

G2P- SOL FINAL WORKSHOP: „Multi-omics-based management of plant genetic resources“

1st announcement

The EU project “Linking genetic resources, genomes and phenotypes of Solanaceous crops (G2P-SOL)” (www.g2p-sol.eu) lasted almost 6 years, from March 2016 to December 2021. Over 50,000 accessions of the four major Solanaceous crops have been catalogued by collecting, in a single database, passport, phenotypic and image data available at worldwide genebanks hosting Solanaceae collections. Over 40,000 of these accessions have been genotyped, and the data have been used to construct core collections representing the genetic and phenotypic variation of the four species. The core collections have been subjected to high density genotyping/resequencing and phenotypic characterization (agronomic/quality traits, metabolomics, tolerance to biotic and abiotic stresses) at multiple locations. The data are being used for GWAS analysis and identification of novel loci controlling such traits. G2P-SOL has also generated/characterized novel prebreeding populations, carrying traits from each crop’s wild gene pools. These data are being stored on a dedicated database with data analysis capabilities.

The aim of the workshop is to present the multi-omic resource generated by G2P-SOL, as well as discuss the path forward with external experts in the field of genetic resources.

The workshop will take place via teleconference on Mon-Thu December 13-15, from 14 to 17.15 Central European Time. Registration is free and is required to participate in the workshop. The program and registration link can be found at

<http://www.g2p-sol.eu/G2P-SOL-Final-Workshop.html>

Day 1: Genotype to Phenotype	
Monday 13th December, 2021 14.00-17.15 CET	
14:00-14:30	Giovanni Giuliano, ENEA, Casaccia Res Ctr, Italy <i>“The G2P-SOL Project: a cornucopia full of Solanaceae”</i>
14:30-15:00	Toni Granell, Institute for Plant Molecular and Cell Biology -IBMCP, Spain <i>“The pheno and genotypic variability in traditional European tomato: an untapped source?”</i>
15:00-15:30	Véronique Lefebvre, Institut National de la Recherche Agronomique, France <i>“TBA”</i>
15:30-15:45	Break
15:45-16:15	Arnaud Bovy, Stichting Dienst Landbouwkundig Onderzoek, Netherlands <i>“Metabolomics-assisted breeding in pepper”</i>
16:15-16:45	Yaniv Semel, Phenome Networks Ltd., Israel <i>“Managing, analyzing and sharing genebank accessions”.</i>
16:45-17:15	General discussion

Day 2: Genomics-assisted breeding Tuesday, 14th December, 2021 14.00-17.15 CET	
14:00-14:30	Dani Zamir, The Hebrew University of Jerusalem, Israel <i>"Epistasis Time"</i>
14:30-15:00	Sanwen Huang, Agricultural Genomics Institute at Shenzhen, China <i>"Genome design of hybrid potato"</i>
15:00-15:30	Ilan Paran, The Agricultural Research Organization of Israel <i>"Genomic tools for pepper breeding and QTL mapping"</i>
15:30-15:45	Break
15:45-16:15	Hannele Lindqvist-Kreuzer, Centro Internacional de la Papa, Peru <i>"Genomics-based potato breeding"</i>
16:15-16:45	Jaime Prohens Tomas, Universidad Politécnica de Valencia, Spain <i>"Introgressomics for utilization of crop relatives for breeding: a case in eggplant"</i>
16:45-17:15	General discussion

Day 3: Biodiversity and genebank management Wednesday, 15th December, 2021 14.00-17.30 CET	
14:00-14:30	Sandra Knapp, Natural History Museum, UK <i>"Exploring morpho-space across Solanum with an expanded dataset"</i>
14:30-15:00	Glenn Bryan, The James Hutton Institute, UK <i>"Using genomic data for the management of Solanaceae germplasm resources"</i>
15:00-15:30	Roberto Papa, Università Politecnica delle Marche, Italy <i>"The INCREASE project: Intelligent Collections of Food-Legume Genetic Resources for European Agrofood Systems"</i>
15:30-15:45	Break
15:45-16:15	María José Díez, Universidad Politécnica de Valencia, Spain <i>"The domestication, diffusion and breeding of tomato from the analysis of 15,000 worldwide accessions"</i>
16:15-16:45	Nils Stein, The Leibniz-Institut fuer Pflanzengenetik und Kulturpflanzenforschung, Germany <i>"Genebank genomics – building the bridge to characterization and evaluation of genebank collections"</i>
16:45-17:30	General discussion - Conclusions