



TWF/44/2 Add.  
ORIGINAL: English  
DATE: May 21, 2013

**INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS**  
Geneva

**TECHNICAL WORKING PARTY FOR FRUIT CROPS**

**Forty-Fourth Session**  
**Napier, New Zealand, April 29 to May 3, 2013**

ADDENDUM TO MOLECULAR TECHNIQUES

*Document prepared by the Office of the Union*

1. The Annex to this document contains the presentation received during the forty-fourth session of the Technical Working Party for Fruit Crops, with regard to the management of peach tree reference collections.

[Annex follows]

Slide 1


**CPVO R&D project – CPV. 8648**  
 May 5, 2008 – May 4, 2011  
**Management of peach tree  
 reference collections**



**CPVO Fruit Open Day**  
 June 15, 2011  
 GEVES - INRA GAFL

Slide 2

**Involvement of the partners**




	France		Hungary	Italy	Spain	
	GEVES	INRA	MgSzH	CRA-FRU	IVIA	CITA
<b>Thematic 1</b> Compilation of <b>morphological data</b>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<b>Thematic 2</b> Creation of standardised <b>digital data</b>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	-	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<b>Thematic 3</b> Generation of <b>molecular marker data</b>	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/> BioGEVES	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<b>Thematic 4</b> Creation of a phenotypic and molecular variety <b>database</b>	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Common varieties (phenotypic harmonization purposes)	11		12	12	12	10
Specific varieties studied by office (without common varieties)	247		54	97	21	75
<b>TOTAL</b>	<b>258</b>		<b>66</b>	<b>109</b>	<b>33</b>	<b>85</b>

*May 2010: Some updating since the inception report*

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## Axis of work

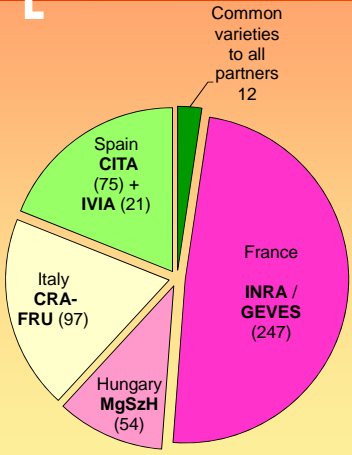
- 7 main axis of work
  - List of varieties included in the project
  - General data on varieties (T01\_varieties table)
  - Applicant phenotypical description (part of T04\_Phenotypical\_Description table)
  - Complete phenotypical description
  - Digital data
  - Biomolecular data
  - Database

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## 1- Varieties included in the project




Country/Institution	Number of Varieties
France (INRA / GEVES)	247
Italy (CRA-FRU)	97
Hungary (MgSzH)	54
Spain (CITA + IVIA)	75 + 21 = 96
Common varieties to all partners	12

- 506 varieties
  - 494 original varieties
  - 10-12 common varieties to all partners
- Officially listed and / or protected (UE / national level)
- Priority done to the latest varieties

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## 2- General data (T01\_Variety table)

- General variety informations
  - such as:  
*Varietal denomination, location into the DUS orchard, number of tree, years of plantation, of protection, of listing, trade mark, breeder...*
- Main entrance of the database  
*The suppression of a variety will destroy all data associated*

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## 3- Applicant phenotypical description

- = *Technical Questionnaire of the Application form*
- A set of phenotypical characteristics + pictures
  - The first information to drive the Examination Office to identify the closest example varieties:
    - ✓ Grouping characteristics
- Exchange of data between Examination Offices

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## 4- Complete phenotypical description (CPVO TP/53/1)




- **Phenotypical ring test**

12 varieties common to all partners

- Aims followed:
  1. to secure the use of reliable characteristics(\*) which can be used in sorts.
  2. Identification of variability between the descriptions (which can be explained and tolerated)

(\*) Selection of 16-18 reliable characteristics to sort the varieties




**68 phenotypical characteristics**

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## 5- Production of standardized digital data




- A protocol to create **standardized digital pictures**

- ❖ *Whatever the picture:*
  - Elements which can influence the picture
    - Place and year of harvest
    - Phenotype x environnement interactions
    - Genotype x environnement interactions
    - Type and setting of the camera

This information can not be a substitute for conventional phenotypic characterization but may summarize a few characteristics.  
*For advanced users only.*



**Pomological view**



**Mass effect view**

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## 6- Generation of molecular fingerprints

- Harmonization of the protocol between 4 biomolecular labs
- Choice of SSR primers for the collections characterization (1st ring test)
  - 16 SSR primers
- Allele scoring (2nd ring test)
  - NIAB's «unified allele score» system
- Characterization of the collections
- Genetic structure of the collection

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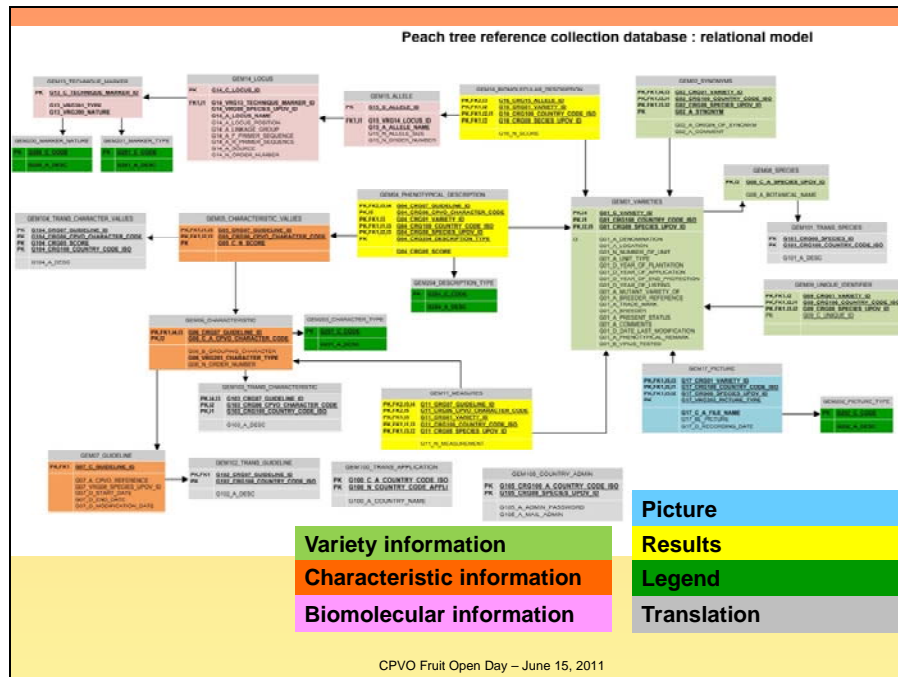
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## 7- Phenotypic and molecular variety database = GEMMA Framework

- **Data model**
  - To integrate different type of data (Molecular data + Digital pictures) what ever the couple Species/Country
  - To support multi language
  - To define access rights
  - To manage different species
- **Web site approach**
  - Easier way to share data
  - Allow to correct problems quickly
  - Easier to manage data such as digital pictures
  - Possibility to provide some useful tools (ie: sorting, ...) automatically available for all users

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CPVO R&D project – CPV. 8648

Management of peach tree  
reference collection



Follow up of the program