Combining systems biology, genome resequencing and MAGIC population to decipher the genetic variation of tomato fruit quality

Laura Pascual, Jiaxin Xu, Nelly Desplat, Yves Y. Gibon, Annick Moing,
Mickael M. Maucourt, Stéphane Bernillon, Catherine C. Deborde, Jean-Paul
Bouchet, Dominique D. Brunel, et al.

Combining systems biology, genome resequencing and MAGIC population to decipher the genetic variation of tomato fruit quality

Laura Pascual[1], Jiaxin Xu[1,2], Nelly Desplat[1], Yves Gibon[3], Annick Moing[3], M. Maucourt[3], S. Bernillon[3], C Deborde[3], Jean Paul Bouchet[1], Dominique Brunel[4], Marie-Christine Le Paslier[4], Mathilde Causse[1]

[1]*INRA, UR1052, GAFL, BP94, F-84143 Montfavet, France;*
[2]*Northwest A&F University, College of Horticulture, Yang Ling, Shaanxin, 712100, P.R.China;*
[3]*INRA, UMR1332 Biologie du Fruit et Pathologie, BP 81, F-33883 Villenave d'Ornon, France;*
[4]*INRA, EPGV, Centre de Génotypage, Evry, France*

Email: mathilde.causse@avignon.inra.fr

Tomato fruit quality is requested by tomato consumers, but complex to improve due to the number of components involved and by their polygenic nature. In order to decipher the genetic diversity and the inheritance of fruit quality components at a global level, we have conducted a large multi-level omic experiment. A set of 8 contrasted lines and 4 of their F1 hybrids were phenotyped for fruit development traits. Fruits were harvested and pericarp samples analysed at 2 stages (cell expansion and orange) and different scales: (1) primary and secondary metabolome profiles, (2) activities of 28 enzymes involved in primary metabolism, (3) proteome profiles revealed by 2D-PAGE and sequencing of 470 spots showing quantitative variations and (4) gene expression analysis by Digital Gene Expression. In parallel, the 8 lines were resequenced and more than 3 millions SNPs identified when aligned on the reference tomato genome.

This experiment allowed us to assess the range of variability and mode of inheritance of the metabolomic, proteomic and transcriptomic data. Correlation networks were constructed to identify regulatory networks. Diversity of candidate genes was analysed, relating the polymorphisms at the sequence level with the protein and gene expression.

A multi-allelic (MAGIC) population was then constructed from the intercoss of the 8 lines and phenotyped for fruit characteristics in two locations. A genetic map composed of 1536 SNP was constructed showing increased recombination frequencies compared to biparental populations. QTL were mapped and related to the variations detected at the genome sequence and expression levels of the parental lines.