Poster Communication Abstract – 3A.24

COMPARATIVE GENOMICS FOR IDENTIFYING FLOWER ORGAN IDENTITY GENES IN PEACH AND OLIVE

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Olea europaea, MADS-box sequences, flower-organ identity genes

Important fruit trees as peach (*Prunus persica* L.) and olive (*Olea europaea* L.) produce fruits with closely similar features, in both cases being drupes. Despite such similarity, the flowering induction pathways of these two species are quite different. In order to shed light on phase transition and flower differentiation, specific bioinformatic analyses were carried out in peach and olive, leading to the identification of MADS-box genes (*i.e.* ABCDE model-related genes). MADS-box genes include floral homeotic genes that participate to the determination of floral organ identity. Since in peach most of the putative MADS-box genes have been already identified and the expression patterns studied, these data were used to validate our bioinformatic approach, which was carried out on the recent public release of the genome. A double experimental approach was set up, starting from available genes whose function was already characterized not only in model plants but also in crop species. HMM patterns were constructed by performing multiple sequence alignments of proteins involved in phase transition and flower differentiation, and used to query the genome for putative orthologs. Concurrently, a BLAST search was carried out using the same set of sequences. Results of both approaches were cross-checked and a list of candidate genes generated and exploited to further validate peach genes previously characterized. The same pipeline was adopted to search for olive candidate genes. Since the genome sequence of this species is not available, a 454 collection recently generated from flower buds at different developmental stages was used as a target. The nucleotide sequences were translated in all possible frames, so that the same approach adopted for peach could be carried out. In peach, the list of candidates was implemented with further members, such as four AP2- and two AP3-like genes, with a putative A and B function, respectively. In olive, a higher number of candidates was identified compared to peach, probably due both to the larger size and the polyploid origin of its genome, as well as to the presence of different alleles of the same gene (being most of the loci heterozygous in olive and homozygous in peach). It is worth mentioning that in this species a total of 21 members were identified, including four AP1, two AP3, three PI, one each of AG, STK and SHP, and eight SEP2, SEP3 and SEP4-like genes. Detailed phylogenetic analyses were performed at the amino acid level, pointing out homogeneous clusters in which candidates of the same class group together with proteins already characterized in model species (*i.e.*, *Arabidopsis* and *Antirrhinum*). Expression analyses of candidates are currently in progress in order to assess the organ specificity and the timing of

expression. The role of these genes in determining discrepancies and similarities in terms of phase transition pathway and fruit type, respectively, will be presented and critically discussed.