



WP 2.09.01 Seed Orchards

PROCEEDINGS

IUFRO

Seed Orchard Conference 2017

SEPTEMBER 4-6, 2017 BÅLSTA, SWEDEN



skogforsk



POLLEN CONTAMINATION AND MATING STRUCTURE IN MARITIME PINE CLONAL SEED ORCHARDS

Laurent Bouffier, French National Institute for Agricultural Research (INRA), Cestas, University Bordeaux, France.
E-mail: laurent.bouffier@inra.fr

Sandrine Debille, Pierre Alazard, Luc Harvengt and Jean-François Trontin, FCBA, Biotechnology and Advanced Forestry Department, Cestas, France

Patrick Pastuszka, French National Institute for Agricultural Research (INRA), Cestas, France

Annie Raffin, French National Institute for Agricultural Research (INRA), Cestas, University Bordeaux, France

Marie-Anne Lelu-Walter, French National Institute for Agricultural Research (INRA), Ardon, France

Brigitte Musch, ONF, Conservatoire Génétique des Arbres Forestiers, Ardon, France

Maritime pine (*Pinus pinaster* Ait.) is a major forest tree species in south-western Europe. In France, a breeding program based on a recurrent selection strategy was initiated in the 1960s with the objective to develop improved varieties for growth and stem straightness. Open-pollinated seed orchards currently supply more than 90% of maritime pine improved stocks for plantation forestry in France (41 million seedlings in 2015-2016). However pollen contamination and mating structure in such seed orchards are still largely unknown.

In this study, we investigated the genetic composition of seed collections from clonal seed orchards through SNP genotyping considering three factors:

- 1) The seed orchard location (3 sites with contrasted pedo-climatic conditions)
- 2) The pollination year (three seed collections: 2011, 2013 and 2014).
- 3) The maternal genotype on which seeds were collected.

Three data sets were analyzed:

- 1) 1,524 offsprings from four maternal parents over three seed orchards and two seed collections (2011, 2013);
- 2) 590 offsprings from 20 maternal parents in one seed orchard (2013);
- 3) 450 offsprings sampled from commercial seedlots from three seed orchards (2014).

Paternity and/or parental analyses were carried out on these 2,564 offsprings with the Cervus software (likelihood inference methodology with 99% confidence level) based on 60 SNPs developed by Vidal *et al.* (2015).

Moreover, each parental genotype was evaluated over two pollination years (2015, 2016) for reproductive phenology traits (precocity of female and male flowering as well as female number of flowers) in the three seed orchards.

Pollen contamination rates were globally high (from 20 to 96%) but highly dependent on seed orchard location. An effect was also detected for both the maternal parent and the pollination year. Even if all parental genotypes contributed as father in the offspring, differential paternal reproductive success was highlighted. This is only partly explained by the variable number of ramets deployed per parental genotype in each orchard. Site and annual variation in pollen contamination can result from a number of geographical (vicinity of plantations), orchard design (zones, ramets/genotype), ontogenetic (orchard age) and environmental factors (pedo-climatic conditions) affecting flowering and/or mating success. Reproductive phenology of parental genotypes and climatic data in each orchard will be presented to tentatively find correlations with pollen contamination rates.

Keywords: *Pinus pinaster* Ait., clonal seed orchard, SNP genotyping, pollen contamination, mating structure

Acknowledgements: This study was supported by a national grant (QUASEGRAINE project, French Ministry of Agriculture/DGAL, n°2014-352, coord. ONF/B. Musch) as well as regional funds from the Conseil Régional d'Aquitaine (IMAF project, n°12009468-052, coord. FCBA) and the Conseil de la Région Centre (IMTEMPERIES project, n°2014-00094511, coord. INRA/M.-A. Lelu-Walter).

We thank also the Maritime Pine Breeding Cooperative (GIS Pin Maritime du Futur) for its support through the FORTIUS project (granted by the Conseil Regional d'Aquitaine and the French Ministry of Agriculture, coord. P. Pastuszka). The SNP genotyping was performed at the Genomic Facility of Bordeaux (granted by the Conseil Regional d'Aquitaine: n°20030304002FA and 20040305003FA, the European Union: FEDER n°2003227 and ANR: n°ANR-10-EQPX-16 Xyloforest).

References:

Vidal, M., Plomion, C., Harvengt, L., Raffin, A., Boury, C. & Bouffier, L. (2015). Paternity recovery in two maritime pine polycross mating designs and consequences for breeding. *Tree Genetics & Genomes* 11(5): 105.