Adaptations

Genetic variation is the ingredient for Natural Selection – Introgression can provide allelic variation

Adaptive introgression from *Populus balsamifera* (balsam poplar) into *P. trichocarpa* (black cottonwood)

Adriana Suarez-Gonzalez, Camille Christe, Armando Geraldes, Charles Hefer, Christian Lexer, Quentin Cronk and Carl Douglas

Poplars as a system to study molecular basis of adaptation in forest trees

- Widespread distributions across environmental gradients
- Hybrids and contact zones
- *P. trichocarpa* reference genome
- Whole genome sequences and SNPs
- Salicoid whole genome duplication shared by all species

Introgression from *balsamifera* into *trichocarpa*

Introgression from *balsamifera* into *trichocarpa*

Geraldes et al. 2014

Genes in chromosome 15

Genetic basis of adaptation in *Populus trichocarpa*

POPCAN

Association analysis

34K SNPs

~500 individuals

Fst outlier test

Geraldes et al. 2014; McKown et al. 2014
INTROGRESSION FROM \textit{balsamifera} INTO \textit{trichocarpa}

\textbf{COMT1: haplotype distribution in} \textit{balsamifera}

\textbf{Candidate genes}

Increased levels of population differentiation at candidate loci in chromosome 15 are mainly driven by introgressed nsSNP.

What is the size of this introgressed region?  
Is this adaptive introgression?  
Are there other introgressed regions?

\textbf{Genes in chromosome 15}

Ancestry inferred for e/ind independently using \textit{Hidden Markov Model} (HMM) for admixture (Price et al 2009)

\textbf{Fst outliers}  
\textbf{Association analysis}  
McKean et al. 2014
Genes in chromosome 15

Fst outliers
Association analysis

Genes in chromosome 12

McKown et al. 2014

Genes in chromosome 6

Fst outliers

Geraldes et al. 2014
Geraldes et al. unpublished

Selected individuals
Ref (25 each sp); Admixed (68)

P. balsamifera  P. trichocarpa

RASPberry: Input data

Ch6  Ch12  Ch15

P. balsamifera  P. trichocarpa

Introgression: from balsamifera to trichocarpa

Proportion of alleles with balsamifera ancestry at each SNP

Sliding window
Size 100 kb, step 20kb

Total: 186,376 SNPs

15 Mb
Pre: 920,351
Post: 56,500 (6.1%)

27 Mb
Pre: 873,992
Post: 52,428 (6%)

15 Mb
Pre: 603,796
Post: 77,448 (13%)
Introgression from balsamifera into trichocarpa

- We found three introgressed regions:
  - One in chromosome 6
  - Two in chromosome 15

- Is this adaptive introgression?
- Are these regions adaptive in *P. trichocarpa* and *P. balsamifera*?

Are introgressed regions adaptive in pure parental species

Tajima D in balsamifera and trichocarpa
Are introgressed alleles different at the functional level?

**COMTs:**
- Catalyze the methylation of lignin precursors
- **COMT2 (ch12)** is involved in developmental lignification
- **COMT1 (ch15)** could be involved in pathogen defense

*COMT sequence alignment*
- nsSNP (P/Q) may cause changes in COMT1 enzyme activity
  - This could result in a competitive disadvantage at lower latitudes

**Gene expression COMT1: RNA-seq**

*Data from C. Hefer*

**Introgressed alleles are different at the functional level**

*Data from A. Capron, C. Hefer*

The nsSNP P/Q is in linkage with a cis-element in the promoter region.
Summary

• Analysis of chromosomes 6, 12 and 15 revealed 3 balsamifera introgressed regions in trichocarpa:
  – 1 in chromosome 6
  – 2 in chromosome 15

• The first introgressed region of chromosome 15 showed signals of adaptive introgression:
  – Is enriched with genes related to developmental processes
  – Has signals of balancing selection in P balsamifera
  – Has alleles that are different at the functional level

• Future work:
  – Functional analysis of COMT1 alleles and other candidates
  – Association analysis of candidate regions using genome-wide SNP data

Linkage disequilibrium (D'):
First introgressed region chr15

Selected individuals
Ref (25 each sp): Admixed (68)

Fst in balsamifera and trichocarpa
P. trichocarpa – balsamifera divergence:
75,000 ya (25 y/g = 3000 gen)

Ancestral rate

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<th>Ne</th>
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<td>5.000 [Levens]</td>
<td>20.000 [Keller]</td>
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Default rate

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<tr>
<td>p/n</td>
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</table>

genome assembly ~422.9 Mb
Yin et al. (genetic map) = genome length 2,300 - 2,500 cM, based on observed # of crossovers in maternal haplotypes, and total observed map length:
defaultRate = 2500 cM / 422.9 Mb = 5.9

Models

| mutation0 | 0.007937 |
| mutation1 | 0.007937 |
| defaultRate | 5 |
| miscopyMutation | 0.01 |

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McKown et al. 2014
<table>
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<tr>
<th>kb</th>
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<th>Geo/Ew correlation</th>
<th>Trait association test</th>
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<td>12.7</td>
<td>ABCB19</td>
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<td>26.5</td>
<td>LSU4</td>
<td>**</td>
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| 137.1 | PR95 | *** | *** | Trait association test
*** | Geo/Ew correlation |
| 162.7 | TFG1 | *** | *** | Trait association test
*** | Geo/Ew correlation |
| 236.7 | COMT1 | *** | Lat | |
| 276.7 | NAC062 | ** | Lat,MCMT,TD,DD_0,EMT | Phenology - Ecophysiology |
| 406.7 | Unknown | *** | Lat,MCMT,DD_0,EMT | |
| 597.7 | Yippee | *** | Lat,MCMT,DD_0 | Phenology |
| 611.3 | Def. zinc finger | ** | *** | Lat,MCMT,DD_0,EMT | Phenology - Ecophysiology |

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**Expression profiles of COMTs**

![Expression profiles of COMTs](www.plexdb.org)