Genomics and reciprocal illumination

The study of local adaptation across an understudied clade of pines

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Adaptation: a phenotypic trait with a functional role that has evolved and is maintained by natural selection. Populations are the units in which adaptation occurs, not individuals.

Temporal components: (evolved)

Spatial components: (variation in selection across landscapes)

Geometry of Local Adaptation

Empirical Study of Local Adaptation

Status of the field pre-genome

Long term adaptive evolution

Local adaptation at fine spatial scales

Benefits of a genome sequence

Outline

Reciprocal Illumination
How common is adaptive evolution in the lineage of soft pines?

Are populations of three soft pine species locally adapted across the Lake Tahoe Basin?

Pre-Genome Studies of Adaptive Evolution

Why?

192 expressed genes examined for patterns of diversity and divergence across 11 species of subgenus Strobus.

- 8 – 16 megagametophytes/species
- P. taeda outgroup
- Bidirectional Sanger sequencing
- Mixture of PineSAP (automated) and CodonCode (manual)
- Inferences using MK framework (DoFE)

Approximate Genomics 0.1

Distribution of Deleterious Fitness Effects (DFE)

Proportion of Adaptive Substitutions (α)

A problem …

Divergence bias
- Primers transferred across up to 80 my of divergence
- Why would highly conserved genes contribute to relatively recent adaptation?
**Approximate Genomics 1.0**

- ddRADseq used to generate hundreds of thousands of SNPs for *Pinus balfouriana*
- Custom SNP calling and genotyping pipeline
- Megagametophyte arrays from four maternal trees
- n = 70–94/tree
- Custom linkage mapping pipeline
- Imputation and error correction needed

**METHODS**

**Next generation linkage mapping**

- Friedline et al. (2015). Tree Genetics and Genomes. Accepted minor rev.
- How common is adaptive evolution in the lineage of soft pines?
- Are populations of three soft pine species locally adapted across the Lake Tahoe Basin?

**Spatial Scale**

- Eckert et al. (2010). Genetics 185: 969-982
- Richardson et al. (2014). TREE 29: 165-176

**Pre-Genome Studies of Adaptive Evolution**

**Methods**

- Sugar pine (*P. lambertiana*)
- Western white pine (*P. monticola*)
- Whitebark pine (*P. albicaulis*)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Units</th>
<th>Sibs</th>
<th>Families</th>
<th>Populations</th>
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</thead>
<tbody>
<tr>
<td>Height</td>
<td>mm</td>
<td>35</td>
<td>111/158/100</td>
<td>8/10/6</td>
</tr>
<tr>
<td>Bud flush</td>
<td>Julian days</td>
<td>35</td>
<td>111/158/100</td>
<td>8/10/6</td>
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<tr>
<td>Root:Shoot</td>
<td>g/g</td>
<td>10</td>
<td>111/158/100</td>
<td>8/10/6</td>
</tr>
<tr>
<td>δ13C</td>
<td>%</td>
<td>5</td>
<td>111/158/100</td>
<td>8/10/6</td>
</tr>
<tr>
<td>δ15N</td>
<td>%</td>
<td>5</td>
<td>111/158/100</td>
<td>8/10/6</td>
</tr>
</tbody>
</table>

**Genetic components of phenotypes are variable within populations (h²).**

**Genetic components of phenotypes are variable among populations (QST).**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Sugar</th>
<th>Western white</th>
<th>Whitebark</th>
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<tbody>
<tr>
<td>Height</td>
<td>0.0248</td>
<td>0.0145</td>
<td>0.0418</td>
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<td>Bud flush</td>
<td>0.0286</td>
<td>0.0754</td>
<td>0.0156</td>
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<tr>
<td>Root:Shoot</td>
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<td>0.1096</td>
<td>0.0310</td>
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<tr>
<td>δ13C</td>
<td>0.0388</td>
<td>0.1724</td>
<td>0.0427</td>
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<tr>
<td>δ15N</td>
<td>0.0000</td>
<td>0.0734</td>
<td>0.0191</td>
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</table>
Local adaptation: Lake Tahoe Basin

Genecology

- Quantitative genetic variation correlated to environment

$Q_{ST} - F_{ST}$

- Traits more differentiated than expected based on candidate genes

Genotype Associations

<table>
<thead>
<tr>
<th>Species</th>
<th>SNPs</th>
<th>Number</th>
<th>Effect (r)</th>
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</thead>
<tbody>
<tr>
<td>Sugar pine</td>
<td>493</td>
<td>20</td>
<td>0.14 – 0.35</td>
</tr>
<tr>
<td>Western white pine</td>
<td>160</td>
<td>10</td>
<td>0.20 – 0.33</td>
</tr>
</tbody>
</table>

Phenotypes

<table>
<thead>
<tr>
<th>Species</th>
<th>SNPs</th>
<th>Significant</th>
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</thead>
<tbody>
<tr>
<td>Sugar pine</td>
<td>493</td>
<td>65 (13.1%)</td>
</tr>
<tr>
<td>Western white pine</td>
<td>160</td>
<td>16 (10.0%)</td>
</tr>
</tbody>
</table>

Environment

Polygenic adaptation

- Carbon isotope ratios
  - δ¹³C
- Contributions of SNPs to $Q_{ST} (Q_s)$
  - $F_{ST}$-like component
  - LD-like component

Conclusions

- What we know from previous research:
  - Markers are the limiting resource
  - Biases
  - Not enough choice
  - Integration of genotypes, phenotypes, and environment can identify pieces of locally adapted genetic architectures
  - This architecture is polygenic

What is next?

- Genome sequences will facilitate:
  - Hypothesis tests about the identity of Cr1
  - Inferences of historical demography, targets of selection, and their interaction.

Cr1 and its identity

- Position of Cr1 is known approximately based on linkage relationships
- Sequence-based candidates for Cr2 can be used for homology-based searches
- Collinearity with loblolly pine can be used in a comparative genomics framework.
Inferences of demography and selection

Population Genomics

Quantitative Genetics

Landscape & Evolutionary Ecology

P. balfouriana subsp. australica

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