

Genetic, genomic and ecophysiological dissection of fruit size and sugar content in tomato

Mathilde M. Causse, Marion Prudent, Nadia Bertin

▶ To cite this version:

Mathilde M. Causse, Marion Prudent, Nadia Bertin. Genetic, genomic and ecophysiological dissection of fruit size and sugar content in tomato. 16. EUCARPIA Meeting Section Vegetables Working Group Tomato, May 2008, Wageningen, Netherlands. 1p. hal-02812667

HAL Id: hal-02812667 https://hal.inrae.fr/hal-02812667v1

Submitted on 6 Jun2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés. Genetic, genomic and ecophysiological dissection of fruit size and sugar content in tomato

Causse Mathilde¹, Prudent Marion^{1,2}, Bertin Nadia²

¹ INRA, UR1052 Génétique et amélioration des fruits et légumes, F-84000 Avignon, France

² INRA, UR1115 Plantes et systèmes de culture horticoles, F-84000 Avignon, France

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. Several experiments were performed in order to analyze this antagonism. First at the genetic level, QTL mapping in several progenies revealed frequent colocalisations of QTLs controlling these two traits with opposite effects. Fine mapping experiments were then performed and, in some cases, close linkage of QTLs in repulsion was shown. In order to try to characterize the molecular bases of these QTLs, transcriptome and proteome analyses of near isogenic lines differing only in the QTL region were performed and revealed several genes putatively involved in the traits.

In a parallel approach, in order to understand which biological processes were underlying this antagonism, a fruit removal experiment was achieved, modifying the source : sink ratio of the plants and plant behaviors under two carbohydrate supply conditions were examined. The role of cell number in fruit size determination was shown and different behaviors of the genotypes identified.