Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - C.52

STEPS TOWARDS THE PRODUCTION OF A FUNCTION MAP IN PEACH (*PRUNUS PERSICA*)

F. BARALE*, B. LAZZARI***, A. ABBOTT**, F. SALAMINI***, C. POZZI***

*) Dipartimento di Produzione Vegetale, Università di Milano, Via Celoria 2, 20133 Milano, Italy
**) Clemson University, Clemson, SC, USA
***) Fondazione Parco Tecnologico Padano, CERSA, Via Einstein, 26900 Lodi, Italy

Prunus persica, Expressed Sequence Tag (EST), Single Nucleotide Polymorphism (SNP), ESTree DB, Candidate gene (CG)

Peach is currently considered a model species for genomics studies in Rosaceae. An international effort is aimed to the improvement of the available EST collections, to the sequencing of gene rich regions and to the production of high-density maps, for integration of QTLs, monogenic traits and functional maps.

We report the development and mapping of genetic markers based upon expressed sequence tags (ESTs) polymorphisms and the positioning of ESTs in a physical framework map for peach genome.

Based on ESTree DB (a collection of 18630 cDNA sequences originated from eight libraries), contigs and EST were selected as candidate genes (CGs) based on sequence similarity with genes relevant for fruit quality, already characterized in other related species like apple, apricot and strawberry.

To rapidly identify SNPs, the ESTs generated from six different peach genotypes (Suncrest, Bolero, Oro, Loring, Fantasia, Redhaven) and from almond were aligned by AutoSNP, a program that allows *in silico* SNP (isSNP) detection. A total of 1863 isSNP was identified and further analysis concentrated on a subset of 67 isSNPs, derived from ESTs representing genes putatively involved in important aspects of the secondary metabolism. A set of mapping populations was also obtained from various germplasm repositories (*Yumyeong* x *O'Henry*, *P. ferganensis x IF7310828, Bolero x Oro* and *Texas* [almond] x *Earlygold* [peach]. Experimental validation of the obtained isSNPs was performed by amplification and sequencing of the polymorphic fragments from parentals of each mapping population. In order to obtain preliminary data for the construction of functional maps, confirmed SNPs were genotyped by minisequencing in selected individuals of the segregating populations.

In a parallel approach a strategy based on the identification of contigs representing putative genes potentially affecting fruit quality was adopted using online resourced offered by the ESTree web site. SNPs were thus scanned by sequencing of amplified products from parental lines of mapping populations. SNPs scoring was conducted on segregating populations by minisequencig.

As a complementary strategy, approximately 200 ESTs were selected to be mapped on a physical framework map, by hybridization on two arrayed BAC libraries whose clones have been fingerprinted. Currently, 17 out of 46 EST which hybridized to the filters containing the BACs clones were localized on physically mapped contigs.