



G2P-SOL

Using Genetic Resource Data for Breeding:

THE G2P-SOL ADVANCED TRAINING SCHOOL

VENUE

Wageningen UR Campus, Wageningen, The Netherlands

DATE

30 April & 1 May 2019

ORGANISER

Dr Richard Finkers (WUR)

Effective vegetable breeding requires a detailed understanding of traits conferring nutrient security, resistance to pests and diseases as well as tolerance to abiotic stresses. At the same time, breeders need the skills to utilize these traits in breeding effectively. This **training school** will provide guidance on how to use vegetable diversity from genebank collections for breeding improved vegetable cultivars.

The **training school** is organized in the framework of the EU-project **G2P-SOL** which aims at bringing into full fruition the seeds from tens of thousands of genetic accessions of the four major solanaceous food crops that are stored in 'genebanks' worldwide, i.e. potato, tomato, pepper and eggplant. Understanding and utilising this genetic diversity is key to the sustainability of agriculture in the face of a changing environment and the appearance of new pests. This is currently hampered by the scarce publicly available information on the variability of collections preserved in different genebanks. Within G2P-SOL, 30,000 accessions from eggplant, pepper, potato and tomato are genotyped while a subset of these plants is phenotyped in detail. In this training school, you will learn about the state-of-the-art methodologies for using and mining the data generated in the project.

WHO SHOULD APPLY

(Junior) vegetable breeders and PhD/Postdoc researchers from breeding institutes with keen interest in exploring natural biodiversity maintained in genebanks more effectively, and utilizing the detailed characterization from state-of-the-art omics technologies.

HOW TO APPLY

If you wish to attend the G2P-SOL advanced Training School on use of genetic resource data for breeding, please fill in the form available [here](#)!

Registration is open until the 31st March 2019.

Acceptance will be on a first come, first serve basis!

Costs incurred by the selected participants cannot be covered by the organiser.

Only the selected participants will be informed via email and will be requested to proceed to the organisation of their travel arrangement. Therefore, we apologise in advance if you will not be selected and would like to thank you for your interest in our project!

The selected participants will receive additional details on the 2-day program as soon as possible.

WHAT WE OFFER

A two-day course with a blend of theory and practise on the use of genetic resources data for breeding.

MODULE 1

Genetic diversity in genebanks (Theo van Hintum, CGN, The Netherlands)

- The genebank landscape: actors and organisations
- Technology in genebanks and the need for it
- The CGN lettuce collection: examples of an integrated approach and its needs
- Core collections, concept, methodology and alternatives

MODULE 2

Sourcing genetic diversity for breeding improved varieties from genebank collections (Roland Schafleitner, World Vegetable Center, Taiwan)

- The need for data and their potential use in a genebank context
- Current technologies and approaches for pheno- and genotyping
- On-going initiatives in the field of assessing diversity and using the data: data production and processing

MODULE 3

G2P-SOL infrastructure (Yaniv Semel, Phenome Networks, Israel)

- Project Unity: A collaborative network which hosts, manages, analyzes and shares phenotypes and genomic data of plant populations
- Browse G2P-SOL data and dynamically view markers' effects on various phenotypes, populations, studies and environments
- QTL and GWAS analysis with Project Unity

MODULE 4

Breeding API (Peter Shelby, BrAPI consortium, USA)

- Breeding API: a standard interface for plant phenotype/genotype databases to serve their data to crop breeding applications
- Showcases on how the Breeding API can be used by end-users:
 - Load data from any BrAPI data source right into R and analyses
 - Visualize geographic information about germplasm and trials by plotting the data on a map
 - Use mobile devices to collect field trial data and directly import it into the BrAPI data source
 - Pull genotypic data from any BrAPI data source and visualize it using tools like [Flapjack](#)

LECTURERS

Dr. Theo van Hintum, Centre for Genetic Resources, the Netherlands

Prof. Dani Zamir, The Hebrew University of Jerusalem

Dr. Yaniv Semel, Phenome Networks

Dr. Maikel Verouden, Wageningen UR

Ir. Matthijs Brouwer, Wageningen UR

Mr. Peter Shelby, Coordinator BrAPI consortium

Dr. Glenn Bryan, James Hutton Institute

Dr. Roland Schafleitner, The World Vegetable Center

