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)
3. The maternal genotype on which seeds were collected.

Three data sets were analyzed:

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

Paternity and/or parental analyses were carried out on these 2,564 offspring 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
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