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Poster Abstract - B.34

TOWARD THE GENETIC AND PHYSICAL MAPPING OF OLIVE

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Olive (*Olea europaea*) is among the oldest of Mediterranean fruit crops. Its long generation time and the tree large size have limited the development of genetic studies and consequently produced a lack of progress in breeding programs.

The molecular-marker-based systems have allowed the development of new approaches to overcome these limitations. Markers closely associated with the traits of interest can be used in the marker assisted selection (MAS).

In perennial crops, as olive, F2 or backcross populations are rarely available, so genetic mapping studies are commonly performed on progenies issued from the cross between two heterozygous parents. In this case, marker data can be analysed as a double pseudo-testcross and a map constructed separately for each parent.

A F1 population obtained by crossing two highly heterozygous cultivars has been analysed to build a genetic linkage map using AFLP, RAPD and SSR markers. The two parental cultivars have been chosen because of their different phenotypes for some traits of agronomic interest like the resistance to *Spilocaea oleagina* and *Verticillium dalhiae* and different bearing precocity. 279 RAPD, 574 AFLP and about 24 (work in progress) SSR markers, were scored on both cultivars. The mapping strategy included two steps: firstly, two maps, one for each parent, have been constructed, using MAPMAKER/EXP v.3.0 software for the segregation ratio analysis. In a second time we started to join the maps in order to produce an integrated map for the species *O. europaea*, using, for this purpose, some anchor loci which are present in both of the parent's maps (SSR and AFLP segregating 3:1 in the progeny). In this second step JoinMap 3.0 software has been used for the segregation ratio analysis.

Taking into account that genome analysis, physical mapping, map-based cloning and sequencing projects require the use of genomic libraries able to contain large DNA fragments, an olive BAC library has been constructed using high-molecular-weight (HMW) DNA from cv. Leccino. The restriction enzyme *Hind* III has been used to generate large size DNA inserts which have been subjected to a double size selection. Selected fragments have been cloned in pBeloBAC11 vector. Preliminary checking showed that the library contains about 200000 clones with an average insert size of 71 Kb, equivalent to 6.5X genome coverage. The BAC library plating is currently in progress.