Valorisation of genetic and genomic resources of tomato for the improvement of fruit quality

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Valorisation of genetic and genomic resources of Tomato for the improvement of fruit quality

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Aims

In this project we intend to develop the resources necessary for high throughput QTL studies in tomato by combining the development of genomic and plant resources including:

(1) a large set of SNPs in expressed sequences and flanking regions based on high throughput sequencing technology.
(2) a set of 4 Illumina VeraCode chips carrying a total of 1536 SNP
(3) Creation and phenotype characterisation of a multiparent advanced generation intercross (MAGIC) population to be used for QTL mapping and latter for fine mapping, as a complement to genetic resources gathered in collections. The population will be characterised for yield related traits and fruit quality (composition in sugars and acids, colour, texture).
(4) Differential Gene Expression profiles and proteome profiles of the 8 parental lines of the MAGIC populations and the 4 F1 hybrids

These resources are developed to be used in the subsequent analyses :
(1) Genotyping a biallelic population in order to precisely map all the markers present on the VeraCode chips
(2) Genotyping the MAGIC population with the Illumina VeraCode chips in order to map QTL
(3) Genotyping several genetic resources (collections of cherry tomato cultivars, of old cultivars and a set of elite genotypes), in order to assess linkage disequilibrium and search for associations between SNP markers and fruit related traits
(4) Expression profile analysis of the genes and proteins characterised at the 2 stages of expression; comparison among genotypes and F1 hybrids. The final expected result is a genetic map of more than 1000 SNPs which will be associated with QTL locations and expression variations of the parental lines and F1 hybrids

Results

After 2 years, many results were obtained :
Genome resequencing
The EPGV has resequenced the full genomes of the 8 parental lines, to a depth of 9x to 26x. We scanned these genomes for SNP after mapping the sequences on the reference tomato genome publicly available. More than 3 millions SNPs were identified, with 80.000 to 1.500.000 depending on the lines. The selection of 1500 SNPs to be used on the Vera Code chip was performed after a screen on the quality of each SNP, their distribution on the genome, and the haplotype they are representing
Creation of the MAGIC population
A MAGIC population of 450 families was produced at INRA and VCo after the intercross of 2 F1 hybrids (AB x CD and EF x GH), followed by the cross of 250 plants ABCD with 250 plants EFGH and reciprocal crosses and then 3 selfing generations. The population will be characterized in 2012.
Characterization of the parental lines for their phenotypes
The 8 parental lines and the 4 resulting hybrids were characterized for their fruit development and sugar, acid and vitamin C content. Thanks to a specific project funded by INRA, the métabolome profiles of the fruits were obtained (60 primary and secondary metabolites + 25 enzyme activities) on the métabolome platform of Bordeaux

Proteome analysis
The proteome of fruits from the 8 parental lines and the 4 resulting hybrids were characterized at 2 stages (cell expansion stage and orange fruits). More than 600 variable spots were identified and 500 spots were sequenced on the Moulon Platform

Transcriptome analysis
The transcriptome profiles of fruits from the 8 parental lines and the 4 resulting hybrids were characterized at cell expansion stage by Digital Gene Expression (subcontracted to MGX, Montpellier). More than 40 million tags were obtained per library (2 libraries per genotypes). The analysis revealed 23.000 different genes, among which 4000 are differentially expressed among the genotypes.

Perspectives

Integration of the data
All the data on the parental lines and F1 are under analyses. The inheritance of each level of traits is studied, and networks of correlations are produced, revealing some interesting features. All the data will be set up in a tomatoIS genome database at URGI (Versailles)

QTL mapping in the MAGIC population
The MAGIC population will be grown and analysed in 2012 in INRA Avignon and Vco Ledenon, together with the genotyping that will be produced in VCo. Genotyping will be done also on a biallelic population derived from the two most distant lines, and in a set of unrelated lines.
Statistical analyses will be performed in 2013.

Publications / Congress

Presentation in PAG 2012

Total permanent scientist

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Temporary contracts

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Maria Tchoumakov (CDD 9 mois en 2011-2012)