

SOL2015



The 12th Solanaceae Conference

October 25 -29, 2015
ENSEIRB Building, Talence

Bordeaux, France



Improvement of pepper fruit quality by molecular breeding

Paran^a, S. Popovsky^a, Y. Borovsky^a, N. Monsonogo^a, O. Zehavi^a, N. Rona^a, A. Bovy^b

^a *Agricultural Research Organization, The Volcani Center, Israel.*

^b *Wageningen University, Netherlands*

For improvement of pepper fruit quality, identification of major genes controlling quality traits and developing molecular markers for use in marker-assisted selection, we conducted several quantitative trait loci (QTL) studies in populations segregating for various quality parameters. These include fruit size and shape, color, pungency, total soluble solids, flavonoid content and water loss during post-harvest storage. For post-harvest water loss we identified two linked QTLs in chromosome 10. Near-isogenic lines (NILs) differing for the QTLs indicated that post-harvest water loss is partly controlled prior to fruit ripening. Furthermore, reduced post-harvest water loss was associated with delayed over-ripening of the fruit on the vine. For flavonoid content, we constructed a highly saturated map of the segregating population using the genotyping by sequencing (GBS) approach. We were able to identify several major effect QTLs controlling multiple metabolites and candidate genes underlying these QTLs. For chlorophyll content in the immature fruit, we identified two major QTLs in chromosomes 10 and 1. The transcription factor CaGLK2 was identified as the likely candidate for underlying the QTL in chromosome 10. We are currently conducting high-resolution mapping at the QTL region in chromosome 1. All together, we were able to identify valuable genetic resources, major QTLs and molecular markers that will be implemented in breeding programs towards improved fruit quality.

A high quality eggplant (*Solanum melongena* L.) genome draft allows the mapping of phenotypic and metabolic QTLs

Delledonne M.1, Dal Molin A.1, Minio A.1, Ferrarini A.1, Venturini, L., Avanzato C.1, , Toppino L.2, Sala T.2, Bassolino L.2, Barchi L.3, Comino C.3, Acquadro A.3, Portis E.3, Rinaldi R.3, Scaglione D.3, Francese G.4, D'Alessandro, A. 4, Mennella G.4, Perrone D.4, Acciarri N.5., Pietrella M.6, Aprea G. 6, Sulli M. 6, , Lanteri S.3, Rotino G.L.2, Giuliano G.6

1University of Verona, 2CREA-ORL, Montanaso Lombardo, 3DISAFA, University of Torino, 4CREA-ORT, Pontecagnano 5CREA-ORA, Monsampolo del Tronto, 6ENEA, Casaccia Research Center, Roma

Eggplant (*Solanum melongena* L. $2n = 2x = 24$, projected genome size 1.1 Gbp) belongs to the Solanaceae family, which also includes a number of other important crops like tomato, potato, pepper and tobacco, whose genome sequences are available. Both its membership to the subgenus *Leptostemonum* and origin from Asia make eggplant of particular interest for comparative genomic analyses within the Solanaceae family.

A high quality eggplant genome assembly was produced from the inbred eggplant line '67/3', which is the male parent of a mapping population composed of 167 F6 RILs, using both Illumina sequencing and Bionano Genomics optical mapping. The hybrid assembly covered 1.2 Gb, with an L50 of >3 Mb. Of these, over 900 Mb were covered by Illumina contigs and anchored to the genetic map obtained with the RIL population. RNA-Seq assisted annotation using Maker resulted in about 39k protein-coding genes. The genome assembly, annotation and RNA-Seq data are being used for comparative analyses with other Solanaceae genomes.

The RIL population has been extensively phenotyped for both visual and metabolic traits. Examples of preliminary QTL mapping for several of these traits will be presented.