

#159: Integrative approach of size and composition of tomato fruit combining ecophysiology, genetic, genomic and metabolomic analysis

M. Causse¹, M. Prudent¹, N. Bertin², P. Thi Do³, P. Tripodi⁴, M. Génard², A. Fernie⁵, S. Grandillo⁴

¹INRA - GAFL, Montfavet, France

²INRA PSH, Avignon, France

³MPI, Potsdam, Germany

⁴CNR IGV, Portici, Italy

⁵Max Planck Institute of Molecular Plant Physiology, Potsdam - Golm, Germany

Combining fruit appearance and organoleptic quality is a new challenge for tomato breeders. Tomato flavor is primarily influenced by sweetness, which is related to sugar content in fruit. High sugar and acid contents are found in wild tomato species, but associated with small fruit size. Increasing sugar content is thus often hampered by this negative relationship.

This antagonism was studied at the genetic, genomic, metabolomic and ecophysiological levels in a population of introgression lines derived from the cross between *Solanum lycopersicum* and *Solanum chmielewskii*. The influence of the carbohydrate supply on quality and ecophysiological traits was carried out, through the modification of the sink:source ratio of the plants via fruit removal experiments. QTL mapping revealed frequent colocalisations of QTL controlling these two traits with opposite effects, in most of the cases. For two regions, colocalisations between fresh weight and sugar content had similar effects and also contained QTL for sugar content relative to dry weight. These regions could be thus involved in carbon allocation to cell structures or to sugar metabolism.

Correlations and QTL colocalisations between quality traits and ecophysiological parameters indicated that cell division, cell expansion and transpiration were involved in the relationship between fruit size and sugar content, and were susceptible to the plant carbon status. Metabolic profiles of three lines revealed the impact of fruit load and G x E interactions on several metabolites. Transcriptome analyses of near isogenic lines helped in the characterization of the molecular bases of QTLs for quality traits and ecophysiological parameters. Pathways underlying sugar metabolism and stress responses were the most susceptible to fruit load. Several genes putatively involved in these traits were then analyzed during fruit development and revealed expression shifts with fruit load and QTL introgressed.