UPOV

International Union for the Protection of New Varieties of Plants

E

Technical Working Party for Agricultural Crops

Fiftieth Session
Arusha, United Republic of Tanzania, June 21 to 25, 2021

TWA/50/7

Original: English
Date: June 7, 2021

VARIETY DESCRIPTION DATABASES

Document prepared by an expert from Austria

Disclaimer: this document does not represent UPOV policies or guidance

The annex to this document contains a copy of a presentation “Integration of molecular data into DUS testing in Durum Wheat”, to be made by an expert from Austria, at the fiftieth session of the Technical Working Party for Agricultural Crops (TWA).

[Annex follows]

Integration of Molecular Data into DUS Testing in Durum Wheat

DURDUS: Use of a standardized method for the efficient management of reference collections (2018 – 2020)

DURDUStools: Development of a common online molecular database and a genetic distance calculation tool (2021 – 2023)

Austrian Agency for Health and Food Safety, Division for Food Security

THE DURDUS/DURDUStools PROJECTS

Objective: Efficient management of reference collections

- A comprehensive **reference collection** has to be present in each entrusted Examination Office (EO) according to UPOV and CPVO rules
  - CPVO: **Austria, France, Hungary, Italy, and Spain** in the case of durum wheat
  - The challenge: Expensive and extensive
  - The aim: **Reduce** the number of plants to be grown in field trials, enable **pre-selection**

  - In total around 640 varieties/candidate varieties have been genotyped
    1. Varieties covered by CPVR
    2. Varieties listed in the Common Catalogue
    3. Candidate varieties

  - Use of a commercial DNA SNP-chip

THE DURDUS/DURDUStools APPROACH

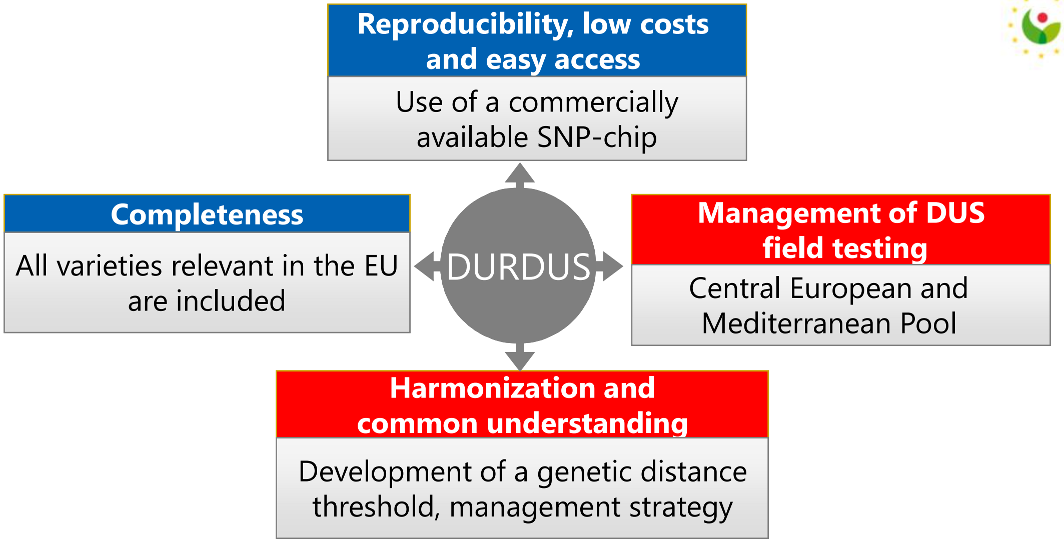
Cost- and resource-efficient, easy-to-use

Follows the UPOV Model "Combining phenotypic and molecular distances in the management of variety collections"

- Cost efficiency
- Resource efficiency
  - Cooperation with a state-of-the-art service provider
  - No lab is needed in the EOs
- Providing an **easily-accessible tool** to be used by the DUS experts of the EOs

KEY FEATURES OF DURDUS/DURDUSTOOLS

Benefits and challenges of the DURDUS approach



Reproducibility, low costs and easy access

Use of a commercially available SNP-chip

Completeness

All varieties relevant in the EU are included

DURDUS

Management of DUS field testing

Central European and Mediterranean Pool

Harmonization and common understanding

Development of a genetic distance threshold, management strategy

CHARACTERISTICS OF THE SNP-CHIPS

SGS Institut Fresenius GmbH – TraitGenetics Section

- 20K and 25K wheat arrays

  - 2018: **20K** Illumina HD technology
    - 15K wheat Illumina array + 5K add-on-array
    - >12,000 of 17,267 functional SNPs suitable for durum wheat

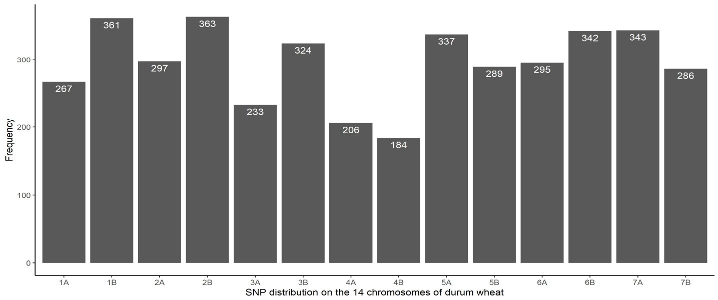
  - 2020: **25K** Illumina XT technology
    - 20K wheat Illumina array + 135K Axiom array + specific markers
    - ~20,000 of 24,145 functional SNPs suitable for durum wheat

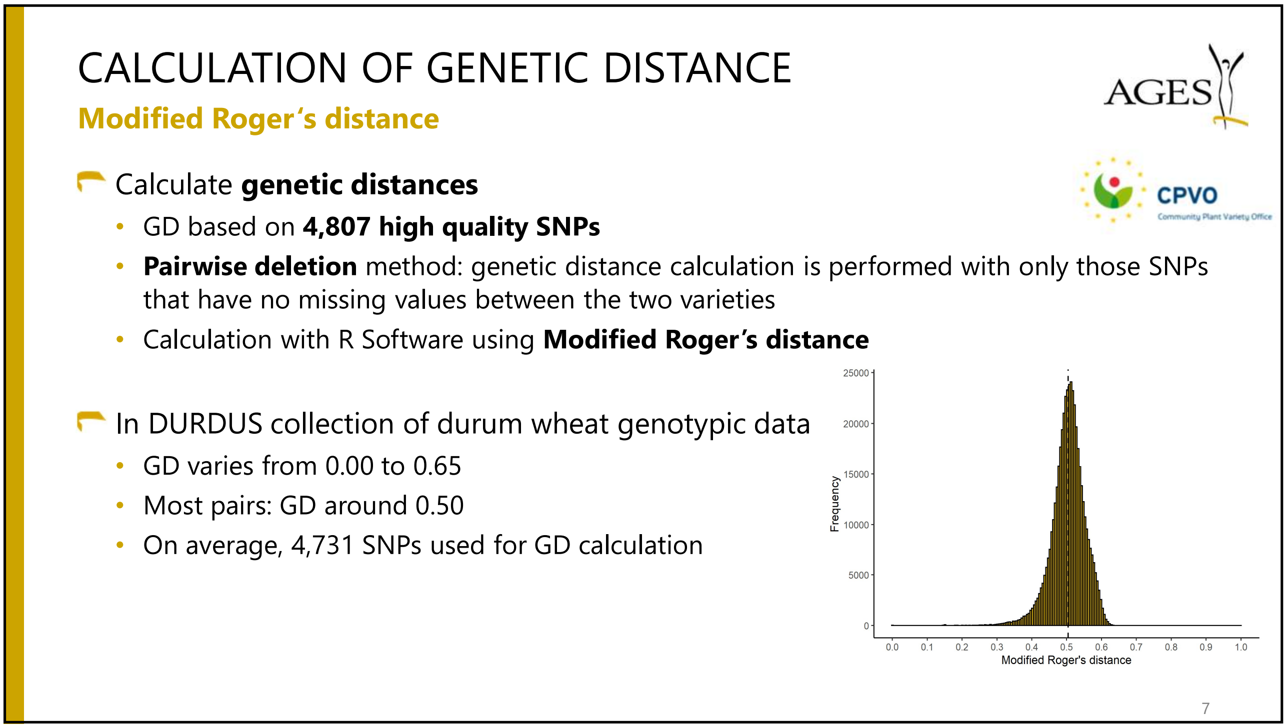
SNP SELECTION IN DURDUS

4,807 high quality, polymorphic SNPs with high discriminatory power

- **4,807 high quality SNPs** selected based on a **quality check:**
  - Present on all used wheat arrays
  - High discriminatory power (GenTrain Score >0.4)
  - Successful amplification
  - <10% missing values
  - Polymorph (MAF>0.01)

- SNPs are evenly distributed on **all durum wheat chromosomes**

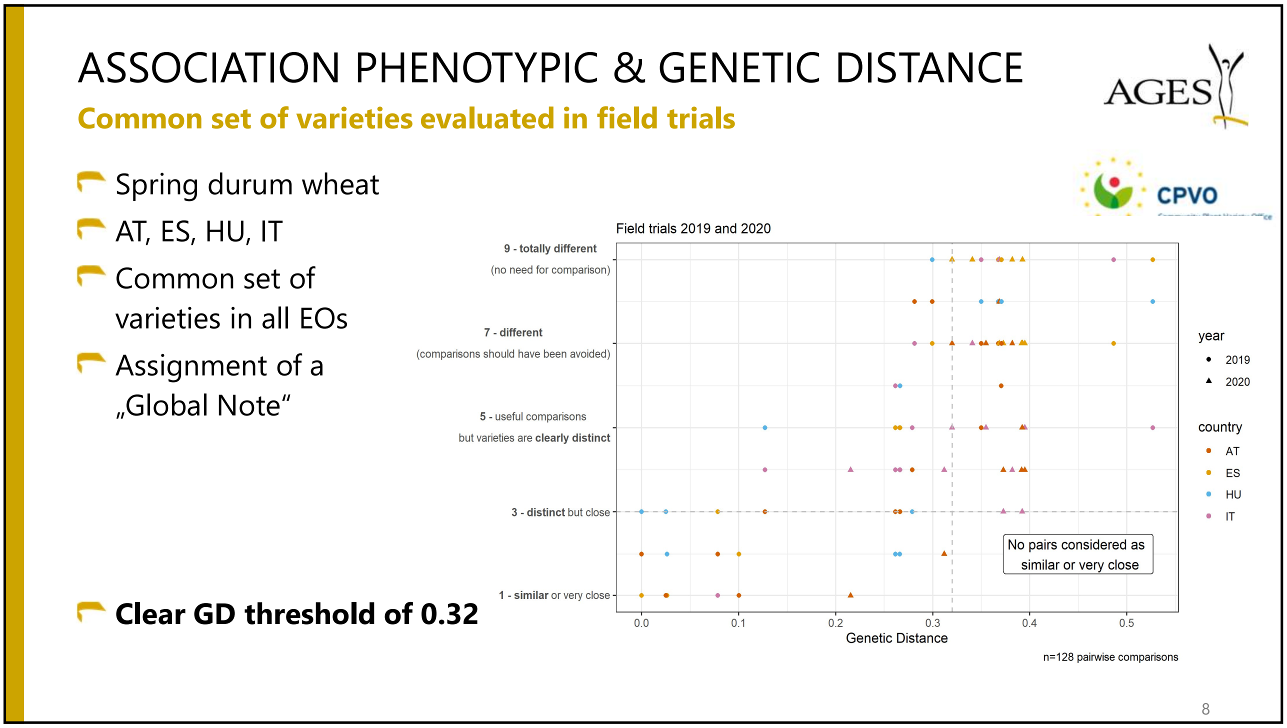




CALCULATION OF GENETIC DISTANCE

Modified Roger's distance

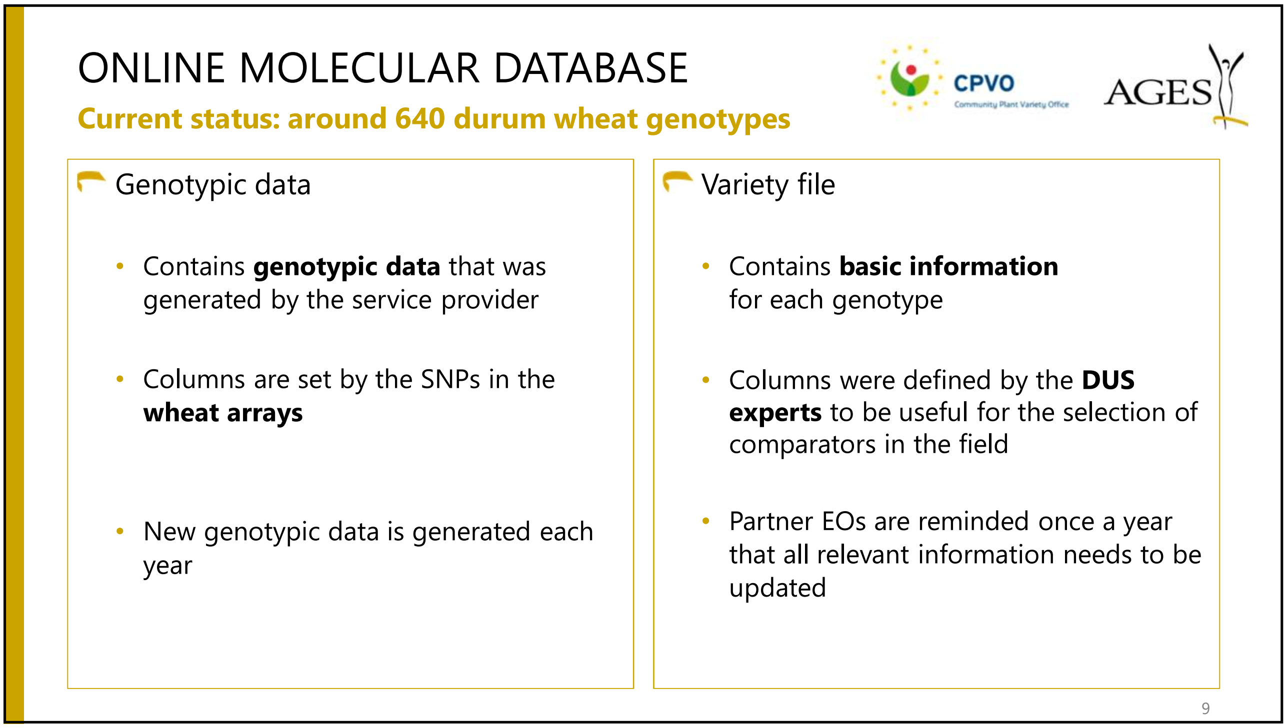
- Calculate **genetic distances**
  - GD based on **4,807 high quality SNPs**
  - **Pairwise deletion** method: genetic distance calculation is performed with only those SNPs that have no missing values between the two varieties
  - Calculation with R Software using **Modified Roger's distance**
- In DURDUS collection of durum wheat genotypic data
  - GD varies from 0.00 to 0.65
  - Most pairs: GD around 0.50
  - On average, 4,731 SNPs used for GD calculation



ASSOCIATION PHENOTYPIC & GENETIC DISTANCE

Common set of varieties evaluated in field trials

- Spring durum wheat
- AT, ES, HU, IT
- Common set of varieties in all EOs
- Assignment of a „Global Note"
- **Clear GD threshold of 0.32**



ONLINE MOLECULAR DATABASE

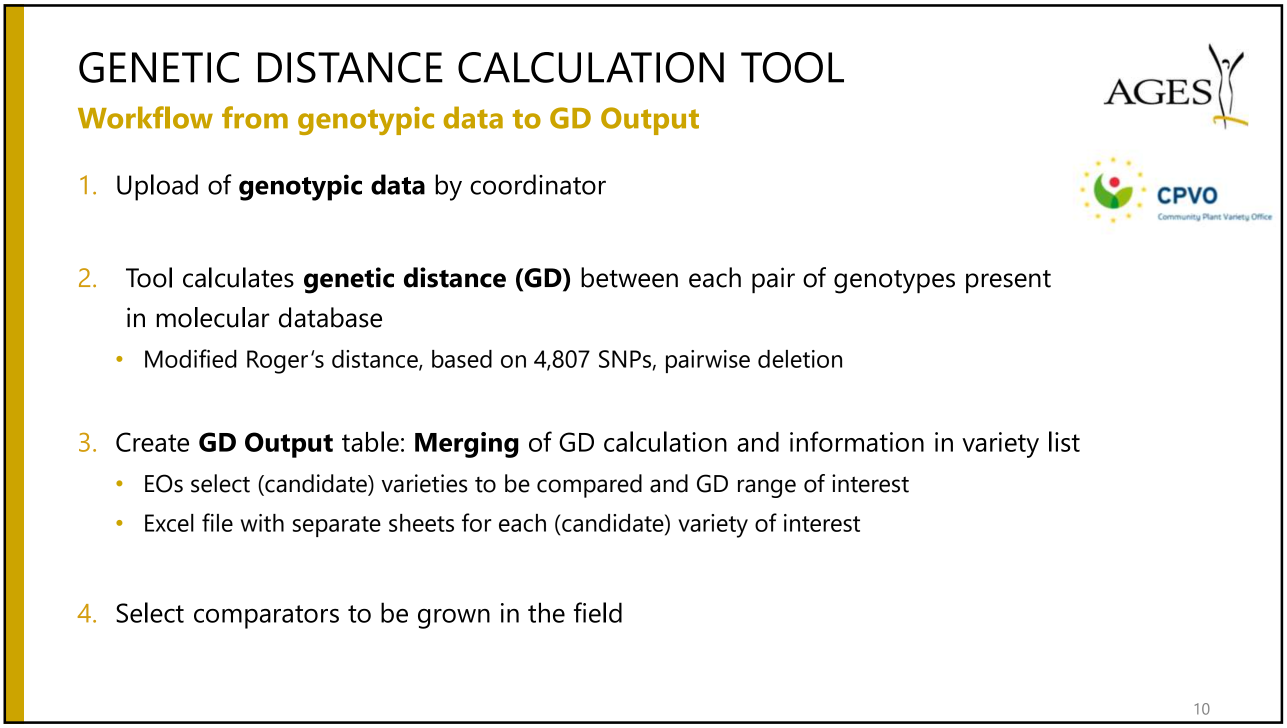
Current status: around 640 durum wheat genotypes

Genotypic data

- Contains **genotypic data** that was generated by the service provider
- Columns are set by the SNPs in the **wheat arrays**
- New genotypic data is generated each year

Variety file

- Contains **basic information** for each genotype
- Columns were defined by the **DUS experts** to be useful for the selection of comparators in the field
- Partner EOs are reminded once a year that all relevant information needs to be updated



GENETIC DISTANCE CALCULATION TOOL

Workflow from genotypic data to GD Output

1. Upload of **genotypic data** by coordinator
2. Tool calculates **genetic distance (GD)** between each pair of genotypes present in molecular database
   - Modified Roger's distance, based on 4,807 SNPs, pairwise deletion
3. Create **GD Output** table: **Merging** of GD calculation and information in variety list
   - EOs select (candidate) varieties to be compared and GD range of interest
   - Excel file with separate sheets for each (candidate) variety of interest
4. Select comparators to be grown in the field

[End of Annex and of document]