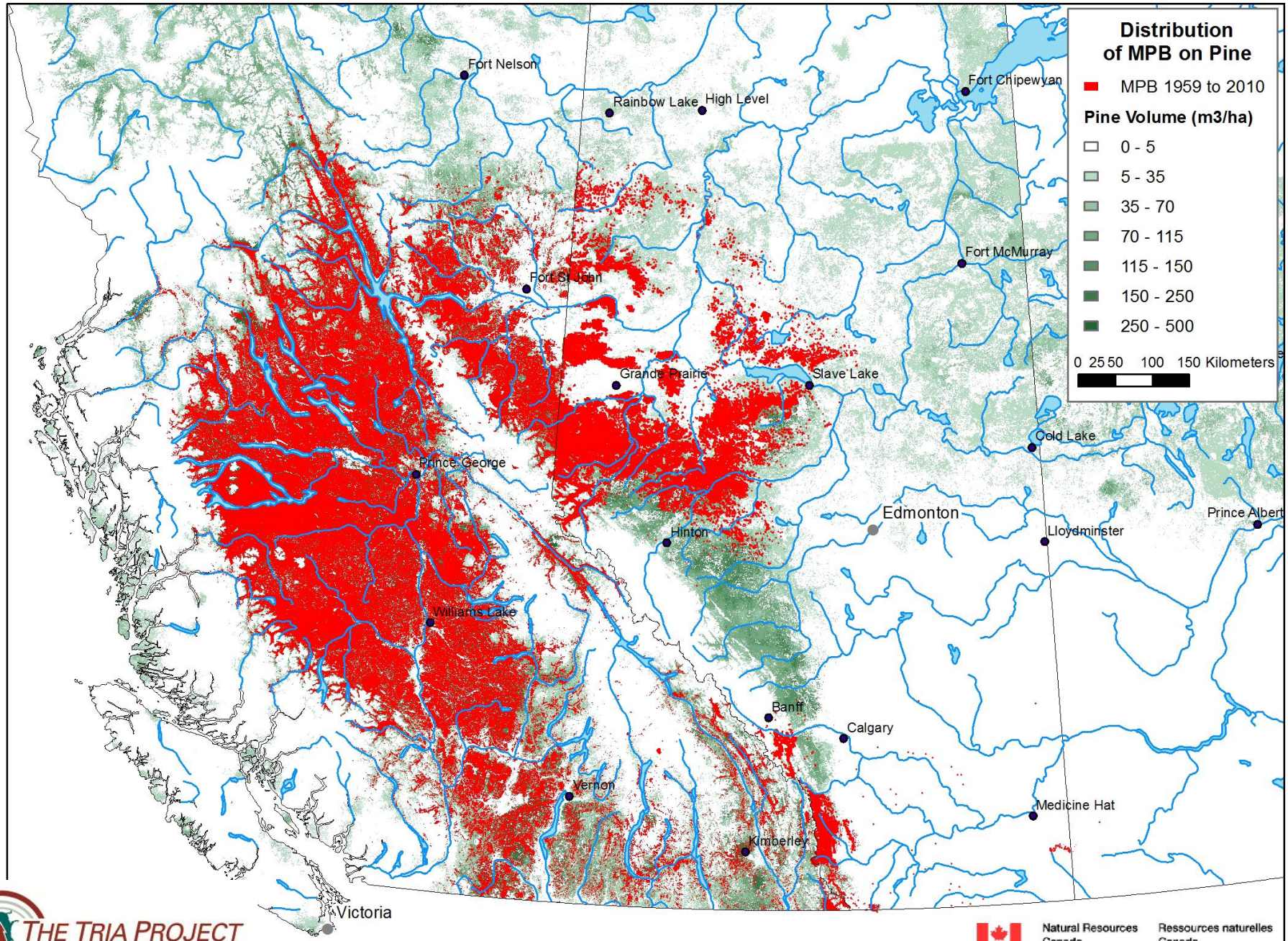
Distribution of MPB on Pine
MPB 1959 to 2010
Pine Volume (m3/ha)
0 - 5
5 - 35
35 - 70
70 - 115
115 - 150
150 - 250
250 - 500
0 25 50 100 150 Kilometers
Fort Nelson
Rainbow Lake
High Level
Fort Chipewyan
Fort McMurray
Fort St John
Grande Prairie
Slave Lake
Cold Lake
Prince George
Edmonton
Hinton
Lloydminster
Prince Albert
Williams Lake
Banff
Calgary
Vernon
Medicine Hat
Kimberley
Victoria
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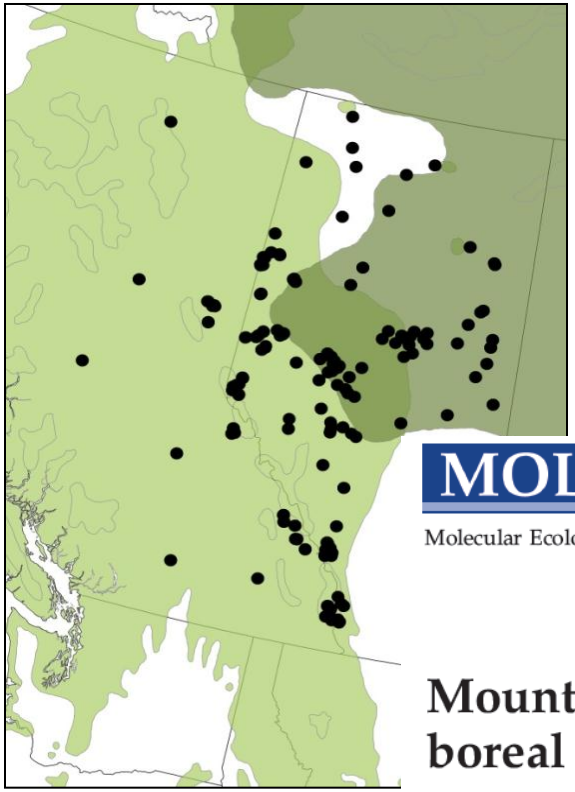
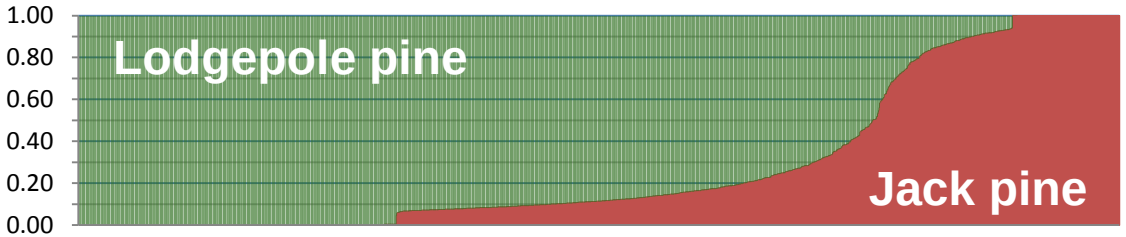
Natural Resources Canada
Ressources naturelles Canada

Using genetic markers to identify MPB-attacked jack pine in spring 2010





MOLECULAR ECOLOGY

Molecular Ecology (2011) 20, 2157–2171 doi: 10.1111/j.1365-294X.2011.05086.x

Mountain pine beetle host-range expansion threatens the boreal forest

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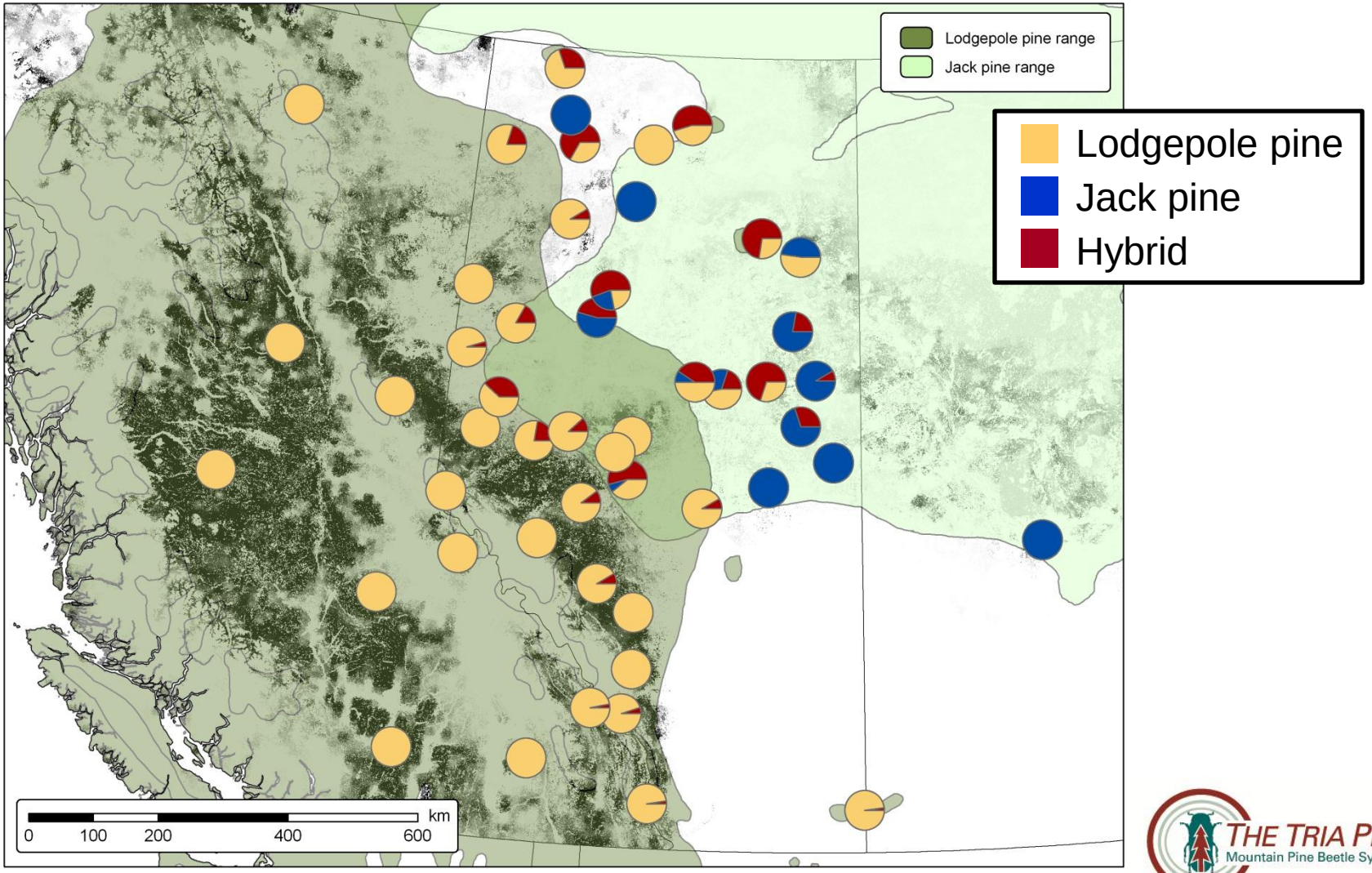
Using genetic markers to identify MPB-attacked jack pine in spring 2010



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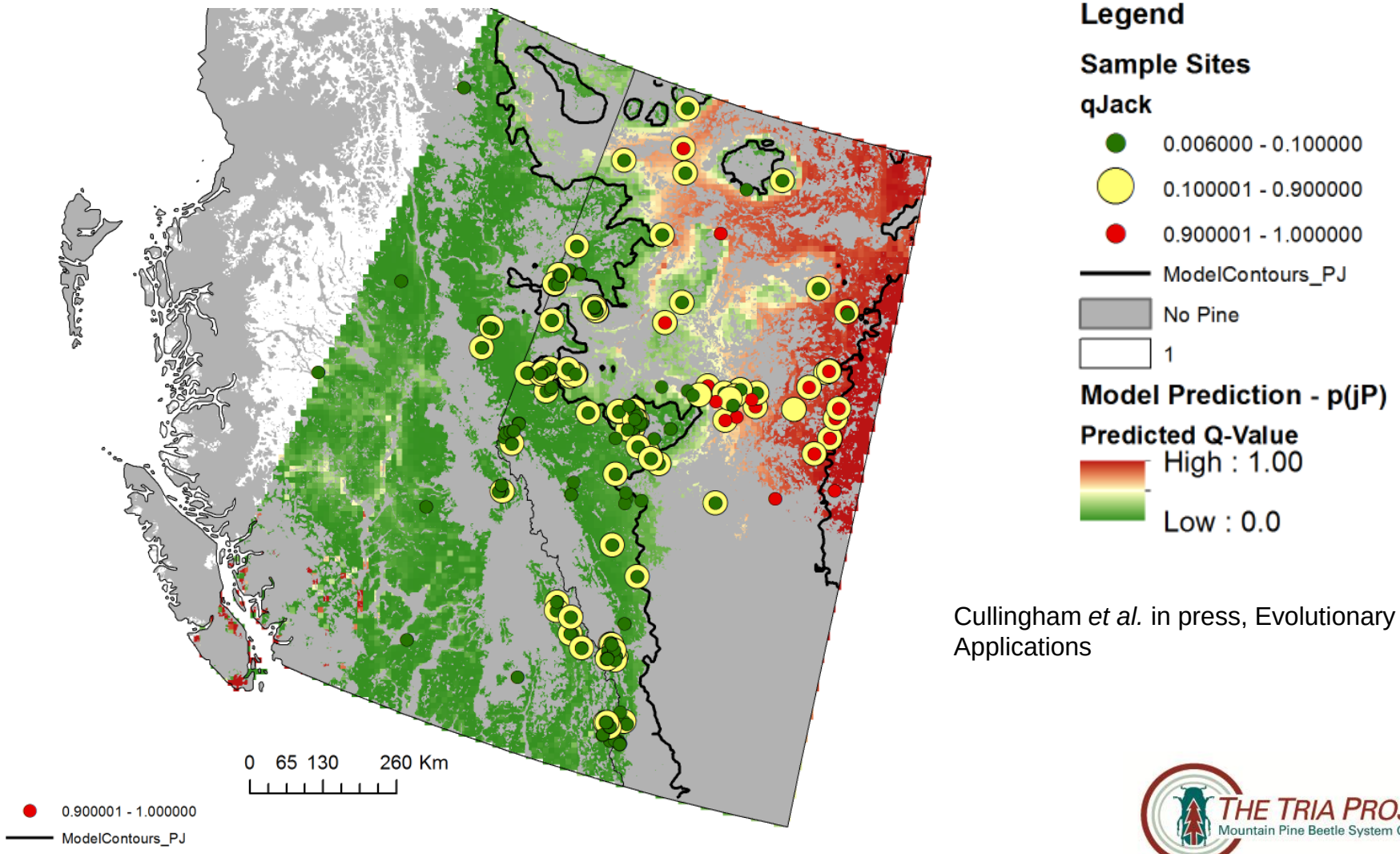
Refining the lodgepole x jack pine hybrid zone



Cullingham *et al.* in press, Evolutionary Applications

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Refining the lodgepole x jack pine hybrid zone

Logistic regression to model the relationship between environment/climate and genetic proportions

Predictor	AIC	Marginal AIC	VIF	Coefficients	LRT*	Effect on p(Pj)
(Intercept)	43498			49.999		
Elevation (m)	50513	7015	6.040	-0.007	7016.8	-
Drought index (CMI)*	46690	3192	2.400	0.058	3193.5	+
Mean Annual Precipitation (MAP)*	43615	117	3.730	-0.001	118.8	-
Summer heat:moisture index (SHM)*	43509	11	3.610	-0.007	12.6	-
Extreme min. temp. (EXT_Cold)*	44524	1026	3.790	-0.307	1027.7	+
Northing - Latitude*	46671	3173	5.490	-0.580	3174.5	-
Easting - Longitude*	46804	3306	2.210	0.233	3307.2	+

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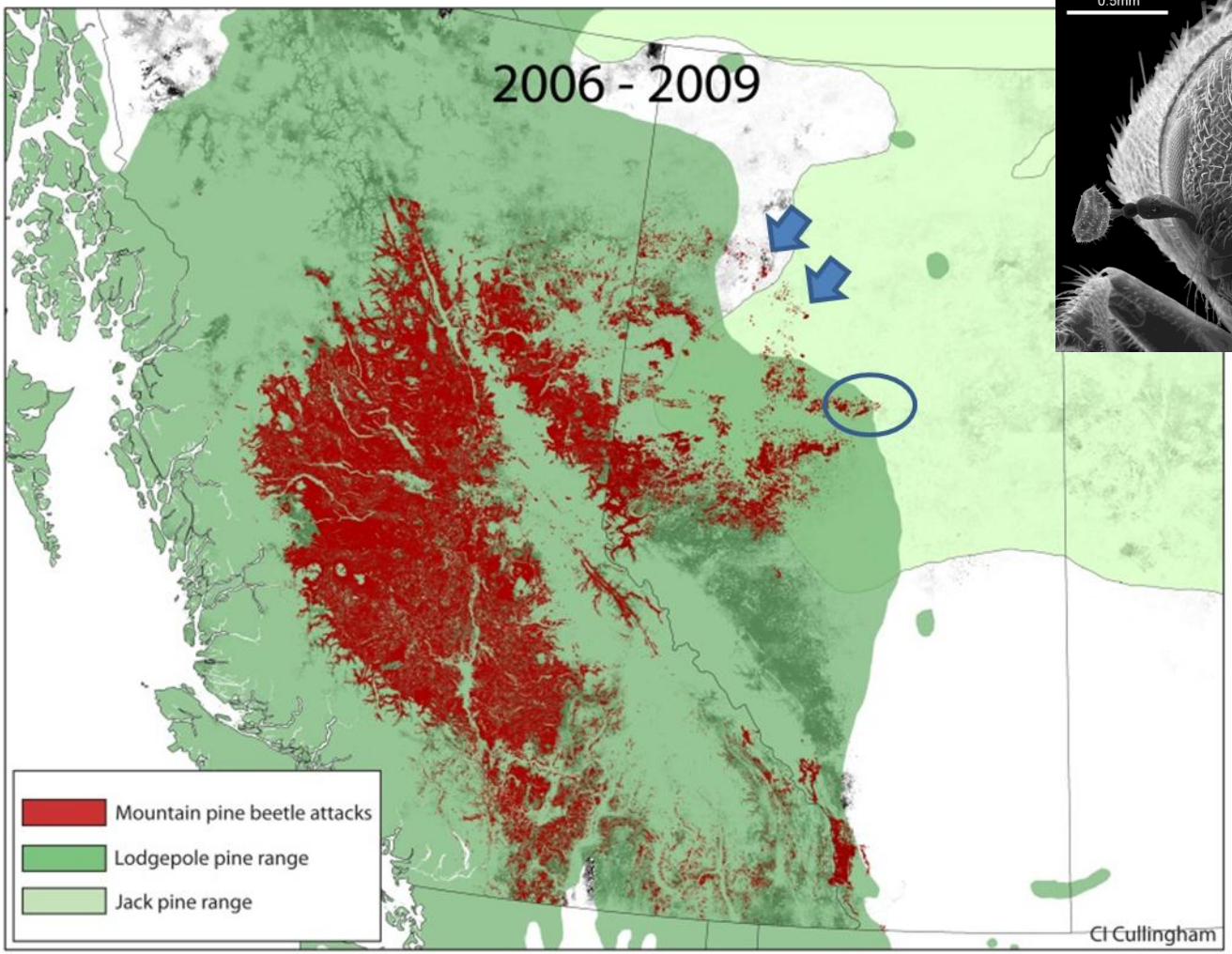
Getting a handle on genetic variation in defense: do lodgepole pine and jack pine defenses differ?



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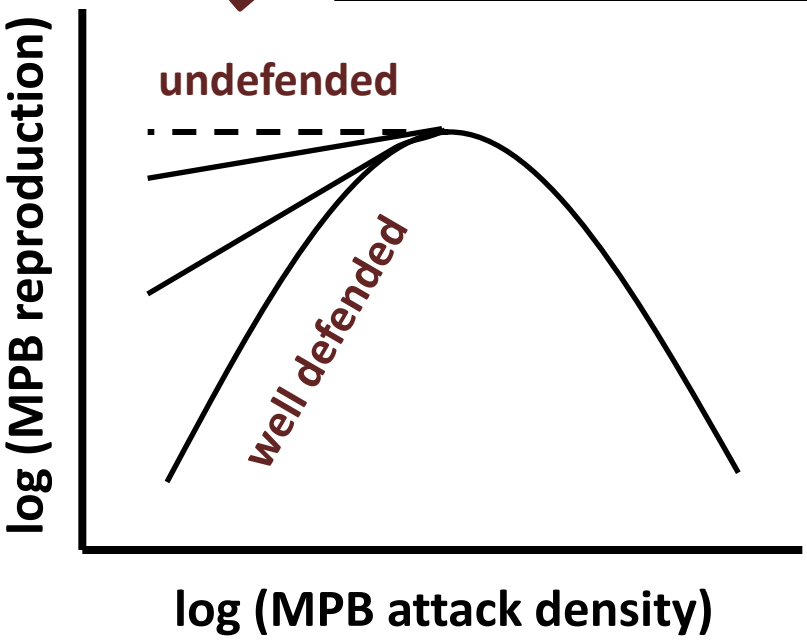
Tree defenses matter at lower MPB attack densities, and are affected by genetics and environment

This part of the curve is affected by host genetics and environment



Genetics: **resistance to MPB attack is moderately heritable in lodgepole pine (Yanchuk *et al*.), but is controlled by many genes with small effects**

Environment: **Stressed trees seem to be favourite targets under lower MPB attack densities, while healthy trees appear to be favoured under higher MPB densities**

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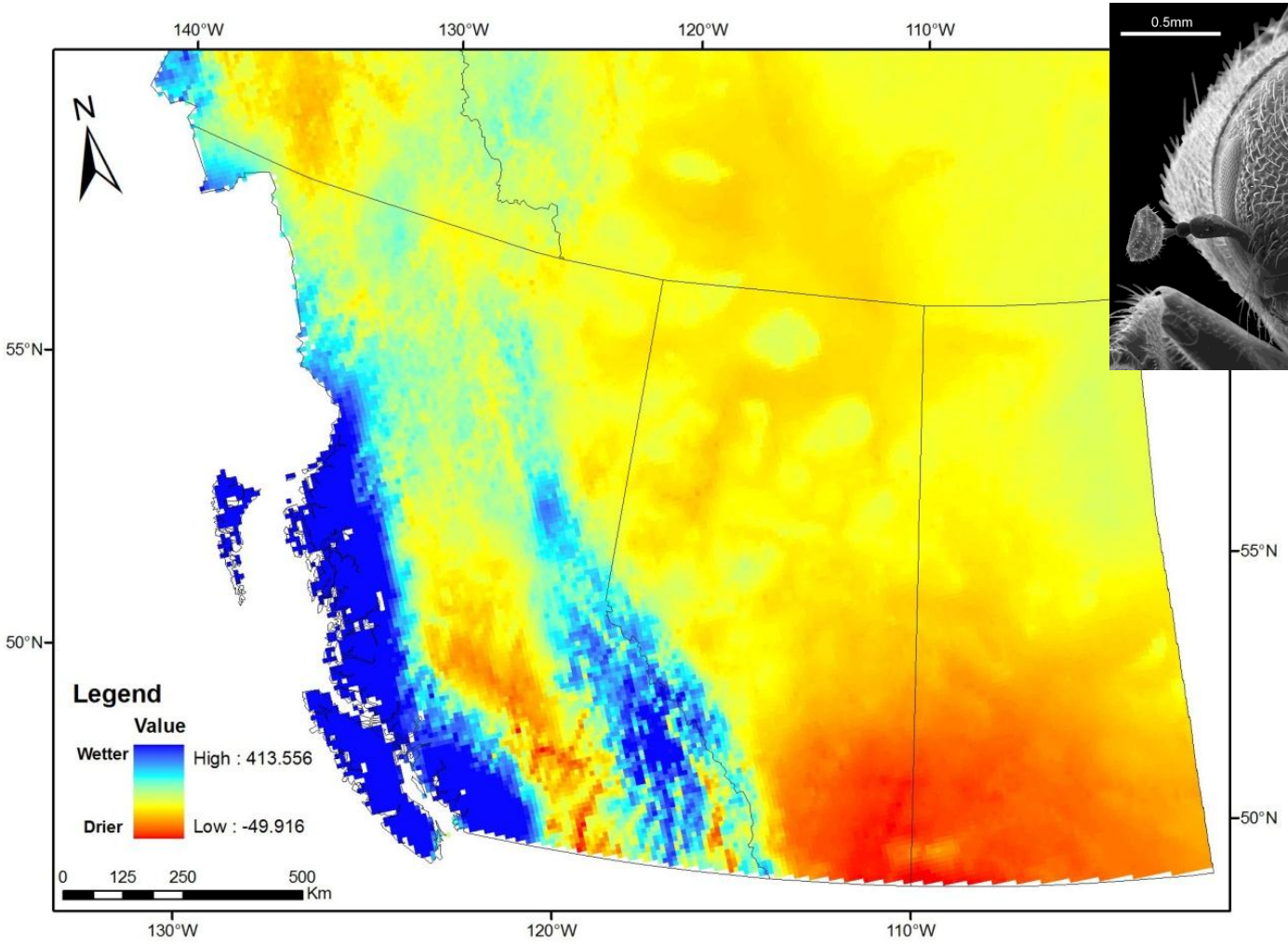
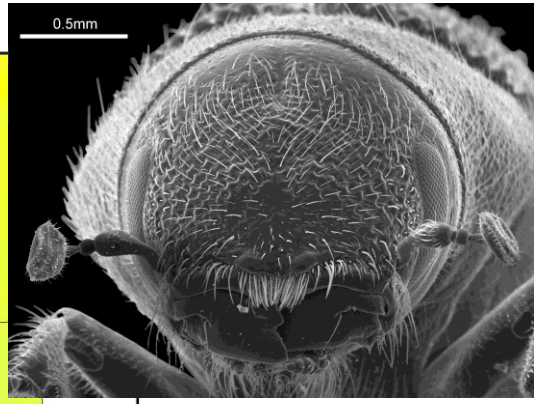
Measuring the effect of climate on defense: does drought affect pine defenses?





Climate Moisture Index (Hogg, 1997) output using BioSim (Barry Cooke)

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Dissecting pine defense responses

Species
- Lodgepole pine
- Jack pine
- Hybrids

Water availability
- Well watered
- Water deficit

Inoculation treatment
- Wound (seedlings only)
- Wound/Inoculation with MPB fungus
- Control

Growth chamber studies

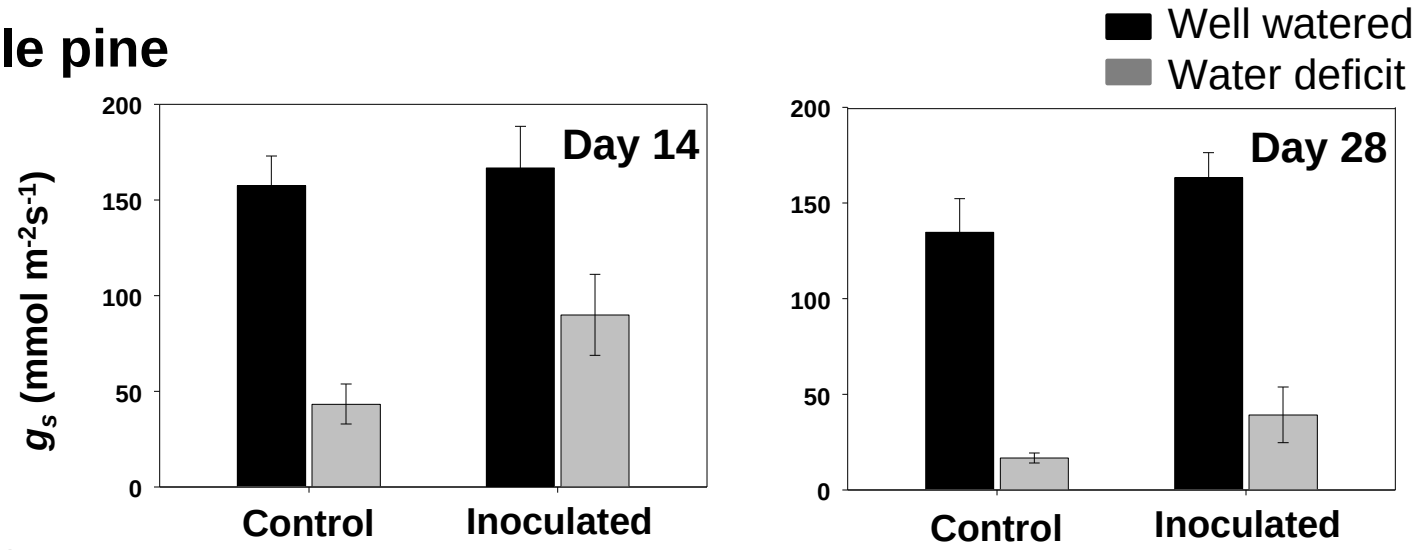
lodgepole & jack pine seedlings

Mature tree field studies

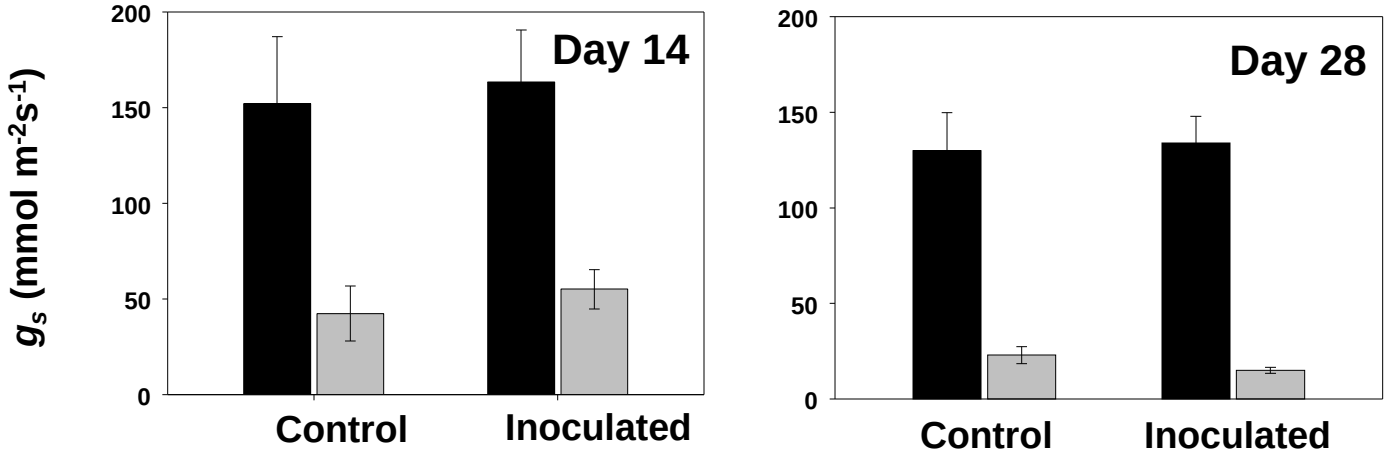
Hybrids, lodgepole & jack pine

Water deficit causes lodgepole and jack pine to close their stomata

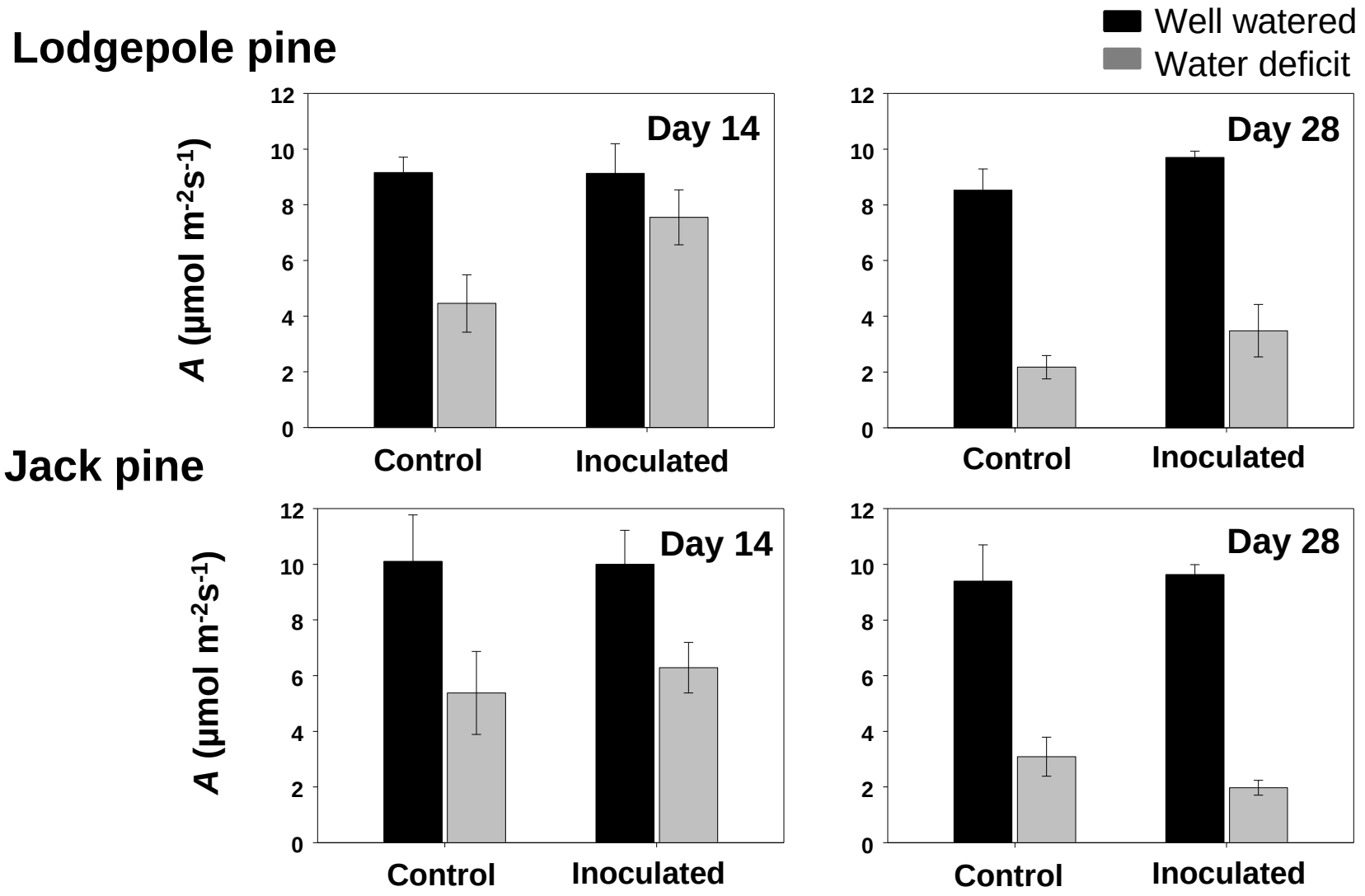
Lodgepole pine



Jack pine

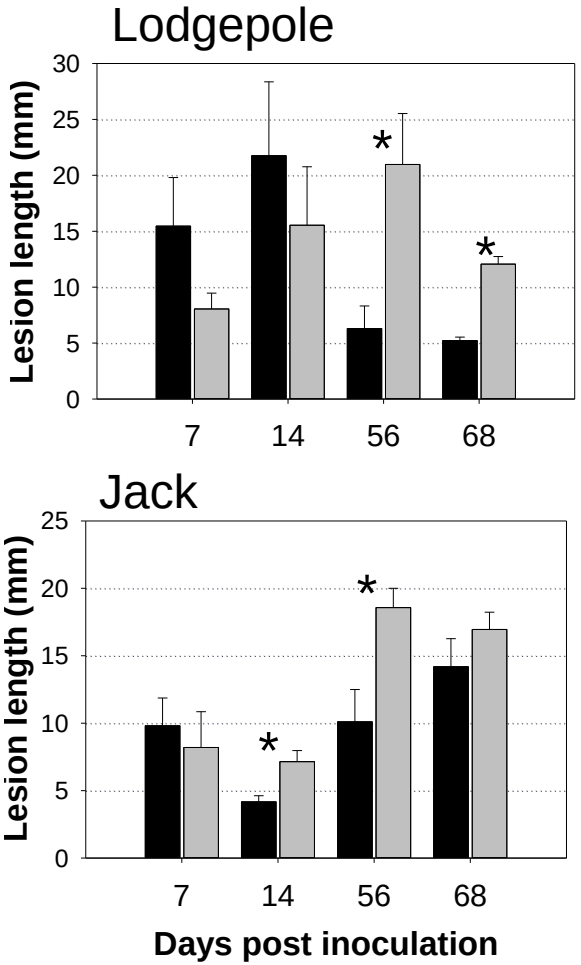


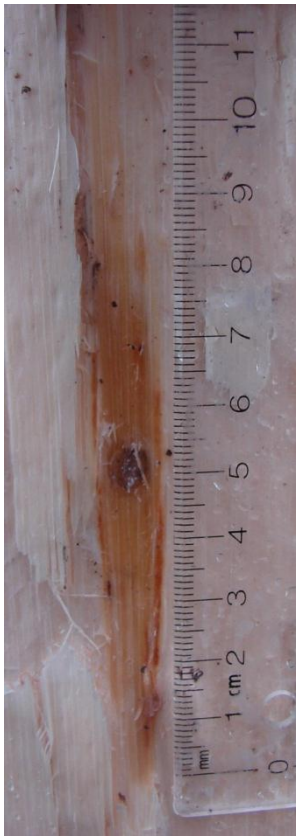
Water deficit reduces photosynthesis in lodgepole and jack pine, reducing carbon gain



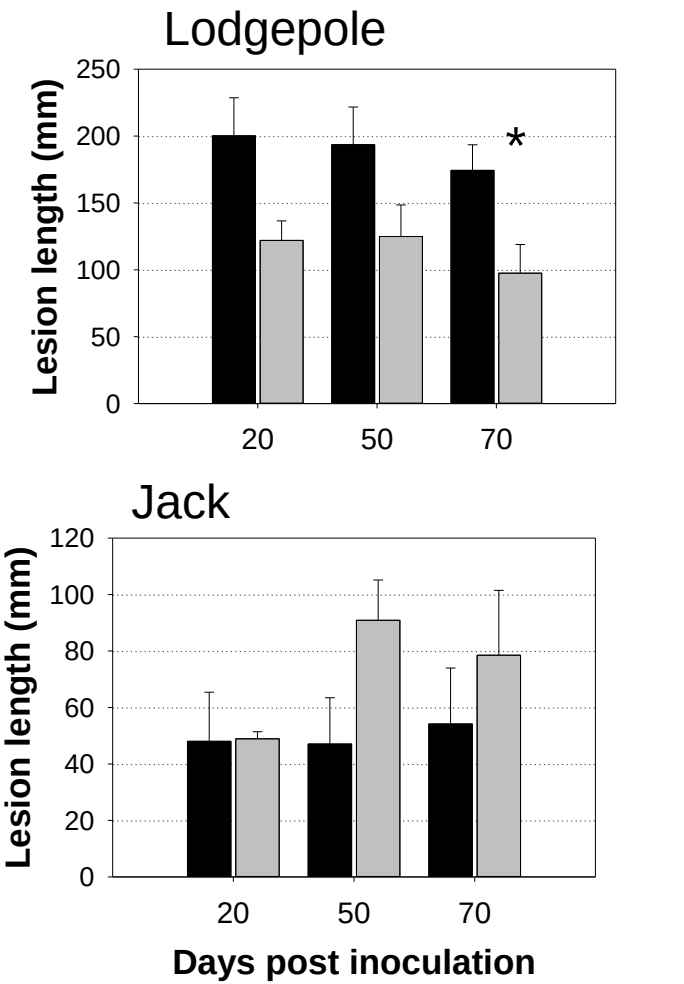
Lesion development differs in lodgepole and jack pine, and is also affected by drought

Seedlings

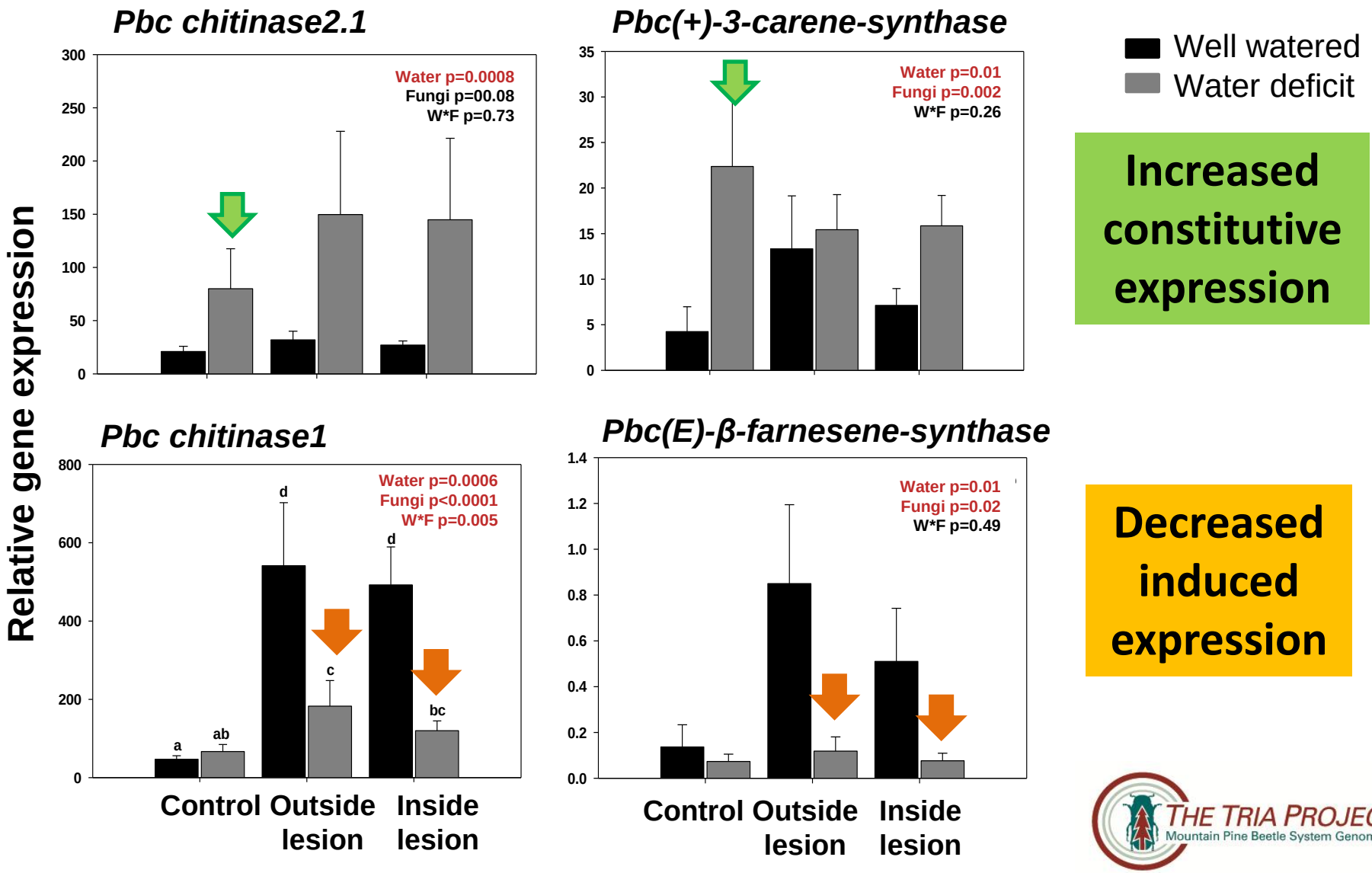




Mature trees



Drought affects gene expression associated with both pre-formed and induced defenses



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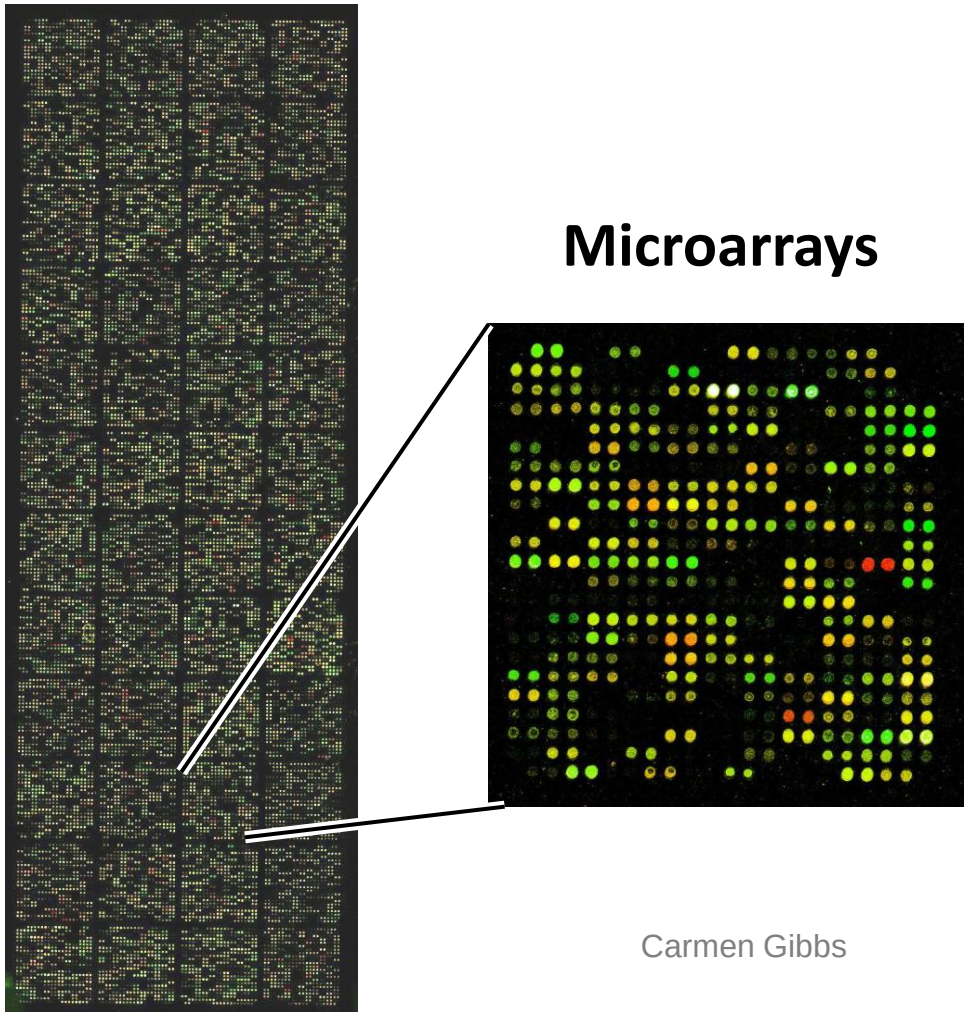
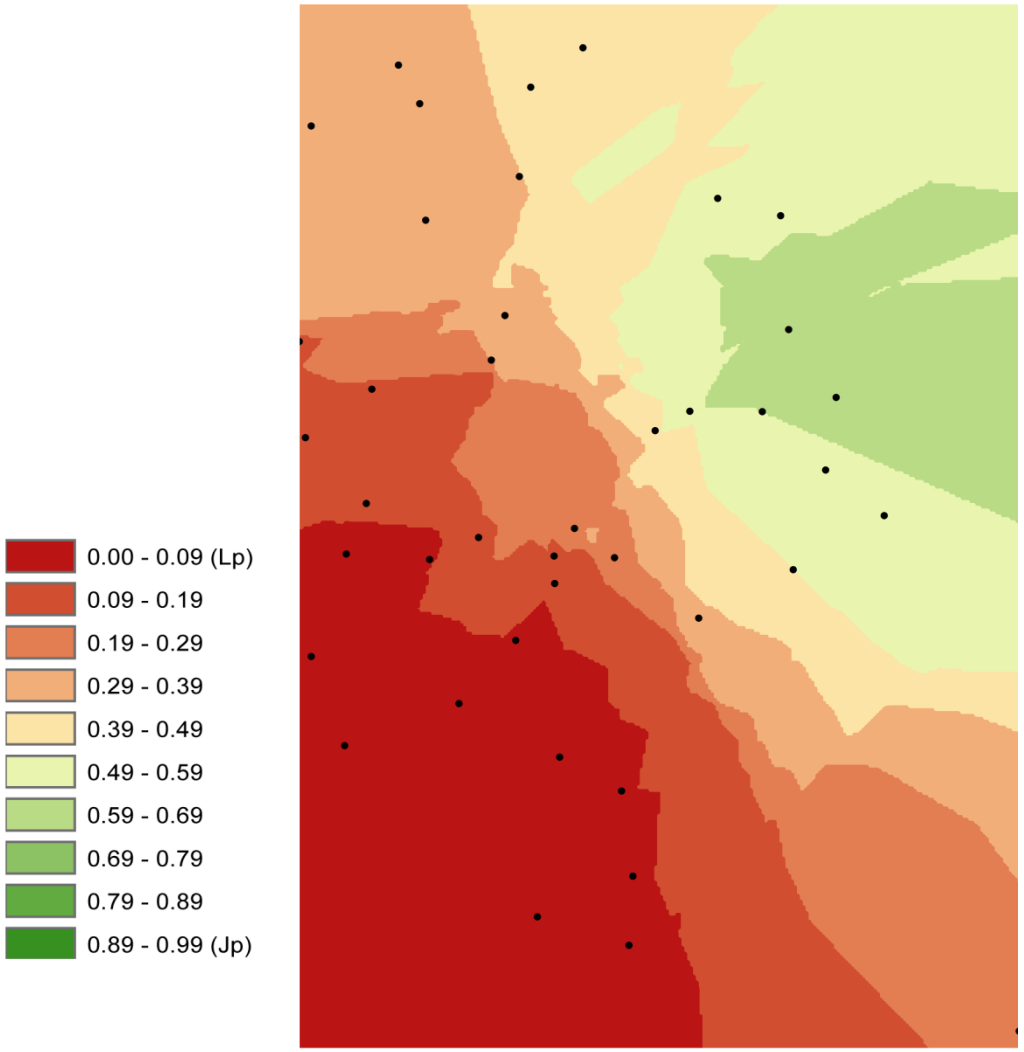
In progress: genomics analyses to look at networks of gene expression in these experiments



Do any of the differentially expressed genes identified in this experiment contribute to genetic variation observed between individuals or species?

Adaptive variation in pines: using genetic markers to discover signatures of selection



Designed 1536 genome-wide genetic markers that are being used for high-throughput analyses of 558 jack, lodgepole and hybrid trees

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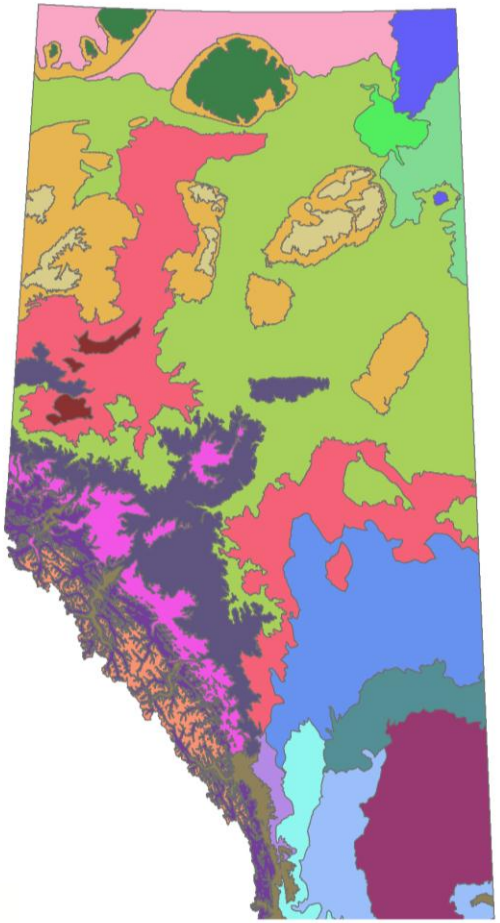
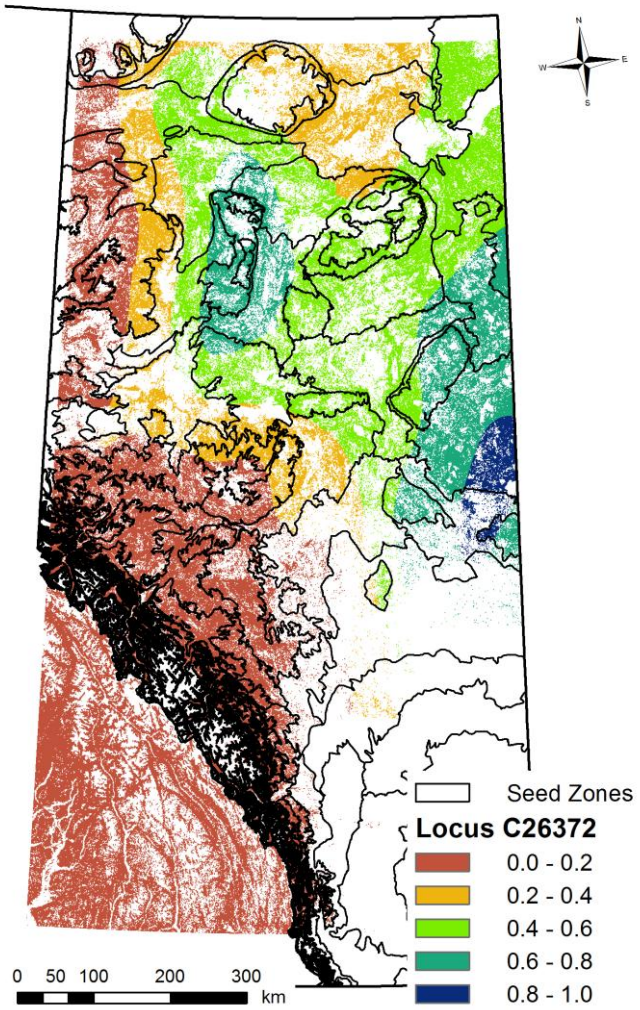
Post-disturbance reforestation: can genetic variation insights be used to refine seed zones?





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Similar genomic approaches are being used to investigate genetic variation in MPB

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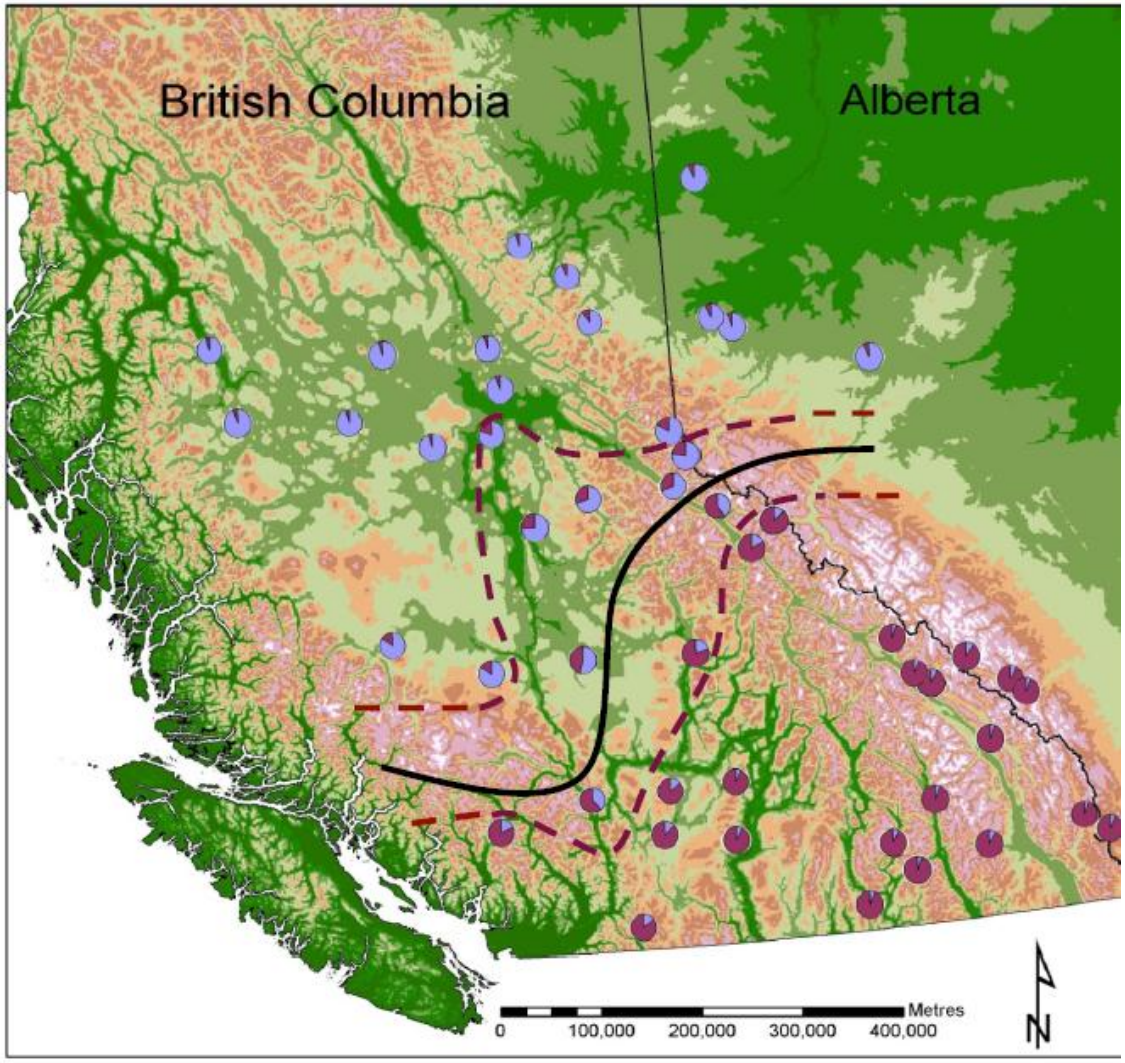
Population genetic analyses to examine MPB dispersal (gene flow) and genetic connectivity



Samarasekara *et al.* Molecular Ecology, in press

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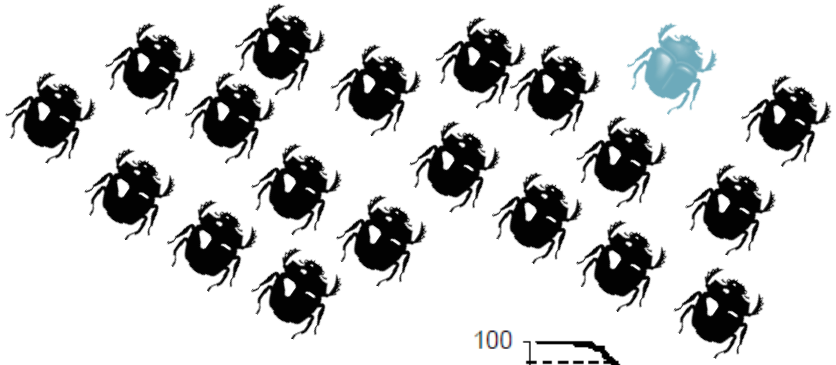
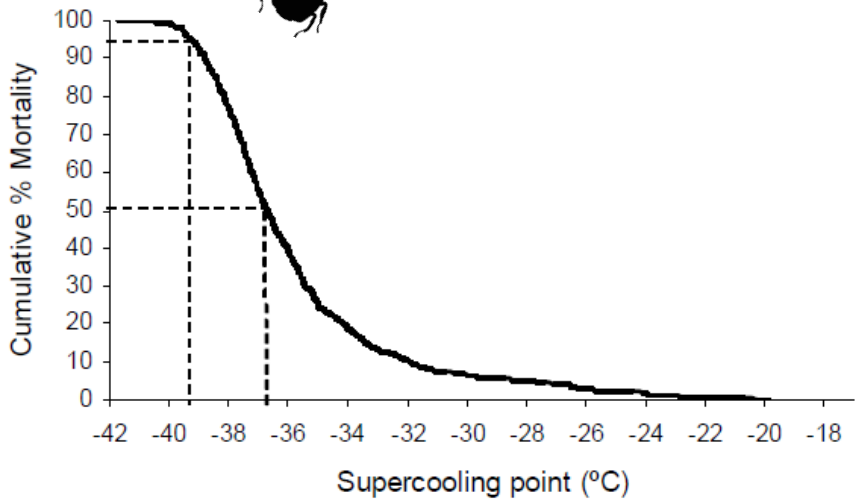
Can we detect signatures of selection for traits such as cold tolerance?

Frequency 5%



Selection (winter cold temperatures)



Frequency 20%

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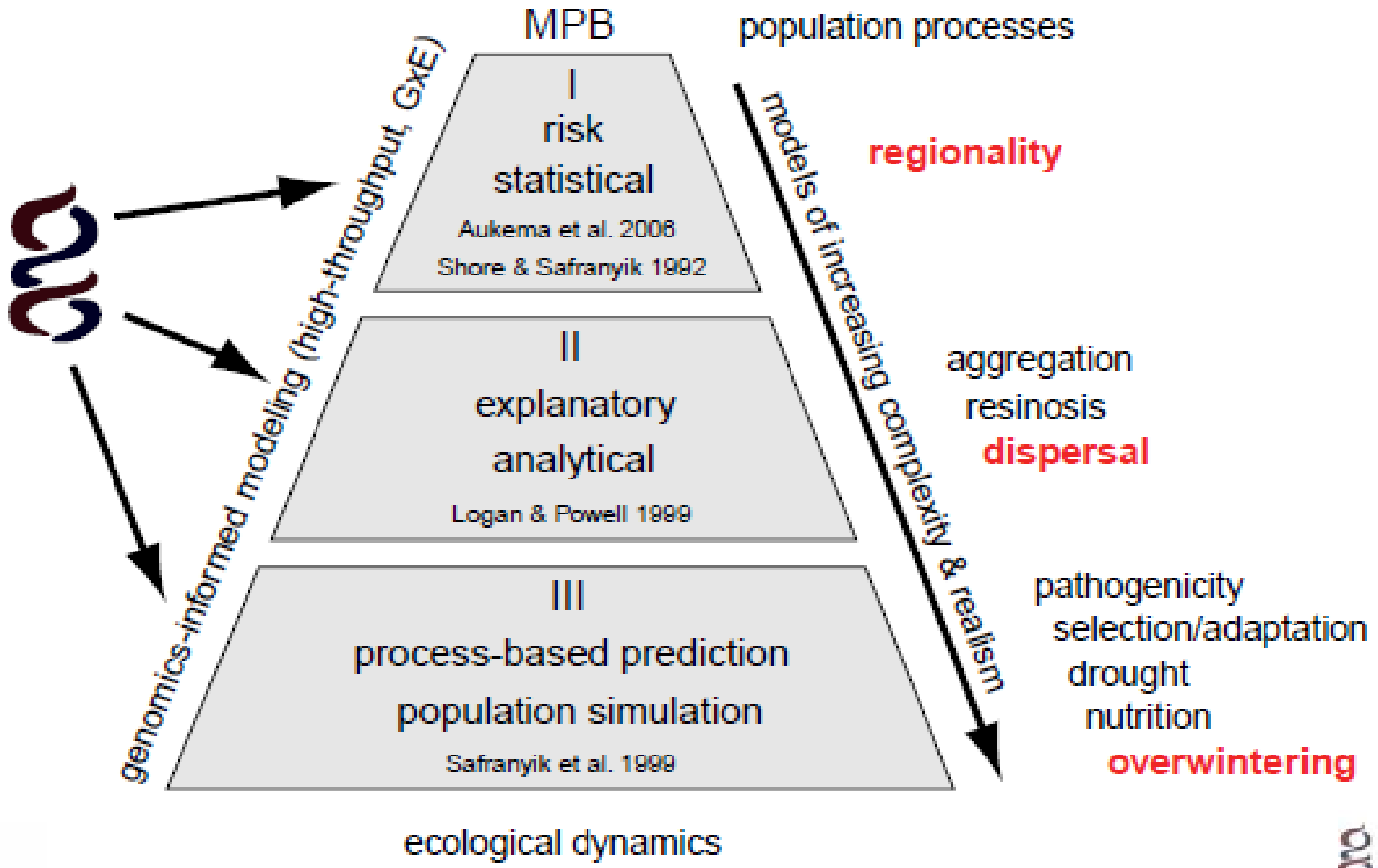
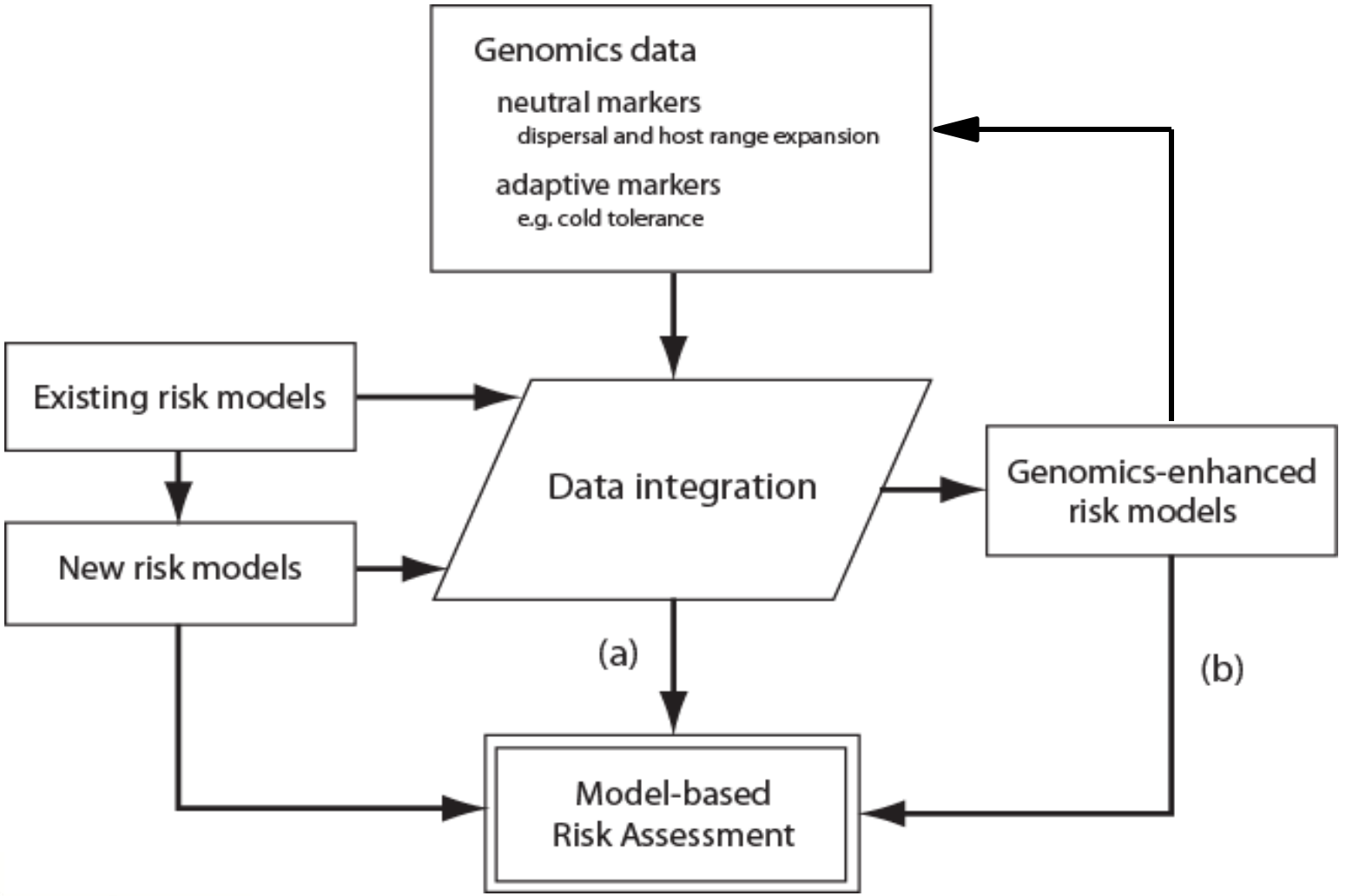
Several genomic insights are being used to inform risk model development



Pathways by which genomics data inform model-based risk assessment



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Summary

The current MPB outbreak has proven to be an excellent system for proof of concept application of genomics to forest management.

- **Pine and MPB populations are heterogeneous**
  - This landscape-level non-uniformity could affect MPB spread, particularly at lower densities and in sub-optimal climates/seasons
- **Genomics is already being used to inform risk assessment and risk modeling**
- **Genomics has potential to inform reforestation and genetic conservation strategies and policies**

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Acknowledgements

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Felix Sperling

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Adriana Arango
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