

Oral presentation. Session 1: Genetic Resources

O1.01

Title: O1.01 American and European Tomato history unveiled using haplotype and GBS analyses

Authors: Blanca, J.* [1], Pons; C. [1,2], Montero-Pau, J. [1], Sanchez-Matarredona, D. [1], Ziarsolo, P. [1], Diez, M.J. [1], Fontanet, L. [3], Fisher, J. [4], Plazas, M. [1], Casals, J. [5], Rambla, J.L. [2], Riccini, A. [6], Palombieri, S. [7], Ruggiero, A. [7], Sulli, M. [8], Grillo, S. [7], Kanellis, A. [9], Giuliano, G. [8], Finkers, R. [10], Cammareri, M. [7], Grandillo, S. [7], Mazzucato A. [6], Causse, M. [3], Prohens, J. [1], Zamir, D. [4], van der Knaap, E. [11], Monforte, A.J. [2], Granell, A. [2], Cañizares, J.# [1]

Affiliations: 1- Instituto de Conservacion y Mejora de la Agrodiversidad Valenciana (COMAV-UPV), Universitat Politecnica de Valencia, Valencia, Spain; 2- Instituto de Biologia Molecular y Celular de Plantas (IBMCP). Consejo Superior de Investigaciones Cientificas (CSIC), Universitat Politecnica de Valencia, Valencia, Spain; 3- INRAE, UR1052, Genetique et Amelioration des Fruits et Legumes, 67 Allee des Chines, Centre de Recherche PACA, Domaine Saint Maurice, CS60094, Montfavet, 84143, France; 4- Hebrew Univ Jerusalem, Robert H Smith Inst Plant Sci & Genet Agr, Rehovot, Israel
5- Department of Agri-Food Engineering and Biotechnology/Miquel Agusti Foundation, UPC-BarcelonaTech, Campus Baix Llobregat, Esteve Terrades, 8, 08860 Castelldefels, Spain; 6- Department of Agriculture and Forest Sciences (DAFNE), Universita degli Studi della Tuscia, Viterbo, Italy; 7- Institute of Biosciences and BioResources (IBBR), National Research Council of Italy (CNR), Via Universita 133, 80055 Portici, Italy; 8- Italian National Agency for New Technologies, Energy and Sustainable Economic Development (ENEA), Casaccia Research Centre, Rome, Italy; 9- Group of Biotechnology of Pharmaceutical Plants, Laboratory of Pharmacognosy, Department of Pharmaceutical Sciences, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece; 10- Wageningen Univ & Res, Plant Breeding, POB 386, NL-6700 AJ Wageningen, Netherlands; 11- Institute of Plant Breeding, Genetics and Genomics, University of Georgia, GA, USA. Department of Horticulture, University of Georgia, GA, USA

Presenting author: jblanca@upv.es

Corresponding author: jcanizares@upv.es

Abstract:

Not many historical or archeological records remain from the tomato journey from *Solanum pimpinellifolium* (SP) to the vintage varieties, however, its domestication, migrations and diversification in Europe can be unveiled using genetic analyses. The study of 628 SP, *Solanum lycopersicum* var. *cerasiforme* (SLC), and *Solanum lycopersicum* var. *lycopersicum* (SLL) revealed: 1) SP evolved into SLC during a migration from Peru and Ecuador, 2) there is a wild SLC Mesoamerican population, 3) there are no wild SLC populations in Ecuador and Peru, 4) Peruvian and Ecuadorian SLC are an admixture of Mesoamerican SLC and SP, 5) SP introgressions in SLC harbor flowering control and light response genes, 6) at least some Mesoamerican SLL derives from domesticated Peruvian and Ecuadorian SLC. A GBS analysis of 1,254 accessions, that included mainly European vintage materials, was used to analyze the European tomato history. The main conclusions were: 1) the vintage materials PCA was organized along a Spanish-Italian axis with mixed origin accessions between these two groups. 2) Spanish and Italian vintage materials were more diverse than the rest. 3) vintage materials have a very low genetic diversity, out of 64,943 only 298 were polymorphic (95% threshold), 4) many of these polymorphic markers are associated with morphological traits like fruit size and color, 5) 25% of the vintage accessions carry introgressions from the wild species. Thus, Spain and Italy became secondary diversity centers and its vintage accessions carry some loci that maintain its high diversity due to balancing artificial selection.

Oral presentation. Session 1: Genetic Resources

O1.02

Title: O1.02 Unlocking the European traditional tomato genetic resources

Authors: Pons, C.*# [1,2], Casals, J. [3], Brouwer, M. [4], Palombieri, S. [5], Fontanet, L. [6], Riccini, A. [7], Rambla, J.L. [2], Ruggiero, A. [5], Figàs, M.R. [1], Plazas, M. [1,2], Sacco, A. [5], Koukounaras, A. [8], Picarella, M.E. [7], Sulli, M. [9], Fisher, J. [10], Ziarsolo, P. [1], Blanca, J. [1], Cañizares, J. [1], Cammareri, M. [5], Vitiello, A. [5], Batelli, G. [5], Kanellis, A.K. [11], Finkers, R. [4], Nikoloudis, K. [12], Soler, S. [1], Giuliano, G. [9], Grillo, S. [5], Grandillo, S. [5], Zamir, D. [10], Mazzucato, A. [7], Causse, M. [6], Diez, M.J. [1], Prohens, J. [1], Monforte, A.J. [2], Granell, A. [2]

Affiliations: 1-Instituto de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV), Universitat Politècnica de València, València, Spain; 2-Instituto de Biología Molecular y Celular de Plantas (IBMCP). Consejo Superior de Investigaciones Científicas (CSIC), Universitat Politècnica de València, València, Spain; 3- Department of Agri-Food Engineering and Biotechnology/Miquel Agustí Foundation, Universitat Politècnica de Catalunya, Campus Baix Llobregat, Esteve Terrades 8, 08860 Castelldefels, Spain; 4- Wageningen Univ & Res, Plant Breeding, POB 386, NL-6700 AJ Wageningen, Netherlands; 5- Institute of Biosciences and BioResources (IBBR), National Research Council of Italy (CNR), Via Università 133, 80055 Portici, Italy; 6- INRAE, UR1052, Génétique et Amélioration des Fruits et Légumes 67 Allé des Chênes, Centre de Recherche PACA, Domaine Saint Maurice, CS60094, Montfavet, 84143, France; 7- Department of Agriculture and Forest Sciences (DAFNE), Università degli Studi della Tuscia, Viterbo, Italy; 8- Aristotle University of Thessaloniki, School of Agriculture, Laboratory of Vegetable Crops, Thessaloniki, 54124 Greece; 9- Italian National Agency for New Technologies, Energy and Sustainable Economic Development (ENEA), Casaccia Research Centre, Rome, Italy; 10- Hebrew University of Jerusalem, Robert H Smith Inst Plant Sci & Genet Agr, Rehovot, Israel; 11- Group of Biotechnology of Pharmaceutical Plants, Laboratory of Pharmacognosy, Department; of Pharmaceutical Sciences, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece; 12-Agroindustrial Cooperative of Tympaki, 70200 Tympaki, Greece

Presenting author: cpons@upvnet.upv.es

Corresponding author: cpons@upvnet.upv.es

Abstract:

The Mediterranean basin countries are considered secondary centres of tomato diversification. However, information on phenotypic and allelic variation of local tomato materials is still limited. To unveil the molecular basis of Southern European tomato phenotypic diversity, we carried out the most comprehensive phenotypic and genomic variability analysis on traditional European tomato by using 1) a collection of 1,499 traditional European tomatoes (TRADITOM collection) and 2) a multipurpose core collection (TCC), comprising 227 European traditional tomato accessions from the original TRADITOM collection, that captured most of genotypic and phenotypic variation and geographical origin present in traditional tomato. The TRADITOM collection was used to gain insights into the phenotypic and genetic architecture of plant and fruit morphological and quality traits. The TCC was used to understand how traditional varieties respond to environmental variation and to investigate the genetic architecture of trait sensitivity to the environment. The results presented here revealed a broad range of phenotypic variability in traditional European tomato and indicated that despite the low polymorphism reported for cultivated and traditional tomato germplasm, as compared to the wild relatives, traditional European tomato is a rich repository of crop genetic diversity, as revealed by both old and new, previously unreported loci.
