



**HAL**  
open science

## Modelling the population history using population genomics : the tomato domestication as a case of study

Christopher Sauvage, Charlotte Aichholz, Gautier Sarah, Manuel Ruiz,  
Mathilde Causse, Jacques David, Sylvain Glemin

### ► To cite this version:

Christopher Sauvage, Charlotte Aichholz, Gautier Sarah, Manuel Ruiz, Mathilde Causse, et al.. Modelling the population history using population genomics : the tomato domestication as a case of study. 12. Solanaceae Conference, Université de Bordeaux (UB). FRA., Oct 2015, Bordeaux, France. hal-01269378

**HAL Id: hal-01269378**

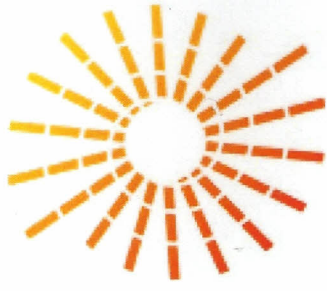
**<https://hal.science/hal-01269378>**

Submitted on 5 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.

SOL2015



# The 12th Solanaceae Conference

October 25 -29, 2015  
ENSEIRB Building, Talence

Bordeaux, France



## Modelling the population history using population genomics : the tomato domestication as a case of study

Christopher Sauvage<sup>a</sup>, Charlotte Aichholz<sup>a,b</sup>, Gautier Sarah<sup>c</sup>, Manuel Ruiz<sup>c</sup>, Mathilde Causse<sup>a</sup>, Jacques David<sup>d</sup> and Sylvain Glémin<sup>e</sup>

<sup>a</sup> Institut National de la Recherche Agronomique, UR1052 GAFL, Génétique et Amélioration des Fruits et Légumes, 67 allée des chênes, CS60094, 84143 Montfavet cedex, France;

<sup>b</sup> Sativa Seeds Sativa Rheinau AG Klosterplatz CH-8462 Rheinau Switzerland ;

<sup>c</sup> CIRAD, UMR AGAP, Baillarguet, F- 34980 Montferrier-sur-Lez, France ;

<sup>d</sup> Montpellier SupAgro, Unité Mixte de Recherche 1334, Amélioration Génétique et Adaptation des Plantes Méditerranéennes et Tropicales, F-34398 Montpellier, France ;

<sup>e</sup> Institut des Sciences de l'Évolution de Montpellier, Unité Mixte de Recherche 5554, Centre National de la Recherche Scientifique, Université Montpellier 2, F-34095 Montpellier, France.

A bottleneck is commonly associated to the study of crop domestication, in which a population experiences a drastic reduction in size and nucleotide diversity. The population genomic era offers new opportunities to document this scenario through the study of the site frequency spectrum (SFS), a powerful method for summarizing genomic data at the genome-wide level. Using a diffusion approximation approach (Gutenkunst et al., 2009) to model SFS, we estimated the demographical history of a major crop, the cultivated tomato (*Solanum lycopersicum*) and its wild relative (*S. pimpinellifolium*). We compared the observed 2 dimensional SFS, obtained from 20 individuals and ~84,500 SNPs markers, to the modelled ones, obtained from four different scenarios. Variants were polarized to ancestral and derived alleles based on the eggplant outgroup sequences. Assuming a mutation rate of  $3 \times 10^{-9}$  and a generation time of 1 year, our results suggest that in the best fitting model, population split occurred ~3750 years ago (95%CI: 2985-4552 yrs), wild tomatoes experienced a dramatic bottleneck (effective population size: -87%; reduction of nucleotide diversity: -63%) that occurred ~420 years ago (95%CI: 337-541 yrs). After this bottleneck, migration rate, from cultivated to wild population, was estimated to less than ~1 migrant per generation. Although, 3.1% of the genes derived from neutral expectations suggesting evolutionary forces acting on. These results demonstrate the power of the approach and provide estimates of demographical parameters that fit previous studies of the tomato domestication (Blanca et al., 2015).