



HAL
open science

The worldwide population structure of over 3,400 eggplant accessions identified by SPET genotyping

Lorenzo Barchi, Ezio Portis, Sergio Lanteri, David Alonso, Maria José Díez, Jaime Prohens, Véronique Lefebvre, Jeremy Salinier, Hatice Filiz Boyaci, Laura Toppino, et al.

► To cite this version:

Lorenzo Barchi, Ezio Portis, Sergio Lanteri, David Alonso, Maria José Díez, et al.. The worldwide population structure of over 3,400 eggplant accessions identified by SPET genotyping. XVII SOLANACEAE2022 International Conference on the Plant Family of Solanaceae, Nov 2022, THES-SALONIKI, Greece. hal-04133464

HAL Id: hal-04133464

<https://hal.inrae.fr/hal-04133464>

Submitted on 19 Jun 2023

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.

Public Domain

XVII SOLANACEAE2022 International Conference on the Plant Family of Solanaceae November 1-5, 2022, THESSALONIKI, GREECE

ORAL PRESENTATIONS

The worldwide population structure of over 3,400 eggplant accessions identified by SPET genotyping.

Lorenzo Barchi¹ , Ezio Portis¹ , Sergio Lanteri¹ , David Alonso² , Maria Josè Díez² , Jaime Prohens² , Veronique Lefebvre³ , Jeremy Salinier³ , Hatice Filiz Boyaci⁴ , Laura Toppino⁵ , Giuseppe Leonardo Rotino⁶ , M. Timothy Rabanus-Wallace⁶ , Andreas Boerner⁶ , Nils Stein^{6,7} , Richard Finkers⁸ , Matthijs Brouwer⁹ , Arnaud G. Bovy⁹ , Roland Schafleitner¹⁰ , Giuseppe Aprea¹¹ and Giovanni Giuliano¹¹

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

2 Instituto Universitario de Conservación y Mejora de la Agrodiversidad Valenciana COMAVUPV, València, Spain

3 INRAE, GAFL, Montfavet, France

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

5 CREA-GB, Montanaso Lombardo, Italy

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

7 Center for Integrated Breeding Research, Georg-August-University Göttingen, Göttingen, Germany

8 Gennovation B.V., Wageningen, Netherlands

9 Wageningen University & Research, Plant Breeding, Wageningen, The Netherlands

10 World Vegetable Center, Tainan, Taiwan

11 ENEA, Rome, Italy

G2P-SOL (<http://www.g2p-sol.eu>) is an EU-funded project, bringing together the main European and international genebanks hosting germplasm of the four major Solanaceous crops: potato, tomato, pepper and eggplant. Within the project, about 5,900 eggplant accessions, including wild relatives of the crop, were inventoried. To provide genomic information on around 3,500 representative accessions, a custom set of 5K SPET probes (single primer enrichment technology, TECAN) was designed targeting SNPs evenly distributed all over the genome but mainly in gene-rich regions. After library preparation, Illumina sequencing and quality filtering, reads were aligned to the eggplant reference genome (version 4.1) using BWA-MEM and SNP calling was performed using GATK4.1.9. By removing accessions with low coverage sequencing data, 3,412 were retained and 120K polymorphic sites identified by applying stringent filtering criteria. Among them, 4,306 were SNPs targeted by the 5K probe set, while the remaining were accessory off-target SNPs. The identified SNPs provided information for identifying putative mislabeled accessions (i.e., wrong species assignment), and duplicates within and between genebanks. Moreover, they are exploitable for setting up screening protocols to avoid the acquisition of duplications by ex-situ maintainers. The population structure and genetic relationships of the eggplant accessions were investigated to build up a core collection for GWAS. Furthermore, based on historical phenotypic data available in genebanks, loci associated with key agronomic traits were identified. Our results demonstrate that SPET technology represents a valid alternative to random complexity reduction methods and arrays, proving a suitable tool for the highthroughput genotyping, management, and enhancement of genebank collections.

Key words: *Solanum melongena*, diversity, SPET

Acknowledgment: This work was supported by the European Commission, Horizon 2020 G2P-SOL project (grant agreement no. 677379). G2P-SOL project.