

Technical Working Party on Automation and Computer Programs TWC/36/12 Rev.**Thirty-Sixth Session**
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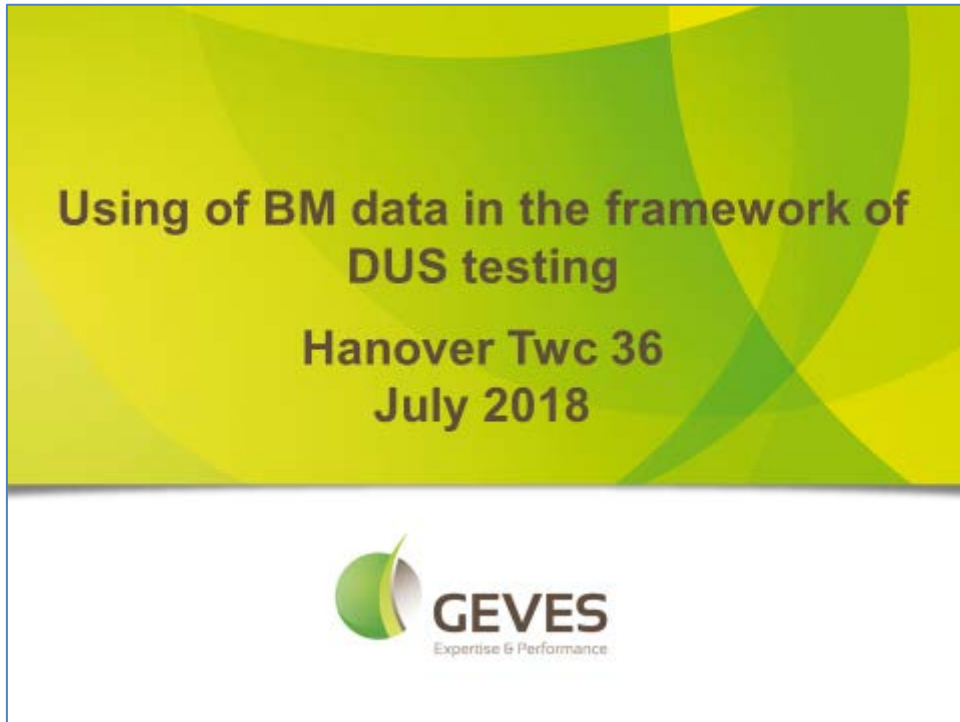
**STATISTICAL METHODS AND SOFTWARE TOOLS FOR MOLECULAR TECHNIQUES IN
DUS EXAMINATION***Document prepared by an expert from France**Disclaimer: this document does not represent UPOV policies or guidance*

The Annex to this document contains a copy of a presentation on “Statistical methods and software tools for molecular techniques in DUS examination”, made at the thirty-sixth session of the Technical Working Party on Automation and Computer Programs (TWC).

[Annex follows]


STATISTICAL METHODS AND SOFTWARE TOOLS FOR MOLECULAR TECHNIQUES IN
DUS EXAMINATION

Presentation prepared by an expert from France

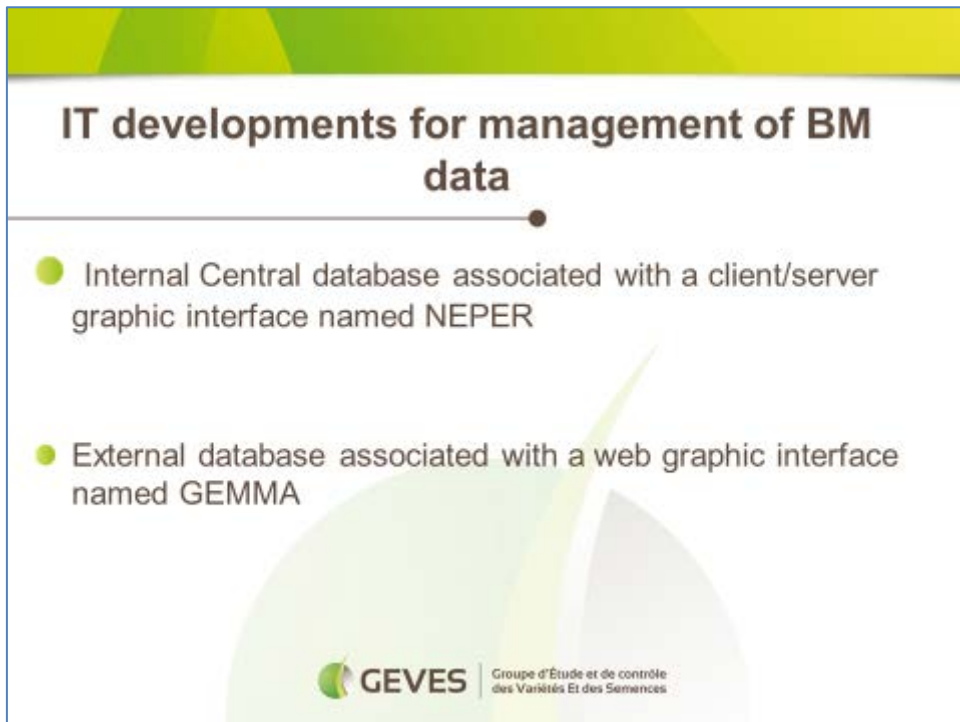


**Using of BM data in the framework of
DUS testing**

**Hanover Twc 36
July 2018**




GEVES
Expertise & Performance



**IT developments for management of BM
data**

- Internal Central database associated with a client/server graphic interface named NEPER
- External database associated with a web graphic interface named GEMMA

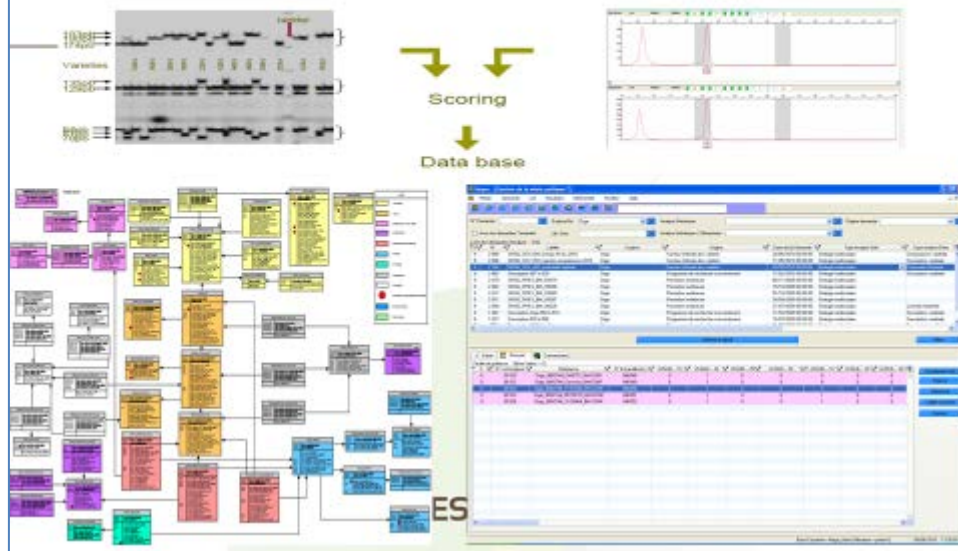


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Internal Central Database NEPER

- Run under Oracle system
- Data model is based on 100 tables
- Database is not accessible from outside
- Concerns around 30 end users
- Store different type of data : Electrophoretic data, chromatographic data, biomolecular data

Internal Central Database NEPER



Internal Central Database NEPER

- Sump up of the data model to focus on storage of BM data

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Internal Central Database NEPER

- BM data are stored as presence or absence of each allele of each locus (large volumes of data, speed of statistical or numerical processes,)
- Up to now, the table that store BM data, reach 30 million lines
- 3 types of markers are stored
 - ISSR (2008)
 - SSR (2008)
 - SNP (2012)

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Internal Central Database NEPER

- Summary on SSR marker

Start Year	End Year	Nb Data	Specie
2009	2018	2427270	Wheat
2007	2018	2022815	Maize
2008	2018	1327179	Sunflower
2008	2018	863531	Barley
2012	2017	779773	Apricot
2010	2018	538529	Pea
2013	2017	386243	Cabbage
2014	2018	335723	Apple
2010	2018	327569	Date Palm
2010	2014	245231	Lettuce
2010	2016	191839	Peach
2008	2018	136412	Rapessed
2015	2017	114415	Pear
2010	2014	113436	Sorghum
2017	2017	89507	Walnut
2015	2017	47502	Cherry
2011	2018	33275	Strawberry
2016	2017	23765	Hazelnut
2010	2016	16580	Triticale
2017	2017	10079	Bean

- Summary on SNP marker

Start Year	End Year	Nb Data	Specie
2011	2018	8602388	Maize
2013	2017	980120	Sorghum
2017	2017	57368	Rapeseed



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External Database GEMMA

- We developed in 2010-2011 a technical website "GEMMA" to share DUS data between different couple Specie/Country.
- This development was made in the framework of CPVO R&D project "CPV8648" (Management of peach three reference collections). This project involved 4 countries: Spain, Hungary, Italy and France.
- In 2017, a new CPVO R&D project "Potato III" (Management of Potato reference collections) have been include in GEMMA website. This project involves 9 countries: Germany, Slovakia, Netherlands, Austria, Ireland, United Kingdom, Spain, Poland and Czech Republic.



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External Database GEMMA

The image displays two screenshots of the GEMMA web application. The left screenshot shows a search results page with a table of entries. The right screenshot shows a detailed view of a specific entry with a table of associated data.

Country	Accession	Accession ID	Accession ID	Accession ID	Accession ID	Accession ID	Accession ID	Accession ID	Accession ID
FR	102	102	102	102	102	102	102	102	102
FR	103	103	103	103	103	103	103	103	103
FR	104	104	104	104	104	104	104	104	104
FR	105	105	105	105	105	105	105	105	105
FR	106	106	106	106	106	106	106	106	106
FR	107	107	107	107	107	107	107	107	107

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Main uses of BM data in the framework of DUS testing

- Computation of genetic distance to be used in the combined approach with morphological distance through the GAIA software

DATABASE

➔

BM DISTANCE

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Main uses of BM data in the framework of DUS testing : Assesment of hybrid conformity

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
		Non Varietal	Type Varietal	S	N°LotSEB	S	N°Cultivar								
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To conclude

- Single database of BM data ? (Pluto, VarietyFinder, ...)
- Type of BM data ? (Genetic distance, DNA profil,)
- Storage format of BM data ?
- Harmonization of referential data ? (locus, allele, marker, ...)
- Strong link between differents information system ?
- Data access methods ? (Text file, Webservice, ...)

Thanks for your attention



[End of annex and of document]