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
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
The Tria Project: A large-scale multidisciplinary collaborative effort

- University of Alberta
- University of BC
- University of Northern BC
- Canadian Forest Service

Physiological Genomics Studies

Biochemistry, Chemical Ecology, Genomic Resources...

Risk Modeling

Population Genomics Studies

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- Bill Sperling
- Talya Truant
- Tyler Watson
- Caroline Whitehouse
- Mack Yuen
Genomes and Genomic Resources

Chromosomes

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

Genome sequence

Expressed gene sequences

…AAGAGAGCCCTGTCGCTAAATGCAAGCCTTGAAGTACC…

(Adapted from Paul & Ferl, 2000)
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.
Population genomics: assessing genetic variation in large numbers of individuals simultaneously

Genomics is the high-throughput analyses of many genes and/or many individuals simultaneously.
Using genetic markers to identify MPB-attacked jack pine in spring 2010

MOLECULAR ECOLOGY
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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
Refining the lodgepole x jack pine hybrid zone

Cullingham et al. in press, Evolutionary Applications
Refining the lodgepole x jack pine hybrid zone

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

<table>
<thead>
<tr>
<th>Predictor</th>
<th>AIC</th>
<th>Marginal AIC</th>
<th>VIF</th>
<th>Coefficients</th>
<th>LRT*</th>
<th>Effect on p(Pj)</th>
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</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>43498</td>
<td></td>
<td></td>
<td>49.999</td>
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<td></td>
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<tr>
<td>Elevation (m)</td>
<td>50513</td>
<td>7015</td>
<td>6.040</td>
<td>-0.007</td>
<td>7016.8</td>
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<tr>
<td>Drought index (CMI)*</td>
<td>46690</td>
<td>3192</td>
<td>2.400</td>
<td>0.058</td>
<td>3193.5</td>
<td>+</td>
</tr>
<tr>
<td>Mean Annual Precipitation (MAP)*</td>
<td>43615</td>
<td>117</td>
<td>3.730</td>
<td>-0.001</td>
<td>118.8</td>
<td>-</td>
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<tr>
<td>Summer heat:moisture index (SHM)*</td>
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<td>11</td>
<td>3.610</td>
<td>-0.007</td>
<td>12.6</td>
<td>-</td>
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<tr>
<td>Extreme min. temp. (EXT_Cold)*</td>
<td>44524</td>
<td>1026</td>
<td>3.790</td>
<td>-0.307</td>
<td>1027.7</td>
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</tr>
<tr>
<td>Northing - Latitude*</td>
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<td>5.490</td>
<td>-0.580</td>
<td>3174.5</td>
<td>-</td>
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<tr>
<td>Easting - Longitude*</td>
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<td>3306</td>
<td>2.210</td>
<td>0.233</td>
<td>3307.2</td>
<td>+</td>
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</tbody>
</table>
Getting a handle on genetic variation in defense: do lodgepole pine and jack pine defenses differ?
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.
Measuring the effect of climate on defense: does drought affect pine defenses?

Climate Moisture Index (Hogg, 1997) output using BioSim (Barry Cooke)
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
Water deficit reduces photosynthesis in lodgepole and jack pine, reducing carbon gain

**Lodgepole pine**

<table>
<thead>
<tr>
<th>Day 14</th>
<th>Day 28</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>Inoculated</td>
</tr>
<tr>
<td>Control</td>
<td>Inoculated</td>
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</tbody>
</table>

**Jack pine**

<table>
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<tr>
<th>Day 14</th>
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</tr>
<tr>
<td>Control</td>
<td>Inoculated</td>
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</tbody>
</table>
Lesion development differs in lodgepole and jack pine, and is also affected by drought.
Drought affects gene expression associated with both pre-formed and induced defenses

**Pbc chitinase2.1**

- Water p=0.0008
- Fungi p=0.08
- W*F p=0.73

**Pbc(+)-3-carene-synthase**

- Water p=0.01
- Fungi p=0.002
- W*F p=0.26

**Pbc chitinase1**

- Water p=0.0006
- Fungi p<0.0001
- W*F p=0.005

**Pbc(E)-β-farnesene-synthase**

- Water p=0.01
- Fungi p=0.02
- W*F p=0.49

**Increased constitutive expression**

**Decreased induced expression**
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
Post-disturbance reforestation: can genetic variation insights be used to refine seed zones?
Similar genomic approaches are being used to investigate genetic variation in MPB
Population genetic analyses to examine MPB dispersal (gene flow) and genetic connectivity

Samarasekara et al. Molecular Ecology, in press
Can we detect signatures of selection for traits such as cold tolerance?

**Selection (winter cold temperatures)**

- Frequency: 5%
- Frequency: 20%

Cumulative % Mortality vs. Supercooling point (°C)
Several genomic insights are being used to inform risk model development.
Pathways by which genomics data inform model-based risk assessment

1. Genomics data:
   - neutral markers
   - dispersal and host range expansion
   - adaptive markers
     - e.g., cold tolerance

2. Data integration
   - Existing risk models
   - New risk models

3. Genomics-enhanced risk models

4. Model-based Risk Assessment

(a) and (b) represent the flow of information from genomics data to model-based risk assessment.
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
Acknowledgements

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