

CONSTRUCTION OF A GENETIC LINKAGE MAP FOR OLIVE USING AFLP, RAPD, SSR AND SNP MARKERS

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Very limited genetic studies and classical breeding programs have been performed on olive. Due to the strategic importance of this fruit crop for the Italian and Mediterranean agricultural production, it would be of main priority to focus the attention on analysing the organization of its genome. As first approach, a linkage mapping program is currently being developed by our groups, aimed at identifying QTL for traits under selection. A genetic linkage map was obtained on a cross population obtained from two highly heterozygous cultivars with contrasting phenotypes for some traits of agronomic interest like bearing precocity and resistance to *Spilocaea oleagina* and *Verticillium dahliae*. The genetic map obtained is based on 574 AFLPs, 279 RAPDs and 62 SSRs. In order to map genes involved in important metabolic pathways, SNP markers were identified and mapped. Two maps, one for each parent, were constructed using MAPMAKER/EXP v.3.0 software, according to the double pseudotest-cross model. All data, including AFLPs segregating 3:1 (heterozygous x heterozygous) and codominant SSR and SNP markers, were afterwards analysed by JoinMap 3.0 software. Forty six linkage groups were obtained for the female and 29 for the male parent, with a coverage percentage of 67.8% and 70.8%, respectively. Anchor loci have allowed joining the homologous pairs of groups from the two maps to produce an integrated map for the species *O. europaea*, including a major group and seven medium groups.