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Poster Abstract – D.78

TOWARD OLIVE GENOME SEQUENCING: FIRST INSIGHTS INTO THE GENOME ORGANIZATION

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One of the fastest ways to obtain insights into the structure, organization and sequence composition of a eukaryotic genome is to sequence a library of randomly sheared genomic DNA. In order to characterize the olive genome, *O. europea* (1C = 1400-1500 Mbp), two libraries were constructed from the cultivar Leccino, one genomic and the other hypomethylated. Genomic fragments in the size range of 3-5 Kb were produced by fragmentation of genomic DNA extracted from nuclei of young leaves, and were then ligated into a plasmid. The ligation mix was first used to transform *E. coli* strain DH10β (mrcA, mrcB, mrcC, mrr) and produce a random genomic library, and inserts from about 3500 clones were selected for sequencing from both ends. The same ligation mix was then used to transform E. coli strain DH5α (MrcA, MrcB, MrcC, Mrr). Since restriction systems for methylated DNA are intact in this strain, so that DNA fragments containing methylated inserts are less likely to survive the cloning process. About 1000 clones from this second library (methyl-filtered library) were sequenced from both ends.

About 5,2 Mbp of sequence was obtained from the random genomic libraries, corresponding to 0,35% of the olive genome. A bioinformatic pipeline has been used to analyse the sequencing data in order to have a first insight into the olive genome structure useful to define strategies for a possible *O. europea* genome sequencing project. Surprisingly, the olive genome differs with respect to the large genome characterised until now for the relative low percentage of transposable elements and the very large number of tandem repetitive sequences (satellite/minisatellite DNAs) which seems to be the major responsible of the olive large genome size.