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POSTER

IUFRO-CTIA joint conference, "Adaptation, Breeding and Conservation in the Era of Forest Tree Genomics and Environmental Change", August 25-28, 2008 – Loews Le Concorde – Québec City, Canada

Association mapping for wood quality in *Pinus pinaster* Aquitaine breeding population

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Improvement of wood quality related traits is currently hampered by costly chemical and technological assays and the necessity to wait until the trees are nearly mature to evaluate wood properties. The availability of a vast quantity of genomic data opens now a new avenue to identify early selection criteria based on molecular information and therefore increase selection efficiency. Association mapping is becoming a method of choice to identify QTN (quantitative trait nucleotide) that contribute to complex trait variation. The implementation of this approach requires on the one hand knowledge of the molecular mechanisms underlying trait variation and polymorphism within candidate genes, and on the other hand the availability of phenotypically well characterized genetic material. We are developing this strategy in the frame of the French maritime pine breeding program, an economically important forest tree species in the South Western Europe. About 500 trees from the breeding population were evaluated for wood physical and chemical properties through the analysis of 2,800 half-sib progenies and 1,500 clones in 8 field tests. These same trees are being genotyped at 185 SNPs obtained from the sequencing of 41 candidate genes, and an additional set of 200 eSNPs detected in 147 EST-contigs (to be used as control). Statistical association between the breeding values of the 500 trees and their respective genotypes will be tested using mixed models accounting for relatedness among individuals of the breeding population.

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Context

Improvement of wood quality related-traits is currently hampered by costly chemical and technological assays, and the necessity to wait until trees are nearly mature to assess wood properties. The availability of a vast quantity of genomic data opens up new opportunities to identify early selection criteria based on molecular information, and thus to increase selection efficiency.

The aim of this study is to identify quantitative trait nucleotides that contribute to wood quality variation.

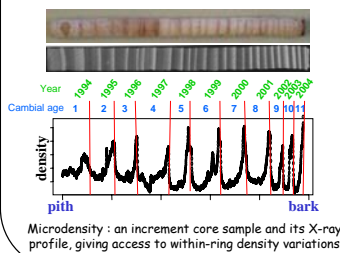


545 trees from the Aquitaine breeding population
1st and 2nd breeding generations - familial relatedness



Phenotyping

	270 G0 plus-trees measured in half-sib progeny tests	275 G1 trees measured in clonal tests
Sample sizes	2800 progeny trees phenotyped in 4 field tests	1500 clones phenotyped in 4 field tests
Studied traits	Height, circumference, straightness, lignin and cellulose contents (NIRS), microdensity.	Height, diameter, straightness, pulping properties, fibers morphology, chemical composition (NIRS), microdensity.



Sampling wood for chemical analyses



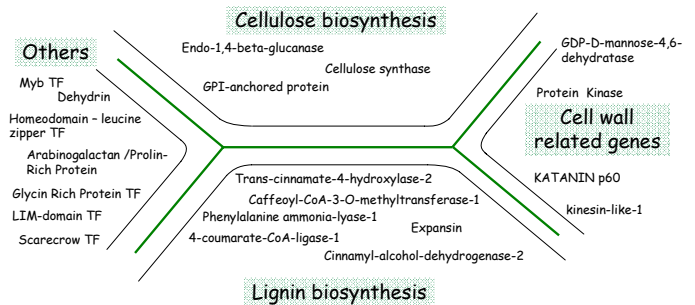
Powdering the samples



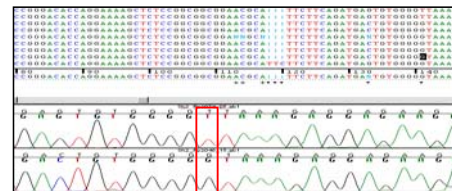
Genotyping

545 trees genotyped at 384 SNPs
(Illumina VeraCode Technology)

→ Candidate genes SNPs : 184 SNPs (from 41 CG)

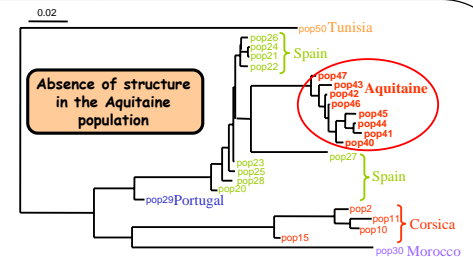
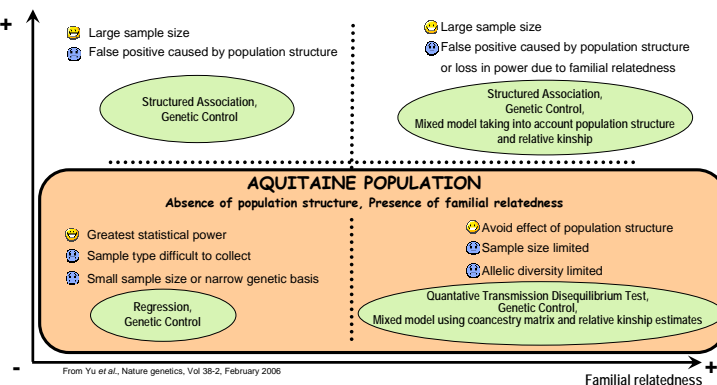


→ Background SNPs : 200 eSNPs (from 147 EST contigs)



Association mapping

Population structure



Statistical associations between the breeding values of the 545 trees and their respective genotypes will be tested using mixed models accounting for relatedness among individuals (G1 trees).

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