



Meta-analysis of GWAS provides new insights into genetic control of tomato flavor.

Jiantao Zhao, Christopher Sauvage, Frédérique Bitton, Mathilde Causse

► To cite this version:

Jiantao Zhao, Christopher Sauvage, Frédérique Bitton, Mathilde Causse. Meta-analysis of GWAS provides new insights into genetic control of tomato flavor.. Plant and Animal Genome 2020, 2020, San Diego, United States. hal-03542371

HAL Id: hal-03542371

<https://hal.inrae.fr/hal-03542371>

Submitted on 25 Jan 2022

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.

Meta-analysis of GWAS provides new insights into genetic control of tomato flavor

Jiantao Zhao, Christopher Sauvage, Frédérique Bitton and Mathilde Causse

¹INRA, UR1052, Génétique et Amélioration des Fruits et Légumes, Domaine Saint Maurice,
67 Allée des Chênes CS 60094 – 84143 Montfavet Cedex, France

⁶Present address: Syngenta, 12 Chemin de l'Hobit, Saint Sauveur 31790, France

Tomato flavor has changed over the course of long-term domestication and intensive breeding. To understand the genetic control of flavor related traits, we performed a meta-analysis of genome-wide association studies (GWAS) for 18 traits, using 775 tomato accessions and 2,316,117 SNPs from three GWAS panels (*Sauvage et al., 2014; Bauchet et al., 2017 and Tieman et al., 2017*). *In a first step, we imputed SNP data to increase genome coverage for two out of three panels and ran EMMAX software for each panel separately. From each run, the genomic inflation factor and standard errors of the beta coefficients were implemented in two meta-GWAS models: the inverse variance-weighted fixed effect and the Han Eskin random-effect model that takes heterogeneity across studies into account. Then, from the meta-GWAS results, we conducted a statistical fine-mapping of the candidate loci following a heuristic linkage disequilibrium (LD) approach.* We discovered 305 significant associations for the contents of sugars, acids, amino acids and flavor-related volatiles. We showed that fruit citrate and malate contents have been impacted by selection during domestication and improvement, while sugar content has undergone less stringent selection. Results suggest that it may be possible to significantly increase volatiles that positively contribute to consumer preferences while reducing unpleasant volatiles, by selection of the relevant allele combinations. Our results provide genetic insights into the influence of human selection on tomato flavor and demonstrate the benefits obtained from meta-analysis.

287 mots