

GENETIC UNIFORMITY OF A WIDESPREAD MEDITERRANEAN TREE, *PINUS PINEA* L.

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phylogeography, microsatellites, EST, diversity, human impact

Phylogeographic studies have used current geographical patterns of genetic diversity to infer the post-glacial history of many tree species. For domesticated species, this inference may be incorrect as a result of human practices in a more recent past. We used 12 chloroplast microsatellites (cpSSRs) to estimate the among and within population genetic variation of 50 *Pinus pinea* L. populations representing the species' current Mediterranean distribution area. A single haplotype was detected in all populations studied except in Lebanon and in two populations from Spain, where 3 and 1 additional haplotypes at very low frequencies were found, respectively. The results found in *P. pinea* are therefore unique and may reflect the recent diffusion of the species westward across the Mediterranean, along with the beginning of offshore sailing and of long-distance trade in the Basin. Confined to a narrow distribution range during successive glacial-interglacial cycles, *P. pinea* may (or not) have experienced further reduction of its genetic diversity with the emergence of traditional agriculture and long distance trading. In order to deeply investigate the genetic uniformity of *P. pinea*, new nuclear markers were developed. Since expressed sequence tags (ESTs) offer an interesting source for marker discovery, a non-normalized cDNA library was constructed from mRNA of young *P. pinea* needles. 1000 ESTs were sequenced to characterize the gene content of the library and a set of EST-SSR were developed and optimised and then used to screen diversity in the same populations. These results are presented and discussed.