

Comparison of genetic structure assessed by amplified fragment length polymorphism and retrotransposon-based sequence-specific amplification polymorphism for portuguese populations of *Pinus pinea* L.

Evaristo, I.; Santos, S.; Tenreiro, R.; Costa, R.

In order to assess genetic diversity within and among populations of *Pinus pinea* L. (stone pine), seven Portuguese populations originating from three Provenance Regions were selected and genotyped using two marker systems. We compared the genetic variation of these populations using retrotransposon-based sequence-specific amplification polymorphism (SSAP) and amplified fragment length polymorphism (AFLP). In total, 105 trees were screened with three primer enzyme combinations (PEC), producing 232 SSAP and 132 AFLP loci. Where SSAP yielded approximately twice-the number of polymorphic fragments compared to AFLP. Differentiation was slightly higher for SSAP, than for AFLP ($F_{ST} = 0.105$ for SSAP and 0.074 for AFLP), and both significantly different from zero, $P < 0.01$. The levels of average genetic diversity within-population found with the two types of marker were not significantly different between SSAPs and AFLPs (26.6% and 22.8%, respectively). The populations that displayed the highest and lowest genetic diversity scores were the same for both markers, and only two populations had significantly different H_e estimates. The neighbor-joining tree based on the Nei's genetic distance displayed some geographic pattern. With the AFLP markers the populations grouped according to the provenance regions where they were sampled, resulting in one well supported cluster with the Southern populations, but with SSAP the pattern was not so coherent. In this study SSAP generated more polymorphic fragments and higher estimates of genetic diversity than AFLP did, due, probably, to the higher mutation rate of retrotransposition relative to base mutation. Nevertheless, congruence was found between estimates obtained with both markers, which is very interesting, for, in general, SSAP markers have lower costs compared to AFLPs, and they might be an interesting alternative marker system, when higher resolution is requested.

Key words: sequence-specific amplification polymorphism, amplified fragment length polymorphism, *Pinus pinea*, genetic structure.