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POSTER

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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.

Association mapping for wood quality in the Pinus pinaster Aquitaine breeding population Camille Lepoittevin^{1,2a}, Pauline Garnier-Géré¹, François Hubert¹, Franck Salin¹, Emmanuelle Eveno¹, Laurent Bouffier^{1,2a}, Jorge Paiva^{3,4}, Delphine Audigeos¹, Valérie Léger¹, Luis Cancino^{1,5}, Denilson Da Silva Perez^{2b}, Luc Harvengt^{2a}, Christophe Plomion¹ 1INRA, UMR BIOGECO, 69 route d'Arcachon, 33612 Cestas, France (lepoittevin@pierroton.inra.fr); 2ª FCBA, Laboratoire de Biotechnologie, Domaine de l'Etancon, 77370 Nangis, France; ^{2b} FCBA, Pôle Nouveaux Matériaux, Domaine Universitaire, BP 251, 38044 Grenoble, France; ³ ITQB/IBET, Laboratory of Plant Cell Biotechnology, ITQB/IBET - Apt 127, 2781-901 Oeiras, Portugal; ⁴ Forestry and Forest Products Group, Tropical Research Institute (IICT), Tapada da Ajuda 1349-017 Lisbon, Portugal; ⁵ Instituto Biologia Vegetal y Biotechnologia, Universidad de Talca, 2 Norte 685, Talca, Chile 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 Genotyping 545 trees genotyped at 384 SNPs 270 GO plus-trees measured in 275 G1 trees measured in clonal (Illumina VeraCode Technology) half-sib progeny tests tests 2800 progeny trees phenotyped in 1500 clones phenotyped in 4 field Sample 4 field tests → Candidate genes SNPs : 184 SNPs (from 41 CG) sizes tests Height, diameter, straightness, Cellulose biosynthesis Height, circumference, Studied pulping properties, fibers straightness, lignin and cellulose GDP-D-mannose-4.6 Endo-1,4-beta-glucanase Others morphology, chemical composition (NIRS), microdensity. traits dehydratase contents (NIRS), microdensity. Cellulose synthase Myb TF Dehydrin GPI-anchored protein Protein Kinose Cell wall Homeodomain - leucin zipper TF related genes Arabinogalactan /Prolin Rich Protein rans-cinnamate-4-hydroxylase-2 KATANIN p60 Glycin Rich Protein Tf Caffeoyl-CoA-3-O-methyltransferase kinesin-like-1 LIM-domain TF Phenylalanine ammonia-lyase-1 Expansir 4-coumarate-CoA-ligase-1 chemical analyses Scarecrow TF Cinnamyl-alcohol-dehydrogenase-2 Lignin biosynthesis → Background SNPs : 200 eSNPs (from 147 EST contigs) Powdering the samples The 200 eSNPs that have been chosen among more than 9000 eSNPs were not singletons and had at least 4 sequences in their externation nitl A 8 8 A 8 8 8 their contig m Microdensity : an increment core sample and its X-ro profile, giving access to within-ring density variation 1 8 Acquiring NIR Spectra, giving access to wood lignin and cellulose contents Association mapping Population structure 0.02 C Large sample size Large sample size False positive caused by population structure False positive caused by population structure Absence of structure or loss in power due to familial relatedness in the Aquitaine population Structured Association, Structured Association. Genetic Control, Mixed model taking into account population structure and relative kinship յեն Genetic Control AQUITAINE POPULATION Absence of ion structure, Presence of familial relatedness ----- Corsica O Avoid effect of population structure Greatest statistical power Sample size limited Dendrogram obtained by hierarchical clustering using a Neighbor-Joining algorithm applied on a Fst distances matrix from 8 SSRs Sample type difficult to collect Allelic diversity limited Small sample size or narrow genetic basis Quantative Transmission Disequilibrium Test, Genetic Control, Mixed model using coancestry matrix and relative kinship estimates Statistical associations between the breeding values of Regression, Genetic Control the 545 trees and their respective genotypes will be tested using mixed models accounting for relatedness among individuals (G1 trees). From Yu et al., Nature genetics, Vol 38-2, February 200 Familial relatedness Acknowledgements : This research is currently supported by grants from ANR (GNP05013C project).

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