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► To cite this version:

José Blanca, Javier Montero-Pau, Christopher Sauvage, Guillaume Bauchet, Eudald Illa, et al.. Genomic variation in tomato, from wild to cultivated. 12. Solanaceae Conference, Oct 2015, Bordeaux, France. hal-02800701

HAL Id: hal-02800701

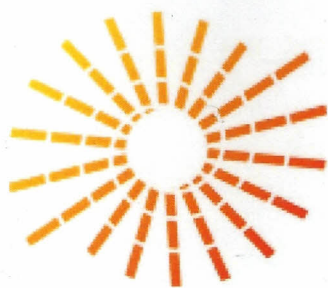
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Submitted on 5 Jun 2020

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SOL2015



The 12th Solanaceae Conference

October 25 -29, 2015
ENSEIRB Building, Talence

Bordeaux, France



Genomic variation in tomato, from wild to cultivated

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Genomic variation of 1008 accessions of *Solanum pimpinellifolium* (SP) and *S. lycopersicum* (SL) was analyzed with the SolCAP genotyping platform. The genotypes for the fruit shape and weight related genes were also obtained. SP was clearly split in the PCA analysis in two distinct groups, one that covered Peru and Southern Ecuador and another located in Northern Ecuador. Most of non-commercial *S. lycopersicum* var. *cerasiforme* (SLC) samples were likely to be semi-domesticated intermediates between the wild and cultivated species, while many commercial cherry tomatoes were dispersed in the PCA with the SPxSLL hybrids. The cultivated alleles for most of the fruit related genes were already found in Ecuadorian and Peruvian SLC. Some of these SLC accessions were collected in markets as cultivated tomatoes. These evidences suggested a first step in the tomato domestication in Peru and Ecuador followed by a further increase in fruit size in Mesoamerica. The genetic diversity indexes showed that the bottleneck in the tomato domestication occurred in the Andean to Mesoamerica migration. The PCA showed that the vintage and modern tomatoes derived mainly from Mesoamerican SLL. A rarefaction analysis showed only a moderately increase in the contemporary SLL variability. This increase is compatible with only few introgressions from wild materials added to the vintage tomato gene pool to create the contemporary materials.