



HAL
open science

Genetic and genomic approach of tomato fruit quality

Mathilde M. Causse, Mireille Faurobert, Jamila Chaïb, Stephane Munos,
Nicolas N. Ranc

► **To cite this version:**

Mathilde M. Causse, Mireille Faurobert, Jamila Chaïb, Stephane Munos, Nicolas N. Ranc. Genetic and genomic approach of tomato fruit quality. Indo French Symposium, Jan 2010, Lucknow, India. hal-02754042

HAL Id: hal-02754042

<https://hal.inrae.fr/hal-02754042>

Submitted on 3 Jun 2020

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.

INDO FRENCH SYMPOSIUM

GENOMICS AND BIOTECHNOLOGY OF FRUIT QUALITY: RECENT ADVANCES

January 18-20, 2010, Lucknow, India



 Indo French Council for Promotion of Advance Research, India

 National Botanical Research Institute, Lucknow, India



Ecole Nationale Supérieure Agronomique Toulouse, Tolosan, France

GENETIC AND GENOMIC APPROACH OF TOMATO FRUIT QUALITY

M. CAUSSE*, M. FAUROBERT, J. CHAÏB, S. MUÑOS, N RANC

INRA, UR1052, Unité de Génétique et Amélioration des Fruits et Légumes, Domaine St Maurice BP 94 – 84143 Montfavet Cédex France

The organoleptic quality of tomato fruit is a complex characteristic involving a set of components such as fruit size, flavour, aroma, texture. Our research program on the bases of fruit quality is focused on genetic polymorphism evaluation and QTL characterization for these traits. We have first mapped QTL controlling quality traits in several populations and introgressed quality trait QTL by marker-assisted selection into elite lines. This introgression program allowed the production of Near Isogenic Lines (NILs) that were characterised at several levels (quality components, metabolome, proteome and transcriptome). We have developed a proteomic analysis of accessions and Near Isogenic Lines (NILs) to identify candidate proteins involved in the genetic variation of fruit quality. Proteins showing either genetic or developmental variations were identified by MALDI-TOF and/or nano-LC-MS/MS. Screening for proteins showing variation of quantity in Near Isogenic lines (NILs) revealed some spots varying according to the allele at the QTL or according to the genetic background. The involvement of some of the candidate proteins was then validated through association studies. The specific case of QTLs carried on chromosome 2 will be presented.