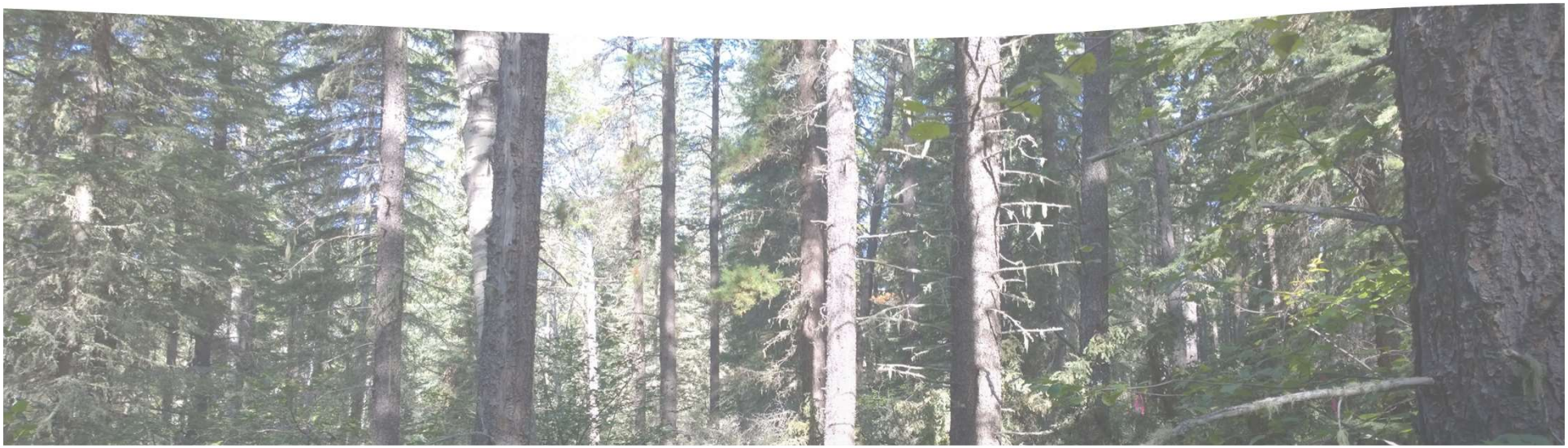
Ministry of Forests, Lands, Natural Resource Operations and Rural Development

UNBC UNIVERSITY OF NORTHERN BRITISH COLUMBIA

Spruce beetle genomics and host tree resistance characteristics

Philip Batista, Christopher Keeling, Dezene Huber, Ward Strong



SBIR^2: Spruce Beetle Infestation Response & Recovery

Our overall objective:

Develop new data on:

1. Spruce beetle genomics
2. Host tree resistance characteristics

This data will be of **immediate use to stakeholders** and that will act as a **foundation for further work**.

Our Team

Phil Batista	Researcher (BCMFLNRORD)	Coordination and data analysis for all aspects of the project
Katherine Bleiker	Research Scientist (CFS)	Insect ecologist with expertise in bark beetle overwintering
Jörg Bohlmann	Professor (UBC)	Expertise in tree and insect genomics
Trevor Doerksen	Research Scientist (BCMFLNRORD)	Expertise in tree breeding and heredity
Dezene Huber	Professor (UNBC)	Expertise in insect ecology
Barry Jaquish	Research Scientist (BCMFLNRORD)	Expertise in tree breeding and heredity
Christopher Keeling	Research Scientist (CFS)	Expertise in tree and insect genomics
Brent Murray	Professor (UNBC)	Expertise in population genetics
Jeanne Robert	Research Scientist (BCMFLNRORD)	Regional Entomologist and expertise in tree and insect genomics
Ward Strong	Research Scientist (BCMFLNRORD)	Expertise in tree and insect genomics
Alvin Yanchuk	Research Scientist (BCMFLNRORD)	Expertise in forest genetics

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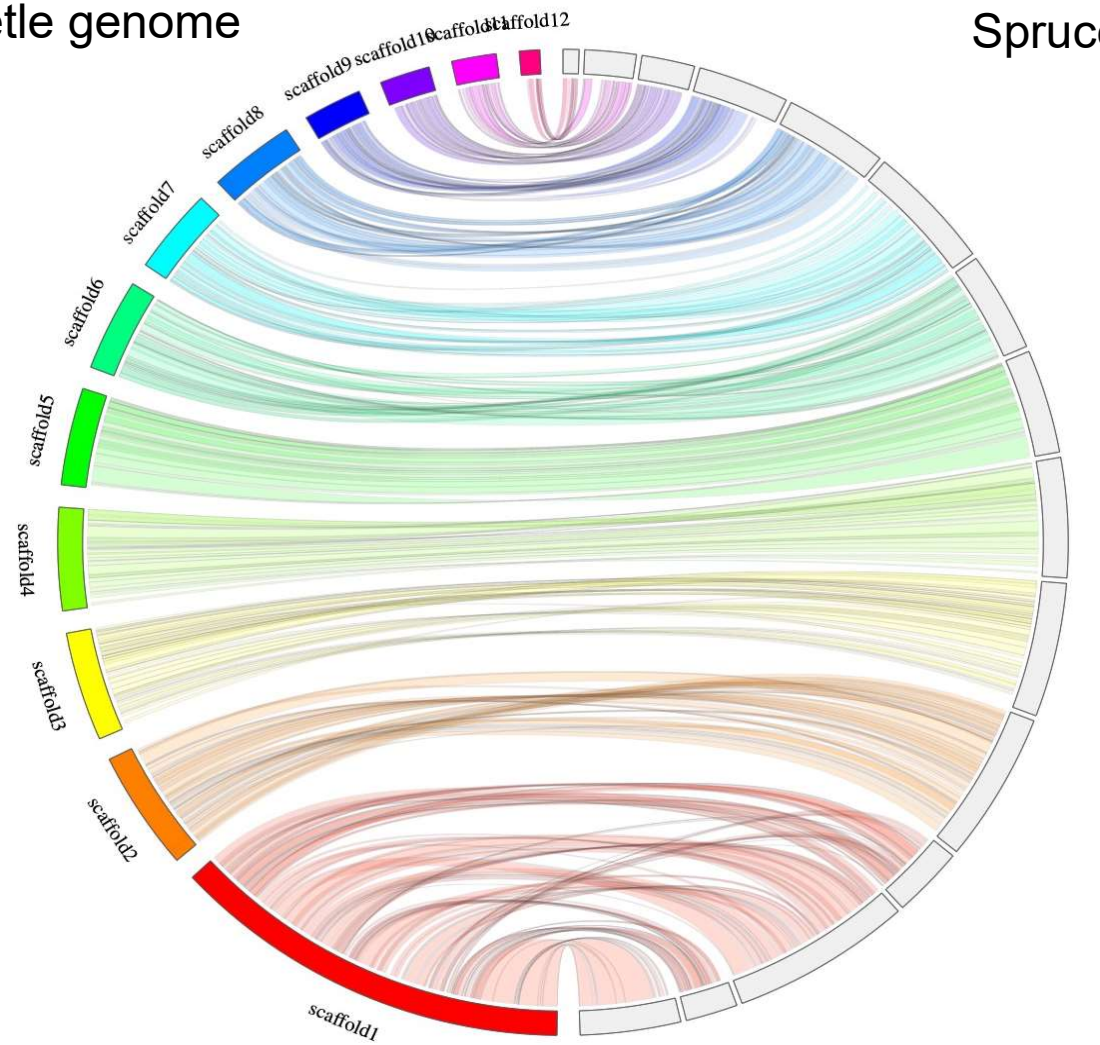
Develop new data on spruce beetle genomics

1. Assemble the first full genome of the spruce beetle and compare it to genome and transcriptome data from other bark beetles (e.g. mountain pine beetle) to better understand the insect's physiology.

Spruce Beetle Genome

Mountain pine beetle genome

Spruce beetle genome



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Both assemblies contain chromosome-sized scaffolds

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Develop new data on spruce beetle genomics

2. Develop spruce beetle population structure data within different regions and hosts in British Columbia for better modelling and management of this forest insect pest.

Spruce Beetle Population Genetics

Favored hosts:

-White spruce (*Picea glauca*)

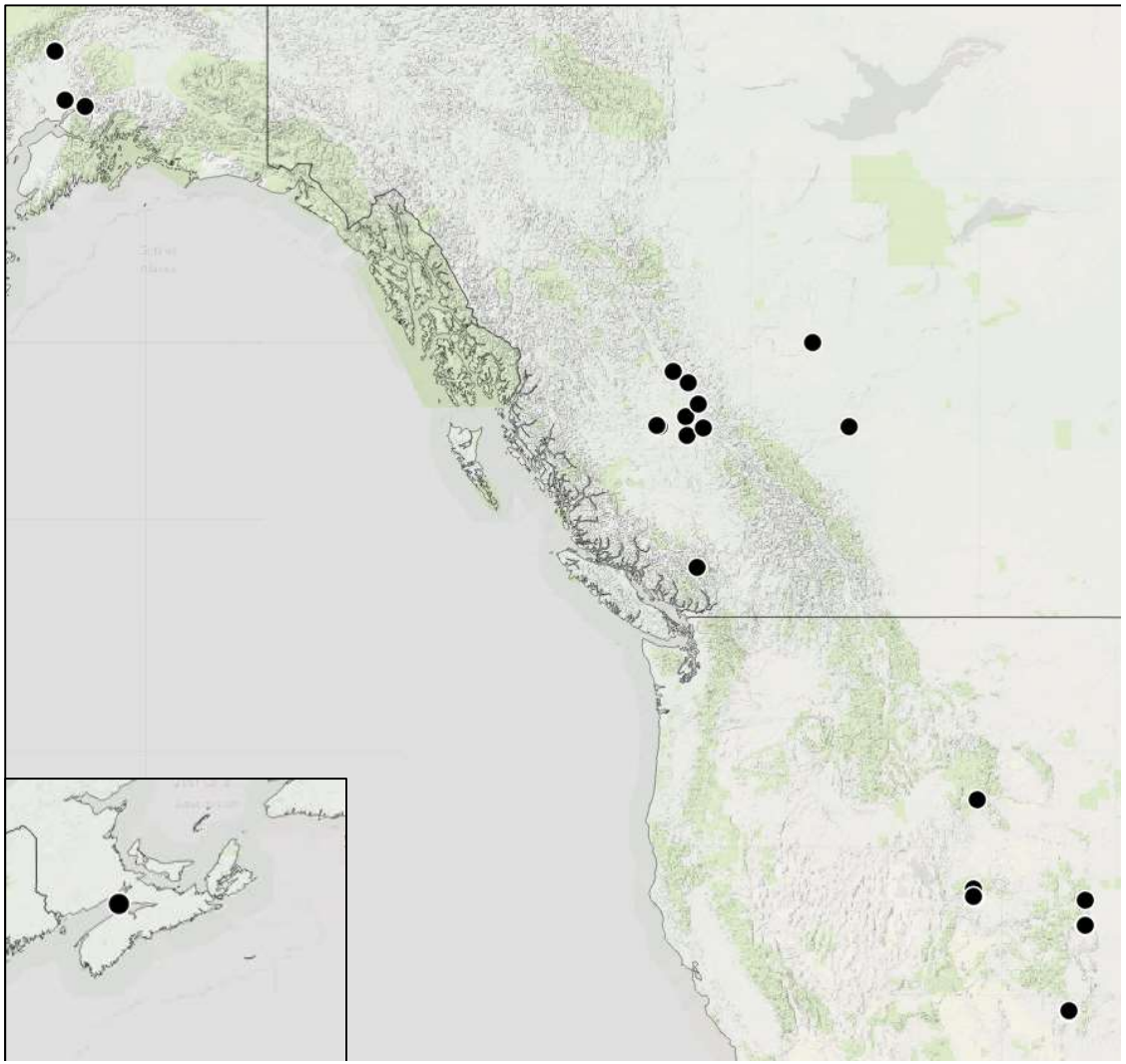
-Engelmann spruce (*Picea engelmannii*)

Range wide population-genetic structure

Spruce Beetle Sampling (2018-2019)

Attention focused on transition area occurring around Prince George.

Using SNP data determine genetic adaptive potential - identify significant outlier loci (under selection).



Summary

What can population structure tell us about pine beetles?

What environmental and evolutionary forces that have shaped these species over time and space.

Basis for functional genetics in identifying the biological significance of genes that show a selective advantage, and what their tolerances are.

(cooler temperatures, developmental timing, longer dispersal flights)

Provide management information, allowing them to target tactics and strategies to specific insect populations.

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Develop new data on spruce beetle genomics

2. generate **tree defense transcriptomic data**, in mature spruce trees with known genetic backgrounds to provide information to tree breeders planning the future forest.

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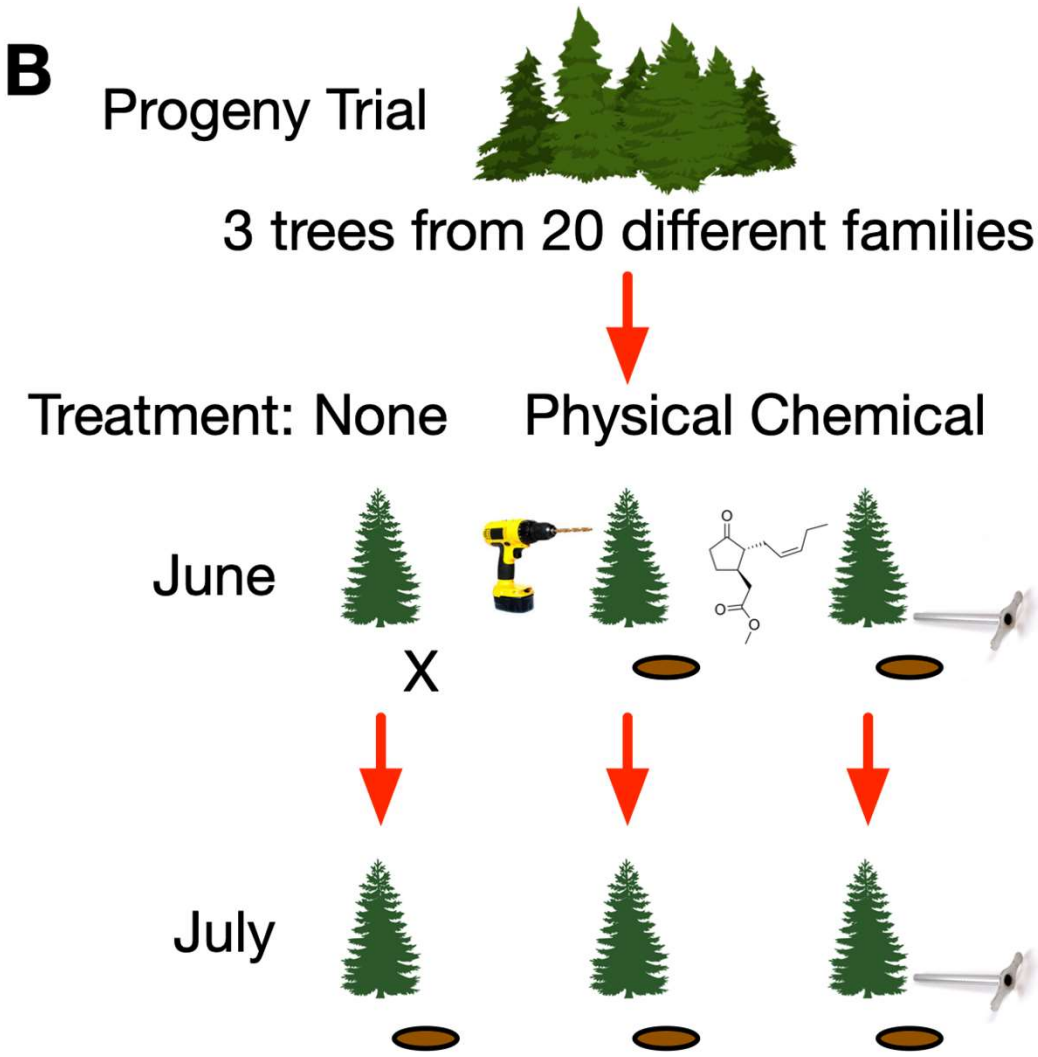

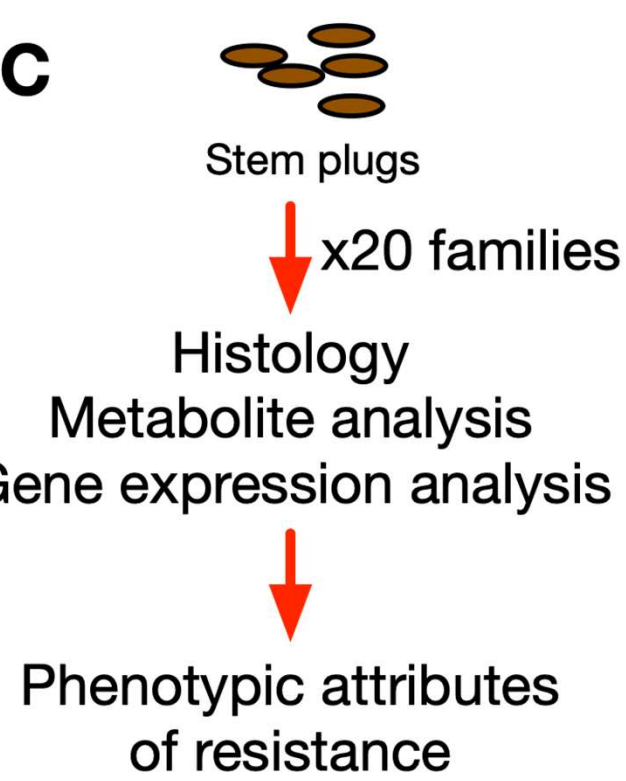

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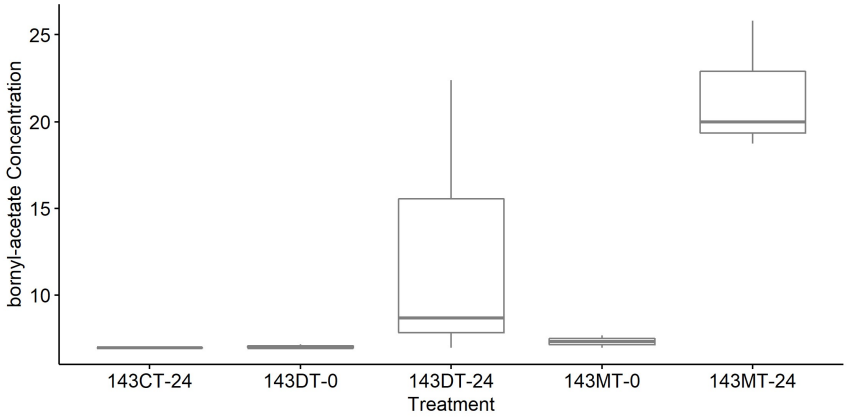
Identification of differences in phenotypic resistance-related traits in a heritability context with well-characterized tree families to guide tree breeding efforts.

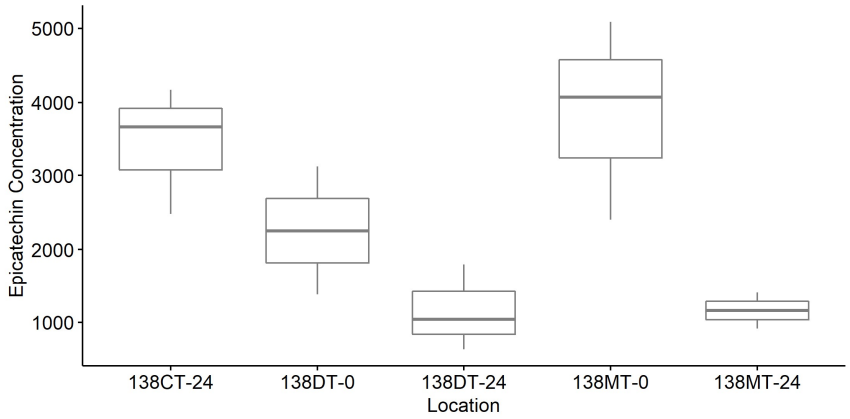
Bornyl Acetate

Insect defensive compound



Epicatechin

Fungal defensive compound



Next step **– Transcriptomics –** identify which genes are turned on/off for tree defense.

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Genome BritishColumbia

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