



HAL
open science

A novel global Capsicum core collection delivers candidate genes for robust agronomic QTLs through a multi-environment GWAS approach

Louis McLeod, Lorenzo Barchi, Giorgio Tumino, Pasquale Tripodi, Giovanni Giuliano, Roeland Voorrips, Ilan Paran, Véronique Lefebvre

► To cite this version:

Louis McLeod, Lorenzo Barchi, Giorgio Tumino, Pasquale Tripodi, Giovanni Giuliano, et al.. A novel global Capsicum core collection delivers candidate genes for robust agronomic QTLs through a multi-environment GWAS approach. 18. Eucarpia Meeting on Genetics and Breeding of Capsicum and Eggplant, Crops Research Institute (MVCRI); Center of Plant Systems Biology and Biotechnology (CPSBB), Sep 2023, Plovdiv, Bulgaria. hal-04670129

HAL Id: hal-04670129

<https://hal.inrae.fr/hal-04670129v1>

Submitted on 11 Aug 2024

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



EUCARPIA

18-21 September 2023

Plovdiv, Bulgaria



Eucarpia 2023

**18th EUCARPIA MEETING ON
Genetics and Breeding of
Capsicum and Eggplant**

14 Oral presentation

TITLE: A NOVEL GLOBAL *CAPSICUM* CORE COLLECTION DELIVERS CANDIDATE GENES FOR ROBUST AGRONOMIC QTLs THROUGH A MULTI-ENVIRONMENT GWAS

APPROA



Authors: McLeod, L.[1,2], Barchi, L.[3], Tumino, G.[4], Tripodi, P.[5], Giuliano G.[6], Voorrips, R.[4], Paran, I.[7], Lefebvre, V.*[1]

Affiliations: 1- INRAE, GAFL, Montfavet, France; 2- INRAE, A2M, Montfavet, France; 3- DISAFA, Department of Agricultural, Forest and Food Sciences, Plant genetics, University of Torino, Grugliasco, Italy; 4- WUR, Wageningen University & Research, Plant Breeding, Wageningen, The Netherlands; 5- CREA, Research Centre for Vegetable and Ornamental Crops, Council for Agricultural Research and Economics, Pontecagnano Faiano, Italy; 6- ENEA, Casaccia Research Centre, Italian National Agency for New Technologies, Energy, and Sustainable Economic Development, Roma, Italy; 7- ARO, Institute of Plant Sciences, Agricultural Research Organization, The Volcani Center, Rishon LeZion, Israel

Presenting author*: veronique.lefebvre@inrae.fr

Corresponding author: LM: louis.mcleod@inrae.fr; VL: veronique.lefebvre@inrae.fr

Abstract: Deciphering the genetic architecture of quantitative traits through genome-wide association mapping on core collections paves the way for breeding adapted crops. We constructed the G2P-SOL pepper world core collection, a set of 423 *Capsicum* spp. accessions of great genotypic and phenotypic variability, representing the diversity of more than 10,000 pepper accessions from 10 major genebanks. To tackle the modulation of complex quantitative traits by the environment and by the genotype-by-environment (GxE) interaction effects, a highly diverse subset of 350 *C. annuum* accessions was extensively phenotyped in a multi-location effort. Multi-environment genome-wide association studies (GWAS) were conducted for 23 agronomic traits pertaining to fruit flavor, color, size and shape, and to plant productivity, vigor and precocity. Robust QTLs and environment-specific QTLs were thus detected, and 97 well-known and new genes potentially underlying 53 of the most high-confidence and robust QTLs

were highlighted. These results assert the usefulness and universality of the G2P-SOL core collection, which will be available upon request for the pepper community, alongside the genotypic and phenotypic data collected as part of the G2P-SOL project. This unique resource will be a key asset in accelerating gene discovery, developing genetic markers for marker-assisted selection, and breeding pepper varieties adapted to various climatic environments.