

## DEVELOPMENT OF AN SNP-BASED GENETIC LINKAGE MAP AND QTL ANALYSIS IN EGGPLANT

BARCHI L.\*\*\*, LANTERI S.\*, PORTIS E.\*, VALÈ G.\*\*\*, ACCIARRI N.\*\*\*\*, CIRIACI T.\*\*\*, TOPPINO L.\*\*\*, ROTINO G.L.\*\*

\*) DIVAPRA Plant Genetics And Breeding, University Of Torino, 10095 Grugliasco (TO)

\*\*) CRA-ORL Research Unit For Vegetable Crops, 26836 Montanaso Lombardo (LO)

\*\*\*) CRA-GPG Genomic Research Centre, 29017 Fiorenzuola d'Arda (PC)

\*\*\*\*) CRA-ORA Research Unit For Vegetable Crops, 63030 Monsanpolo Del Tronto (AP)

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The eggplant (*Solanum melongena*) genome is relatively unexplored, especially compared to those of the other major *Solanaceae* crops tomato and potato. Genetic maps based on both inter-specific and intra-specific crosses have been developed in the last years. The most recent inter-specific map is constituted of 347 COS and RFLP markers spanning 1,535 cM, while the 2 most recent intra-specific maps comprise 238 markers and 236 markers, spanning 718.7 and 951.4 cM respectively. The level of marker saturation is however still low for fine mapping and genomic synteny studies. We recently combined the developed Restriction-site Associated DNA (RAD) approach with Illumina DNA sequencing to effect the rapid and mass discovery of both SNP and SSR markers for eggplant (1).

A subset of 384 SNPs was used to genotype an F<sub>2</sub> intraspecific mapping population and integrated into a previously developed genetic linkage map (2) encompassing a total of 426 markers, including 343 SNPs, 43 SSRs, 28 COSs, 11 RFLPs and 1 CAPS. The framework map included 418 markers spanning 1,388 cM with an average map distance of 3.32 cM. Thanks to RFLP and COS markers, the chromosome assignment of all the linkage groups (LG) identified was performed. The length of eggplant chromosomes ranged from 152 cM (E6) to 78.6 cM (E8).

The newly developed map was then used for performing QTL analyses on several agronomical traits related to fruit quality, plant architecture and plant development, phenotyped in two locations. Preliminary results are available for traits as fruit weight, fruit shape and anthocyanins content in leaves, revealing the identification of at least one major QTL for each of these traits. Further ongoing analyses are allowing a comparison of the QTLs identified in the two environments, thus making possible a reliable identification of genomic regions involved in the control of key horticultural traits.

### REFERENCES

- 1) Barchi et al. *BMC Genomics* 2011 12:304
- 2) Barchi et al. *Genome* 2007 50: 51-60