Poster Abstract – 5.07

HIGH-THROUGHPUT GENOTYPING AND HIGH-RESOLUTION PHENOTYPING FOR A COMPREHENSIVE QTL MAPPING RELATED TO APPLE FRUIT CRISPNESS

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fruit quality, high resolution phenotyping, high-throughput markers genotyping, QTL mapping

In the definition of fruit quality in apple, crispness is certainly the major characteristic. Crispness, which is associated to the cell wall disruption mechanism and turgor pressure, is perceived as emitted sound during compression.

Besides its sensorial perception, a crispy apple is generally more appreciated because its higher flavour and aroma release.

In this context we performed a pilot study aimed to discovery the QTLs putatively involved in the control of the "crispy" phenotype.

To perform our investigation we genotyped two mapping populations, Fuji x Delearly and Fuji x Pink Lady, with two type of molecular markers. First, a series of SSR (CH and Hi series) were extended in a multiplex system with an ABI 3730 DNA analyzer, to build up the maps scaffold, necessary for linkage groups comparison with other reference maps.

The second category was represented by a set of SNP markers (ad hoc identified between the two haplomes of the heterozygous Golden Delicious genome), genotyped in high throughput using SNPlex™ (Applied Biosystem) and Golden Gate genotyping assay (Illumina).

High resolution phenotyping, addressed to dissect most of the fruit flesh complexity, was carried out analyzing a series of acoustic and mechanical parameters via a TA.XT Texture Analyzer instrument (Stable Micro Systems) equipped with an acoustic detector.

The preliminary QTL mapping study identified significative genomic regions on these two populations possibly involved in the control of fruit crispness and firmness. These regions will be further explored in order to identify the gene set included in the QTL interval, with the final aim to investigate the allele mining of these future candidate genes in a wider apple collection.