COANCESTRY AMONG WIND POLLINATED PROGENIES FROM A *PINUS PINASTER* SEED ORCHARD IN A PROGENY TRIAL.

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Introduction

Maritime pine (*Pinus pinaster* Ait.) is an important commercial species in southwest Europe. In Portugal, *P. pinaster* is one of the most important native species, covering 1 Mha. It is the only source of long fibre for pulp and paper and the main source for solid sawn timber industries. A tree improvement plan has been developed since the early 80s with the aim of increasing volume and stem form. A genetic improvement program management implies the knowledge of the genetic parameters, of the way these parameters affect the genetic gains, and how the progenitors transmit to the progeny the traits under improvement. The knowledge of the coefficient of coancestry is a requirement for estimating variance components and other genetic parameters for any quantitative trait. In populations where plus trees are typically selected, pedigrees are usually unknown, and it is assumed that all plus trees are genetically unrelated, as it was in the Portuguese *Pinus pinaster* improvement program. In forest trees, deviations from this assumption lead to greater inbreeding and loss of genetic gain. Thus, knowing the value of the coancestry coefficient among parents and within their progeny can be useful to improve the heritability estimation (additive *vs.* non additive variance) and to decide how to select the trees within the families in a combined selection scheme. The aim of this work is to estimate a mean value of the coancestry coefficient of the families present in a progeny trial originated from seed collected in a clonal seed orchard, and in what way this affects heritability estimations.

Material and Methods

To accomplish this objective 125 offspring from a sub sample of six families from a progeny test planted at Mata do Escaroupim were analyzed. Seeds for the progeny test were originated by open pollination of 46 plus trees maintained at Escaroupim Clonal Seed Orchard. Total genomic DNA was isolated from needles following Doyle and Doyle (1990) protocol, with some modifications. Offsrping were genotyped for five highly polymorphic microsatellite markers: two chloroplast microsatellite loci (Pt87268 and Pt1254) and three nuclear microsatellites (Itph4516, Ctg275 and Ctg4363). The amplification conditions for the different molecular markers are described in Robledo-Arnuncio *et al.* (2004) (cpSSRs), González-Martínez *et al.* (2002) (Itph4516) and Chagné *et al.* (2004) (Ctg275 and Ctg4363). Estimates of correlated mating within families were obtained following Hardy *et al*. (2004) by using the freely available software SPAGeDi 1.2 (Hardy & Vekemans 2002). Narrow sense heritability was estimated using ASREML (Gilmour et al. 1998).

Results and Discussion

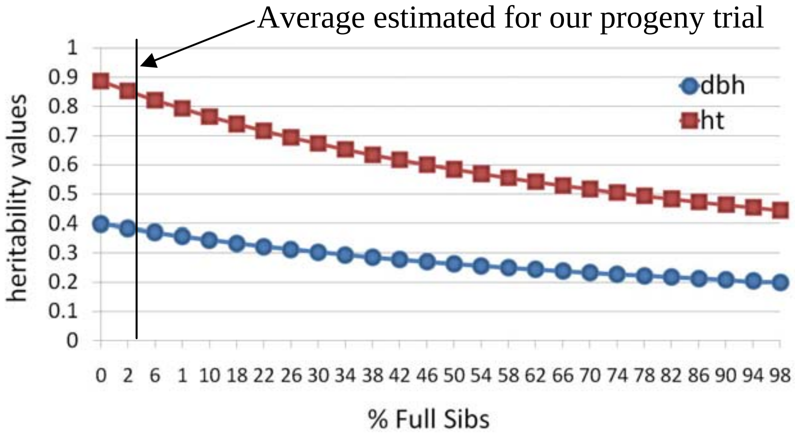
The percentage of full-sibs slightly differed among families, being 4% the average value within the families studied (Table 1) presents estimates of correlated mating (i.e. percentage of full-sibs) within families. The mean value of the genetic covariance coefficient of the families present in this progeny trial was then of 0.26. Adjusted heritabilities for different percentages of full-sibs found in an open-pollinated progeny trial are represented in Figure 1. Differences between the unadjusted and adjusted heritability values were more pronounced in total height (0.40 and 0.38, respectively) than in diameter (0.90 and 0.89, respectively), but they did not imply severe bias (<5%).

We can conclude that in a *Pinus pinaster* open-pollinated trial the associated error in heritability estimates due to the inclusion of full-sibs, when assuming a coefficient of relation amongst open pollinated sibs of ¼, is low.

Table 1: Marker-based estimates of correlated mating

Fam	nuSSR	cpSSR	Mean
50	0.0284	0.0614	0.0449
14	0.0282	-0.0319	-0.0018
32	0.0072	0.0840	0.0456
59	0.0416	0.0513	0.0464
15	-0.0032	0.1507	0.0737
General mean		0.0418	

Figure 1: Adjusted heritability for different percentages of full-sibs found in an open-pollinated progeny trial



Average estimated for our progeny trial

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