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Worldwide Population Structure of Eggplant Identified by SPET Genotyping over 3,400 Accessions

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Barchi L. (Orateur), Portis E., Lanteri S., Alonso D., Diez M.J., Prohens J., Lefebvre V., Salinier J., Boyaci H.F., Unlu A., Toppino L., Rotino G.L., Rabanus-Wallace M.T., Borner A., Stein N., Finkers R., Brouwer M., Bovy A., Schafleitner R., Aprea G., Giuliano G.

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Worldwide Population Structure of Eggplant Identified by SPET Genotyping over 3,400 Accessions.

Sunday, January 9, 2022
8:30 PM - 8:50 PM

- *Palm 5-6*

Abstract

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, have been 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. DNA samples were prepared by the genebanks, while library preparation and Illumina sequencing was performed by IGA Technology Services. After quality filtering, reads were aligned to the eggplant reference genome sequence (version 4.1) using BWA-MEM and SNP calling was performed using GATK-4.1.9.

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), 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 high-throughput genotyping, management, and enhancement of genebank collections.

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