

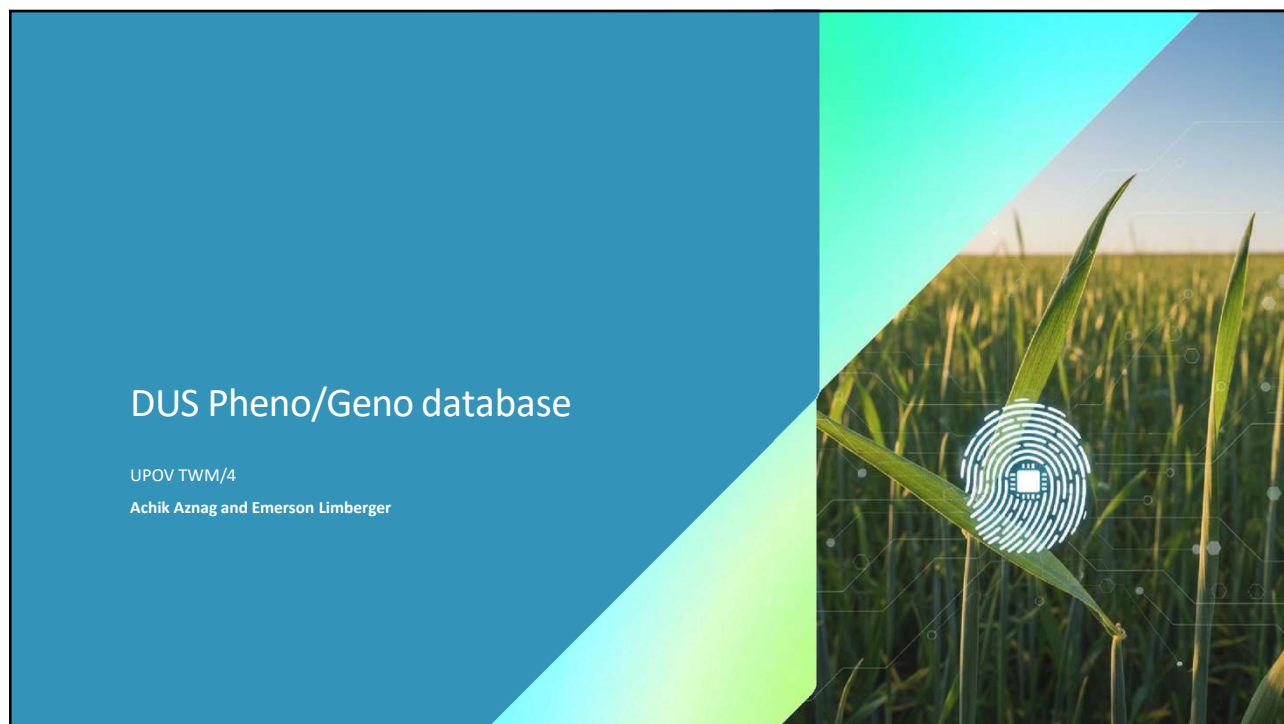
**Technical Working Party on Testing Methods and Techniques****TWM/4/16****Fourth Session****Cambridge, United Kingdom, June 2 to 5, 2026****Original:** English**Date:** May 11, 2026

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**DUS PHENO/GENO DATABASE***Document prepared by an expert from the International Seed Federation (ISF)**Disclaimer: this document does not represent UPOV policies or guidance*

The annex to this document contains a copy of a presentation “DUS Pheno/Geno database”, to be made by an expert from the International Seed Federation (ISF), at the fourth session of the TWM.

[Annex follows]



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## Goal

Provide a **database framework** for UPOV and PBR offices to store and share data related with **DUS information** that covers simultaneously morphological characteristics (Phenotypes) and molecular information (Genotypes) for **plant varieties**.

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## Momentum from TWM/3

Many great proposals were presented in Beijing, including TWM/3/23

The atmosphere allowed for a spirit of collaboration

Profit from the momentum and turn into deliverables

Possibility to implement the “confidentiality of molecular information”  
(TWM/9/4) through server authentication

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## Concept

### Simple:

- Minimalist design covering what’s necessary

### Data Agnostic:

- Species, Authority, Marker Type etc

### Robust:

- Well defined keys that contemplate the foundation

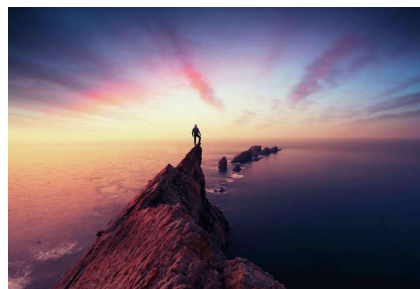
### Flexible:

- Allows for changes in data without interruptions  
– version changes in TGs

### Secure:

- Enhance data security by moving away of Excel and PDF files

Big Picture



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## Scope

Purely a database to store and manage molecular data (**genotypes**) and morphological characteristics (**phenotypes**) related with DUS → no software analysis

Data integrity → genotypic concordance

Reciprocal imputations between genotypes and phenotypes → to serve the current requirement of association between markers and morphological characteristics

Robust → following technical guidelines and already harmonized terminology under UPOV documentation and systems

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## Scope

Data integrity → genotypic concordance

Variety	RST-24	Authority
Alpha	A/C	A
Beta	A/C	A
Gamma	C/C	A



Variety	RST-24	Authority
Alpha	A/A	B
Beta	A/C	B
Gamma	C/C	B

Variety	RST-24	Authority
Alpha	--	UPOV
Beta	A/C	UPOV
Gamma	C/C	UPOV

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## Scope

Reciprocal imputations between genotypes and phenotypes → to serve the current requirement of association between markers and morphological characteristics

Variety	Marker 12	Petal Color
Alpha	A/A	White
Beta	--	Pink
Gamma	C/C	--

**Imputation** →

Variety	Marker 12	Petal Color
Alpha	A/A	White
Beta	A/C	Pink
Gamma	C/C	<i>Red</i>

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## Scenarios and implications

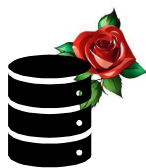
### Example Authority A

Databases built to fit specific requirements limited to vegetable crops



### Example Authority B

Databases built to fit specific requirements limited to flowers and other asexually propagated crops



### Example Authority C

Databases built to fit specific requirements limited to agricultural crops



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## Scenarios and implications

### Example Authority A

Stores SNPs only as:

A/A  
C/C  
G/G  
T/T

Uses **alpha characters** and  
backslash is the compulsory  
**delimiter**



### Example Authority B

Stores SNPs only as:

AA  
CC  
GG  
TT

Uses **alpha characters** and does not  
support delimiters



### Example Authority C

Stores SNPs only as:

1,1  
2,2  
3,3  
4,4

Uses **numeric characters** and comma is  
the compulsory **delimiter**



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## Scenarios and implications

### Example Authority A

#### Molecular Assays

- Marker ID
- Marker Name
- Primer Name
- 3' Seq
- 5' Seq

#### Variety

- Variety ID
- Variety Name
- Specie

#### Genotyping Table

- Sample ID
  - Variety ID
  - Marker ID
- Observation

### Example Authority B

#### Main Table

- Entry ID
- Entry Name
- Entry Type
- Entry Value

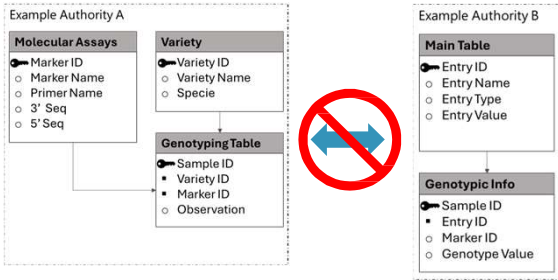
#### Genotypic Info

- Sample ID
  - Entry ID
- Marker ID
- Genotype Value

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## Dataflow and communication

How do we store information?



What do we want to share?

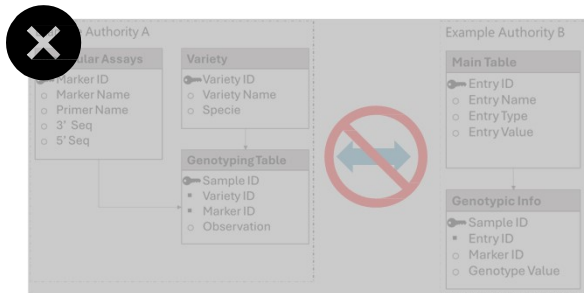
Variety	RST-24	RSTV Virus
Alpha	A/A	Resistant
Beta	A/C	Resistant
Gamma	C/C	Susceptible

**Why are those not compatible?**

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## Dataflow and communication

How do we store information?



What do we want to share?

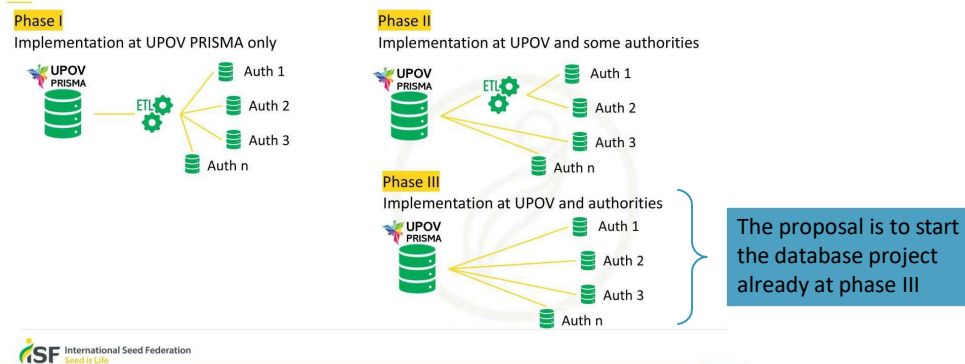
Variety	RST-24	RSTV Virus
Alpha	A/A	Resistant
Beta	A/C	Resistant
Gamma	C/C	Susceptible

**Reposition ourselves to a generic and common perspective**

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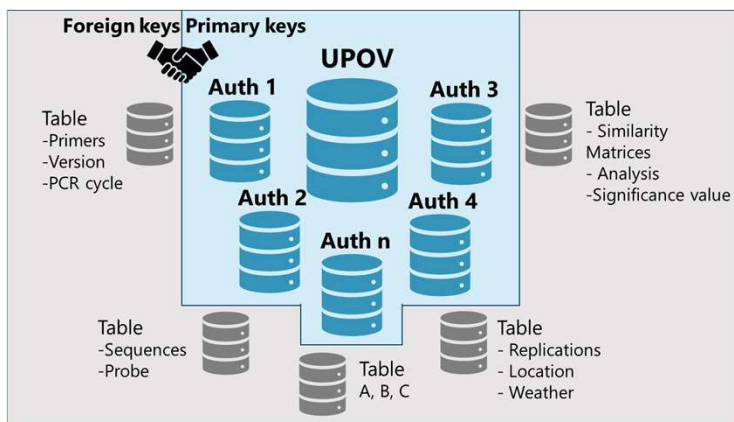
## UPOV PRISMA – similar concept

### Types of data connection



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## Central database and satellite databases

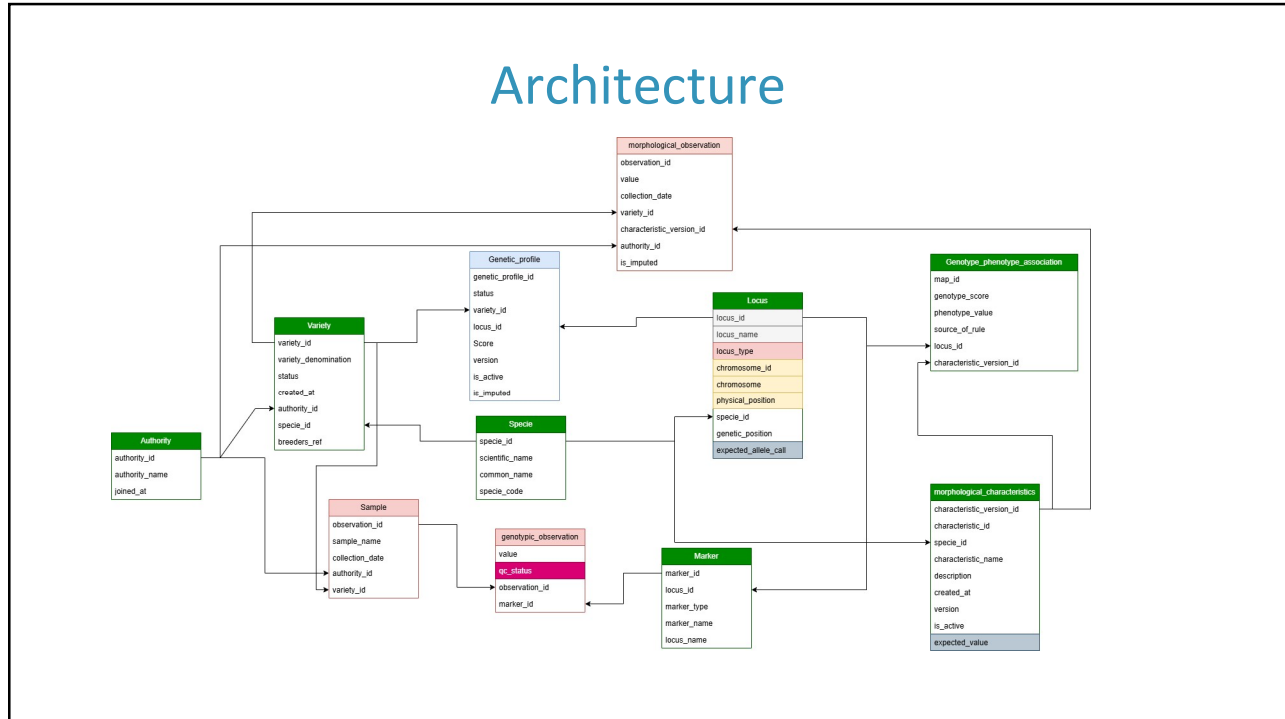


The design allows authorities customized tables and attributes without detriment to the core data and data connection.

Mutual tables, attributes, values and types.

Independent tables, attributes, values and types to accommodate specific needs that are not shared.

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## Demonstration

Agriculture Communications 1 (2023) 100006

Contents lists available at [ScienceDirect](#)

**Agriculture Communications**

journal homepage: [www.sciencedirect.com/journal/agriculture-communications](http://www.sciencedirect.com/journal/agriculture-communications)

**Evaluation of SNP fingerprinting for variety identification of tomato by DUS testing**

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**HIGHLIGHTS**

- 116 tomato varieties were identified by both SNP fingerprinting and DUS testing.
- A set of 16 core SNPs and 18 core DUS traits were selected to efficiently identify varieties.
- SNP fingerprinting and DUS testing had a consistent result in variety identification.

**The data used is from the publication from Zhang et al., 2023**

Genotype and phenotypes were randomly assigned and do not represent the real state of the varieties, because that data was not shared.

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## Demonstration

### Consolidated genetic profile

Genetic_profile_id	Status	Variety_id	Locus_id	Score	Version	Is_active	Is_imputed	Locus	Variety
1	consistent	2	1	A;G	2026-01-05 14:14:41	True	False	Locus	Variety
2	consistent	2	27	C;C	2026-01-05 14:14:41	True	False	Locus	Variety
3	consistent	3	1	A;A	2026-01-05 14:14:41	True	False	Locus	Variety
4	consistent	3	27	T;T	2026-01-05 14:14:41	True	False	Locus	Variety
5	consistent	4	1	A;A	2026-01-05 14:14:41	True	False	Locus	Variety
6	consistent	4	27	T;T	2026-01-05 14:14:41	True	False	Locus	Variety
7	consistent	5	1	A;A	2026-01-05 14:14:41	True	False	Locus	Variety

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## Demonstration

### Phenotypic and genotypic annotation

Map_id	Genotype_score	Phenotype_value	Source_of_rule	Locus_id	Characteristic_version_id	Locus	Morphological_characteristics
1	A;A	3	QTL Study	1	18	Locus	Morphological_characteristics
2	A;G	2	QTL Study	1	18	Locus	Morphological_characteristics
3	G;G	1	QTL Study	1	18	Locus	Morphological_characteristics
4	C;C	1	GWAS	27	22	Locus	Morphological_characteristics
5	C;T	1	GWAS	27	22	Locus	Morphological_characteristics
6	T;T	2	GWAS	27	22	Locus	Morphological_characteristics

Locus_id	1
Locus_name	FQSNP-0413
Locus_type	SNP
Chromosome_id	1
Chromosome	1
Physical_position	348230
Specie_id	SOLAN_LYC
Genetic_position	null
Expected_allele_call	G/A
Specie	Specie
Genetic_profiles	Genetic_profiles
Genotype_phenotype_associations	Genotype_phenotype_associations
Markers	Markers

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## Demonstration

Phenotypic or  
genotypic  
imputations

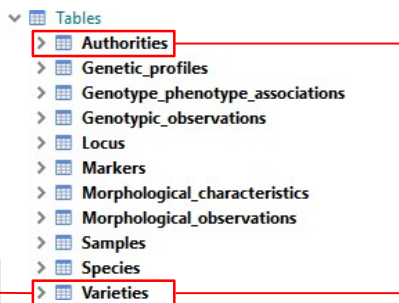
Observation_id	Value	Collection_date	Variety_id	Characteristic_version_id	Authority_id	Is_imputed	Authority	Morphological_characteristics	Variety
1	1	6/15/2025	1	18	CHN	False	Authority	Morphological_characteristics	Variety
2	1	6/15/2025	1	22	CHN	False	Authority	Morphological_characteristics	Variety
3	2	6/15/2025	2	18	CHN	False	Authority	Morphological_characteristics	Variety
4	1	6/15/2025	2	22	CHN	False	Authority	Morphological_characteristics	Variety
5	3	6/18/2025	3	18	CHN	False	Authority	Morphological_characteristics	Variety
6	2	6/18/2025	3	22	CHN	False	Authority	Morphological_characteristics	Variety
7	3	6/18/2025	4	18	CHN	False	Authority	Morphological_characteristics	Variety
8	2	6/18/2025	4	22	CHN	False	Authority	Morphological_characteristics	Variety
9	3	7/10/2025	5	18	CHN	False	Authority	Morphological_characteristics	Variety
10	2	7/10/2025	5	22	CHN	False	Authority	Morphological_characteristics	Variety
23	3	7/10/2025	7	18	CHN	True	Authority	Morphological_characteristics	Variety
24	1	7/10/2025	7	22	CHN	True	Authority	Morphological_characteristics	Variety
25	3	7/10/2025	8	18	CHN	True	Authority	Morphological_characteristics	Variety
26	2	7/10/2025	8	22	CHN	True	Authority	Morphological_characteristics	Variety
27	3	7/10/2025	9	18	CHN	True	Authority	Morphological_characteristics	Variety
28	2	7/10/2025	9	22	CHN	True	Authority	Morphological_characteristics	Variety
29	3	7/10/2025	10	18	CHN	True	Authority	Morphological_characteristics	Variety
30	2	7/10/2025	10	22	CHN	True	Authority	Morphological_characteristics	Variety
31	1	7/10/2025	11	18	CHN	True	Authority	Morphological_characteristics	Variety
32	1	7/10/2025	11	22	CHN	True	Authority	Morphological_characteristics	Variety
33	null	7/10/2025	12	18	CHN	False	Authority	Morphological_characteristics	Variety
34	null	7/10/2025	12	22	CHN	False	Authority	Morphological_characteristics	Variety

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## Demonstration

Code based solutions:

- Accounting for GxE interactions
- Fitting reference scores
- Finding most similar



**Within-Case Analysis**  
Most similar

**Cross-Case Analysis**  
GxE interaction

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## Next steps

Continue sharing the concept and help defining a generic framework

Test and validation by interested PBR offices and UPOV

Connection with existing repositories and services:

- PLUTO
- ePVP DUS exchange module

**PROPOSAL: Creation of an official working group with authorities and breeders**

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# Thank you!

Contact: [Emerson.Limberger@corteva.com](mailto:Emerson.Limberger@corteva.com)

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