



**HAL**  
open science

## Towards understanding of metabolic diversity of pepper fruit

Yuri Tikunov, Louis McLeod, Giorgio Tumino, Y Wu, Jérémy Salinier, Lorenzo Barchi, Roland Schafleitner, Richard Finkers, Mathjis Brouwer, Felice Boyaci, et al.

### ► To cite this version:

Yuri Tikunov, Louis McLeod, Giorgio Tumino, Y Wu, Jérémy Salinier, et al.. Towards understanding of metabolic diversity of pepper fruit. XVII SOLANACEAE2022 International Conference on the Plant Family of Solanaceae, Nov 2022, THESSALONIKI, Greece. hal-04133409

**HAL Id: hal-04133409**

**<https://hal.inrae.fr/hal-04133409>**

Submitted on 19 Jun 2023

**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.

Public Domain

XVII SOLANACEAE2022 International Conference on the Plant Family of Solanaceae November 1-5, 2022, THESSALONIKI, GREECE

#### ORAL PRESENTATIONS

Towards understanding of metabolic diversity of pepper fruit

Yury Tikunov<sup>1</sup>, Louis Mcleod<sup>2</sup>, Giorgio Tumino<sup>1</sup>, Yi Wu<sup>1</sup>, Jérémy Salinier<sup>2</sup>, Lorenzo Barchi<sup>3</sup>, Roland Schafleitner<sup>7</sup>, Richard Finkers<sup>1</sup>, Matthijs Brouwer<sup>1</sup>, Filiz Boyaci<sup>10</sup>, Gancho Pasev<sup>11</sup>, Ilan Paran<sup>4</sup>, Nils Stein<sup>8</sup>, Jaime Prohens<sup>9</sup>, Giovanni Giuliano<sup>5</sup>, Pasquale Tripodi<sup>6</sup>, Véronique Lefebvre<sup>2</sup>, Arnaud Bovy<sup>1</sup>

1 Wageningen University & Research, 6708 PB Wageningen, The Netherlands

2 Unité de Génétique et Amélioration des Fruits et Légumes (GAFL), L'Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement (INRAE), Montfavet, F-84140, France

3 Department of Agricultural, Forest and Food Sciences (DISAFA), Plant Genetics, University of Torino, Grugliasco, 10095, Italy

4 Institute of Plant Sciences, Agricultural Research Organization, Volcani Center, Bet Dagan, 50250, Israel

5 Casaccia Research Centre, Italian National Agency for New Technologies, Energy, and Sustainable Economic Development, Rome, 00123, Italy

6 Research Centre for Vegetable and Ornamental Crops, Council for Agricultural Research and Economics (CREA), Pontecagnano Faiano, 84098, Italy

7 Genetic Resources and Seed Unit, World Vegetable Centre, Shanhua 74151, Taiwan

8 Genome Diversity, Department Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

9 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València (UPV), 46022 València, Spain

10 Bati Akdeniz Agricultural Research Institute, 07100 Antalya, Turkey

11 Maritsa Vegetable Crops Research Institute, 4003 Plovdiv, Bulgaria

Among the Solanacea crops pepper – *Capsicum* spp – is the only one that can make one either smile or cry owing to presence of specific metabolites which pepper fruits accumulate. Diverse and recognizable flavor of bell pepper or chilli pepper is determined by specific volatile compounds, pungency, caused by capsaicinoids, is essential in some 44 World's cuisines, fruit color is determined by carotenoids and flavonoids, nutritional quality – by vitamins and antioxidants. World's gene banks possess a great genetic and phenotypic diversity of pepper that could be used to diversify the cultivated pepper germplasm. To study how the genetic diversity of the most cultivated pepper species *C. annuum* translates into metabolic diversity ripe fruits of a core collection of 450 accessions developed in the EU Horizon 2020 G2P-SOL project (<http://www.g2psol.eu/>) were profiled using different metabolomics platforms for volatile aroma compounds using GC-MS and for non-volatile secondary metabolites using LC-MS. Wide qualitative and quantitative metabolic variation was observed. Volatile esters, alkanes, terpenes and oxylipin volatiles determined the variation in the composition of aroma compounds. Flavonoids and capsaicinoids had the major contribution to the variation in semi-polar secondary metabolite composition. Compounds from the abovementioned

groups revealed highly similar quantitative patterns across the core collection suggesting a coordinate regulation of compounds that belong to the same biosynthetic origin. GWAS was performed using SNP data obtained using genotyping-by-sequencing and revealed multiple associations of the metabolic variation with genomic loci harboring known and novel candidate genes.

Key words: Capsicum, metabolomics, GWAS, fruit quality

Acknowledgment: This study was carried out as a part of G2P-SOL project, funded by the European Union Horizon 2020 research and innovation program under Grant Agreement No. 677379. We are also grateful to all the partners involved in G2P-SOL project.