



HAL
open science

Improving modern breeding in tomato: the crucial role of genetic resources

Christopher Sauvage, Mathilde Causse

► To cite this version:

Christopher Sauvage, Mathilde Causse. Improving modern breeding in tomato: the crucial role of genetic resources. 13. Japan Solanaceae Consortium (JSOL2016), Nov 2016, Tokyo, Japan. 2016. hal-01604959

HAL Id: hal-01604959

<https://hal.science/hal-01604959v1>

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.

The 13th Japan Solanaceae Consortium (JSOL2016) 25/11/2016 Tokyo

Improving modern breeding in tomato: the crucial role of genetic resources

Christopher Sauvage and Mathilde Causse

INRA, UR 1052 Centre de Recherche PACA, Domaine Saint Maurice, 67 Allée des Chênes, CS60094, 84140, Montfavet Cedex

The tomato is one of the most produced vegetable in the world and this species is also a model in science to the study of fruit development. Over the past 60 years, many sampling campaigns in Central and South America (source area) helped preserving more than 80,000 accessions of this species, including most of its crop wild relatives. In parallel, the contribution of molecular biology through the development of molecular markers was used to map many QTLs for traits of agronomic interest such as fruit quality and resistance to biotic and abiotic stresses. Since 2012, date of publication of the tomato genome, the combination of the rich genetic resources and high-throughput genomics was used to extend the work to a genome-wide scale to better understand its dynamic, to identify large amount of polymorphic sites but also revisiting scientific questions, such as the evolutionary history (i.e. domestication) of this species and the study of the genetic architecture of quantitative traits through new approaches such as genome-wide association study (GWAS) or genomic selection genomics. The genetic resources of this species are essential for fundamental scientific research but also for the genetic improvement of this species.