UPOV

International Union for the Protection of New Varieties of Plants

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Working Group on Biochemical and Molecular Techniques and DNA-Profiling in Particular

BMT/19/4 Rev.

Nineteenth Session
Alexandria, United States of America, September 23 to 25, 2020

Original: English
Date: September 7, 2020

CPVO REPORT ON IMODDUS: UPDATE ON R&D PROJECTS

Document prepared by an expert from the European Union

Disclaimer: this document does not represent UPOV policies or guidance

The annex to this document contains a copy of a presentation on "CPVO report on IMODDUS: update on R&D projects", prepared by an expert from the European Union, to be made at the nineteenth session of the BMT.

[Annex follows]

CPVO
Community Plant Variety Office

UPOV-BMT19 (2020)

CPVO report on IMODDUS :
update on R&D projects

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IMODDUS Background

- The CPVO Administrative Council adopted a R&D Strategy for the period 2015-2020.
- The strategy includes the set up of a CPVO BMT working group for the promotion of the use of bio-molecular techniques in DUS testing and variety identification.
- Its name is CPVO **IMODDUS** which stands for **I**ntegration of **MO**lecular **D**ata into **DUS** testing.
- IMODDUS works as a think-tank on developing a strategy on how to integrate BMT into DUS testing.
- IMODDUS has a **practical approach** which aims to assist the CPVO identifying and assessing R&D project proposals for species where BMT could improve the quality and potentially cost efficiency of DUS testing.

IMODDUS Activities

Meetings

- April 2016, January 2017, April 2018
- No meeting in 2019 → INVITE consortium
- Meeting cancelled in 2020 (Covid19)

Reviewing of R&D proposals

- 2020 : follow-up project on Durum wheat ('DURDUStools')

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On going IMODDUS projects

Tomato

"*International harmonisation and validation of a SNP for the management of tomato reference collection*"

- Granted co-financing in February 2019.
- coordinated by Naktuinbouw; partners are all EU entrusted examination offices for Tomato: GEVES; COBORU; NÉBIH; INIA; DGAV and CREA.
- The Beijing Sub-Center for DUS testing (CAAS) in China, the Korean Seed & Variety Service from the Republic of Korea and the Center for Seeds and Seedlings, NARO (NCSS) in Japan participate on their own fundings.
- Euroseeds is also partner to the project.
- Results expected to be available in 2021.
- If successful → follow-up project for the complete characterization of the collection and the application of the markers to its management following UPOV model (e.g. French bean approach)

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On going IMODDUS projects

Hemp

"*Development of a SNP marker set in Cannabis to support DUS testing*"

- Context: importing plant material for DUS testing of pharmaceutical varieties is particularly demanding in terms of time and money, which creates reluctance of titleholders to submit reference varieties.
- Aim : identifying a SNP marker set for Cannabis to help identify precisely what reference varieties are needed for the testing (French bean model) and limit the request for materials.
- Coordinator : Naktuinbouw (NL), partner : NEBIH (HUN)
- The project started in 2020 and will last 24 months.
- If successful → follow-up project for the complete characterization of the collection and potential application of the markers following UPOV model (e.g. French bean approach)

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On going IMODDUS projects

Oilseed rape

"*Developing a strategy to apply SNP molecular markers in the framework of winter oilseed rape DUS testing*."

- Granted co-financing in March 2019.
- Goordinated by GEVES (FR), Bundessortenamt (GER) as project partner.
- Follow up project of an earlier project which validated a set of SNP markers for KasPAR assay on bulk samples as a tool for the management of the reference collection (concluded in 2018).
- Aims at developing a method to use genetic data in the two different testing systems GAIA in France and COY in Germany in the framework of existing or new UPOV models.
- Before the end of the project, all EU entrusted examination offices will be invited to discuss the outcome of the project results and prepare a 2nd follow-up to extend the genotyping to the whole collections.
- Expected to be finalized in 2021.

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On going IMODDUS projects

Apple

"*Developing molecular markers allowing the distinction of apple mutants (sports)"*

- Granted co-financing in March 2018
- coordinator : INRA-IRHS (FR), project partner : GEVES (FR)
- expected to be finalised in October 2021 (18 months extension due to Covid19)

- Evaluation of differences between 7 Gala mutants (2 trees on 2 years) :

1. Standardized phenotyping of fruit color on the basis of hyperspectral images recorded automatically from conveyer machines: intensity, surface, stripes and metabolites (anthoc.)
2. Whole genome sequencing to detect genetic differences (SNPs, TEs, indels, copy number variations)
3. Epigenetic differences assessed genome-wide at the DNA methylation level (DMRs)
4. Tanscriptomic data (RNA sequencing on apple skin) to identify differentially expressed genes

→ identification of genes potentially involved in the phenotypic changes of mutants

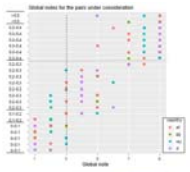
On going IMODDUS projects

Durum wheat

"*Integration of molecular data into DUS testing in Durum wheat* "

- Aim: Efficient management of reference collections
- Granted co-financing in December 2017
- Coordinator : Austrian Agency for Health and Food Safety (AGES)
- Project partners are INIA (ES), GEVES (FR) CREA – SCS (IT), NÉBIH (HU)
  = all CPVO entrusted Examination Offices.
- Expected to be finalised end 2020

Threshold for genetic distance identified according to the maize approach (visual appreciation by experts of a set of variety pairs with defined GD):
Modified Rogers distance = 0.3



(8.194 high quality SNPs from Illumina 25K array from TraitGenetics, tested on ~600 varieties)

- call for tender SFS-29 of Horizon 2020 programme on "Innovation in plant variety testing" in 2017.

- "INnovations in plant VarIety Testing in Europe to foster the introduction of new varieties better adapted to varying biotic and abiotic conditions and to more sustainable crop management practices"
  - Duration : 60 months
  - Budget : 8 Million euros
  - Aim : improving both efficiency of variety testing and availability of information to stakeholders on variety performance under a range of production conditions and biotic and abiotic stresses.

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Species

7 "model" crops :

maize, wheat, rye grass, sunflower, potato, tomato, apple

+ 3 "application" crops :

lucerne, soybean, rapeseed

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Technical approaches

High throughput phenotyping tools to speed up observations and provide detailed and accurate phenotypic data.

Genomic data for :

- new sets of molecular markers to improve the management of reference collections for DUS testing (reduce the number of reference varieties used in the field when a candidate variety is tested).

- new markers linked to a range of phenotypic traits to accelerate the assessment of certain DUS characteristics."

Modelling to make prediction of variety behaviour in various environments.

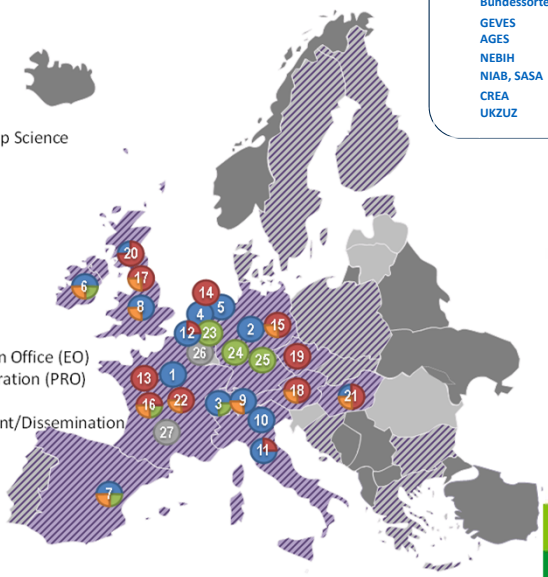
Consortium (29 partners)

INVITE
CPVO Network of EOs

Non-profit
1 – INRA
2 – UH
3 – FiBL
4 – WU
5 – DLO
6 – Teagasc
7 – IRTA
8 – JHI
9 – Agroscope
10 – RCL
11 – CREA
12 – CRA-W
13 – CPVO
14 – Naktuinbouw
15 – BSA
16 – GEVES
17 – NIAB
18 – AGES
19 – UKZUZ
20 – SASA
21 – NEBIH
22 – ACTA

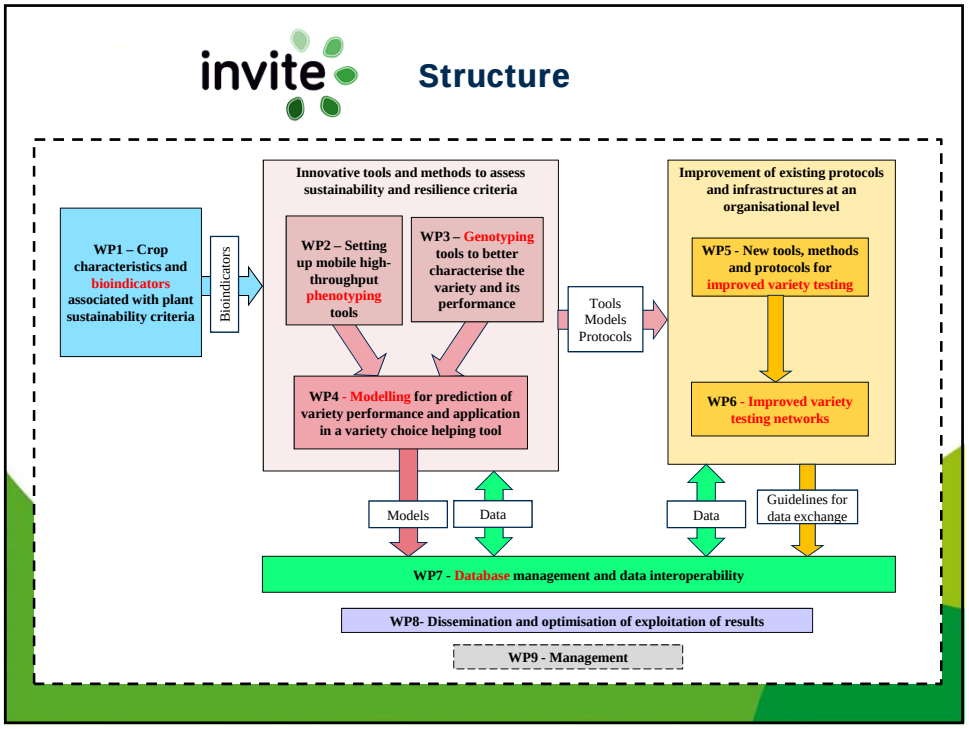
Industry
23 – ESA
24 – NPZ
25 – Bayer Crop Science
26 – ARCADIA
27 – IT

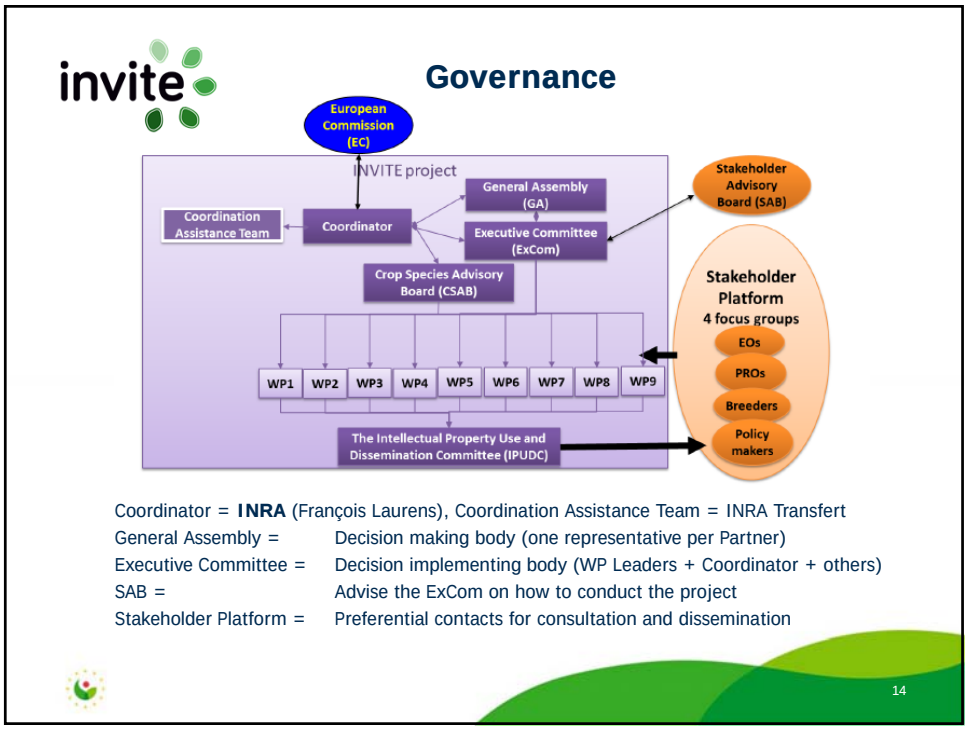
Activities
- Research
- Examination Office (EO)
- Post-Registration (PRO)
- Breeding
- Management/Dissemination



EOs

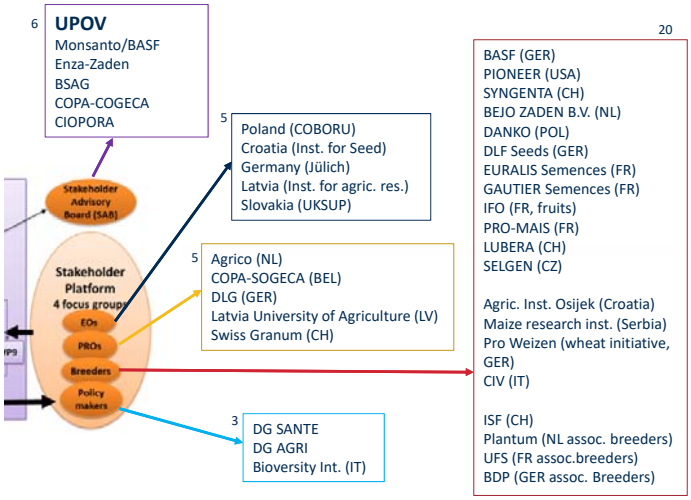
CPVO	EU
CRA-W, ILVO	BE
Naktuinbouw	NL
Bundessortenamt	GER
GEVES	FR
AGES	AU
NEBIH	HU
NIAB, SASA	UK
CREA	IT
UKZUZ	CZ





Coordinator = **INRA** (François Laurens), Coordination Assistance Team = INRA Transfert
General Assembly = Decision making body (one representative per Partner)
Executive Committee = Decision implementing body (WP Leaders + Coordinator + others)
SAB = Advise the ExCom on how to conduct the project
Stakeholder Platform = Preferential contacts for consultation and dissemination

Stakeholders
(39 representatives)



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WP3: Genotyping tools to characterize varieties and their performance

Karl Schmid (University of Hohenheim, Germany)

- **Task 3.1: Genome wide marker sets for distinguishing heterogeneous and open pollinated varieties PRG (TEAGASC, INRA, Agroscope, GEVES, CPVO, BioSS)**
- **Task 3.2: Genome wide marker sets for line and hybrid varieties**
  WHEAT, MAIZE, SOYBEAN (UHOH, NIAB, INRA, GEVES, CPVO)
- **Task 3.3: Identification of specific markers for DUS related traits and development of genotyping assays using these markers**
  POTATO, TOMATO, APPLE (NIAB, INRA, GEVES, CPVO, WU)
- **Task 3.4: GWAS mapping and genomic prediction of DUS traits**
  WHEAT, MAIZE, PRG, SOYBEAN (UHOH, NIAB, INRA, BioSS)
- **Task 3.5: Improved models for marker-based evaluation of D and U**
  WHEAT, MAIZE, PRG, SOYBEAN (UHOH, BioSS)

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WP5: Integration of new methods and tools in advanced variety testing protocols and demonstration in field trials

Aurélia GOULEAU (GEVES, France)
Cécile COLLONNIER (CPVO)

- **Task 5.1: Demonstration in field test conditions of the applicability of phenotypic tools**
- **Task 5.2: New procedures using molecular tools for optimization of DUS testing management of reference collection and direct evaluation of specific traits.**
- **Task 5.3: Development and proposals of new protocols to integrate the sustainability and resilience criteria for specific traits linked to biotic and abiotic stresses through multi criteria evaluation under conventional and organic cropping**

- **Task 5.2: New procedures using molecular tools for optimization of DUS testing management of reference collection and direct evaluation of specific traits.**

Related WP: WP1, WP3	Wheat	Rye-grass	potato	apple	tomato	Soy bean	lucerne
Management of reference collection	GEVES, IRTA, CREA, AGES, NIAB M24-M36 WP3 → set of molecular markers (M24)	BIOSS, ILVO, NIAB, NAKT, TEAGASC M24-M36 WP3 → set of molecular markers (M24)					GEVES, INRA, CREA M24-M48 Eucleg → ?
Certification	GEVES, ACTA M24-M36 WP3 → set of molecular markers (M24)						
Molecular markers linked to traits of interest			SASA, NAKT: disease M36-M48 WP3 → Gene specific markers (M36)	ACTA, IRTA,: disease M36-M48 WP3 → Gene specific markers (M36)	GEVES, CREA NAKT: disease M18-M36	CREA, : drought M1-M30	
Epigenetic markers				ACTA, GEVES: color M46-M52 WP1→ Epigenetic bioindicators (M54)			
Reflexion on the integration of molecular markers and on the use of statistical approaches to describe varieties and to address uniformity issues for variety testing M40-M52 WP3 → Novel marker-based method (M48)							

Thanks for your attention !

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[End of Annex and of document]