



**HAL**  
open science

## Development of highly-multiplexed SNP arrays in Maritime pine for multi-objective genetic applications

Christophe Plomion, Emilie E. Chancerel, Camille Lepoittevin, Isabelle Lesur,  
S.C. González-Martínez, G.G. Vendramin, M.T. Cervera

► **To cite this version:**

Christophe Plomion, Emilie E. Chancerel, Camille Lepoittevin, Isabelle Lesur, S.C. González-Martínez, et al.. Development of highly-multiplexed SNP arrays in Maritime pine for multi-objective genetic applications. IUFRO Tree Biotechnology Conference 2011 “From genomes to integration and delivery”, Jun 2011, Bahia, Brazil. 3 p., 2011. hal-02808550

**HAL Id: hal-02808550**

**<https://hal.inrae.fr/hal-02808550>**

Submitted on 6 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## **Development of highly-multiplexed SNP arrays in Maritime pine for multi-objective genetic applications**

Plomion C<sup>1</sup>, Chancerel E<sup>1</sup>, Lepoittevin C<sup>1</sup>, Lesur I<sup>1</sup>, González-Martínez SC<sup>2</sup>, Vendramin GG<sup>3</sup>, Cervera MT<sup>2</sup>

1/ INRA, UMR1202 BIOGECO, F-33610 Cestas, France ;

2/ INIA, Center of Forest Research (CIFOR), E-28040 Madrid, Spain ;

3/ CNR-IGV, Firenze, Italy

Single Nucleotide Polymorphisms (SNPs) are the most abundant form of genetic variation in the genome. In this poster, we reviewed what has been achieved in terms of highly-multiplexed SNP genotyping assay construction in maritime pine (*Pinus pinaster* Ait.), the main conifer used for commercial plantation in southwestern Europe. Seven custom SNP-assays (384 and 1536-plex), oriented towards broad applications, have been designed. We illustrated here the usefulness of this genotyping technology to address specific questions related to i/ genetic diversity and population structure analysis, ii/ linkage and QTL mapping and iii/ association mapping.

With respect to genetic diversity and differentiation, a custom VeraCode assay for 384 SNPs mostly based on a larger array designed for linkage mapping (see below) allowed to obtain less blurred, albeit similar, breeding zone boundaries than a set of 12 nuSSRs screened on the same individuals. Levels of diversity were also more accurately estimated, showing clear differences among gene pools. Interestingly, a relatively small subset of SNPs would be enough to develop an application tool for origin certification, which could have a notable impact on current operational practices.

In terms of linkage mapping, a custom GoldenGate assay for 1,536 SNPs detected through the resequencing of gene fragments (in vitro SNPs) and from Sanger-derived Expressed Sequenced Tags (in silico SNPs) was established. Offspring from two mapping pedigrees were genotyped. A consensus map comprising 357 SNPs from 292 different loci was constructed and the analysis of sequence homology between mapped markers and their orthologs in a *Pinus taeda* linkage map, made it possible to align the 12 linkage groups of both species. Moreover, QTL detection for different traits is underway.

In terms of association mapping, a custom GoldenGate assay with 384 SNPs was built and used to genotype 160 unrelated plus-trees from a half-sib experimental design for which breeding values (for height growth, circumference, stem straightness at 8 years, lignin content and extractives at 31 years) were available. Taking into account multiple testing, one single SNP in a gene encoding a putative fasciclin-like arabinogalactan protein was found to be associated with growth traits.

We conclude that the VeraCode/GoldenGate assays can be used successfully for high-throughput SNP genotyping in maritime pine, a conifer species that has a genome seven times the size of the human genome. This first generation of SNP-arrays has been recently upgraded to an Infinium-array (containing 10.5k SNPs) thanks to deep sequencing based on new generation sequencing technologies. The Infinium-array also includes SNPs from comparative

orthologous sequences with other major conifer species, providing a wider collection of anchor points for comparative genomics among these major groups of forest trees.