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ORAL PRESENTATIONS

SPET genotyping of over 15,000 accessions of tomato reveals the genetic structure and history of the tomato germplasm at world level

Blanca Jose, Aprea Giuseppe, Ferrante Paola, Fain V.V., Alonso David, Barchi Lorenzo, Schafleitner Roland, Brandt R., Wallace Mark Timothy, Böerner Andreas, Stein Nils, Salinier Jérémy, Lefebvre Véronique, Bovy Arnaud, Boyaci Hatice Filiz, Pasev Gancho, Tringovska Ivanoka, Zamir Dani, Prohens Jaime, Canizares J, Díez Maria Jose, Giuliano Giovanni

1 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana – Universitat Politècnica de València (COMAV-UPV), València, Spain

2 Italian National Agency for new Technologies, Energy and Sustainable Economic Development (ENEA), Casaccia Res. Ctr., Rome, Italy

3 Department of Science, University of Rome “Roma Tre”, Rome, Italy

4 DISAFA, Plant Genetics and Breeding, University of Torino, Grugliasco, Italy

5 The World Vegetable Center (AVRDC), Shanhua, Tainan, Taiwan

6 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

7 National Research Institute for Agriculture, Food and the Environment (INRAE), GAFL, Montfavet-Avignon, France

8 Wageningen University and Research (WUR), Wageningen, The Netherlands

9 Bati Akdeniz Agricultural Research Institute (BATEM), Antalya, Türkiye

10 Maritsa Vegetable Crops Research Institute (MVCRI), Agricultural Academy, Plovdiv, Bulgaria

11 Faculty of Agriculture, Hebrew University of Jerusalem, Rehovot, Israel

*These authors have contributed equally to the study

Tens of thousands tomato accessions are conserved in genebanks all over the world, constituting a valuable source of genes of interest for tomato breeding. Genetic characterization of such large collections can improve their management. The G2P-SOL project has carried out the largest-scale tomato genotyping to date, by designing a 5k probe Single Primer Enrichment (SPET) tomato platform, and used it to genotype a collection of over 15,000 accessions from worldwide genebanks. Besides wild species, the main genetic groups found were: wild *S. lycopersicum* var. *cerasiforme* (SLC) from Meso- and Southamerica, early vintage cultivated tomatoes, that genetically are closer to SLC than to the bulk of *S. lycopersicum* var. *lycopersicum* (SLL), vintage tomatoes, mainly from Spain, early improved materials with no introgressions, and more recent materials that do include wild species introgressions. The structure of the early vintage 36 accessions mirrored the early history of the cultivated tomatoes. They were widely spread across Meso- and South America, probably because they were the cultivated tomatoes in those regions before the Spanish arrival. Interestingly, they were also found in other geographic regions controlled or influenced by the Spaniards during the between XVII, and XVIII centuries, such as the western Pacific (mainly the Philippines) and the Mediterranean. History has left many marks in the tomato genomes. For instance, the Italian San

Marzano is genetically closer to a population of ovoid brasilian early breeds that genetically are better characterized as SLC than to most European vintage tomatoes, that are SLL.

Key words: tomato, history, diversity, populations