International Union for the Protection of New Varieties of Plants

E

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

BMT/16/9 Rev.

Sixteenth Session
La Rochelle, France, November 7 to 10, 2017

Original: English
Date: November 9, 2017

THE USE OF MOLECULAR DISTANCE AS A CHARACTERISTIC? ASSESSMENT OF THE REFERENCE VARIETY MODEL BASED ON GEVES SNP MAIZE DATA

Document prepared by experts from France

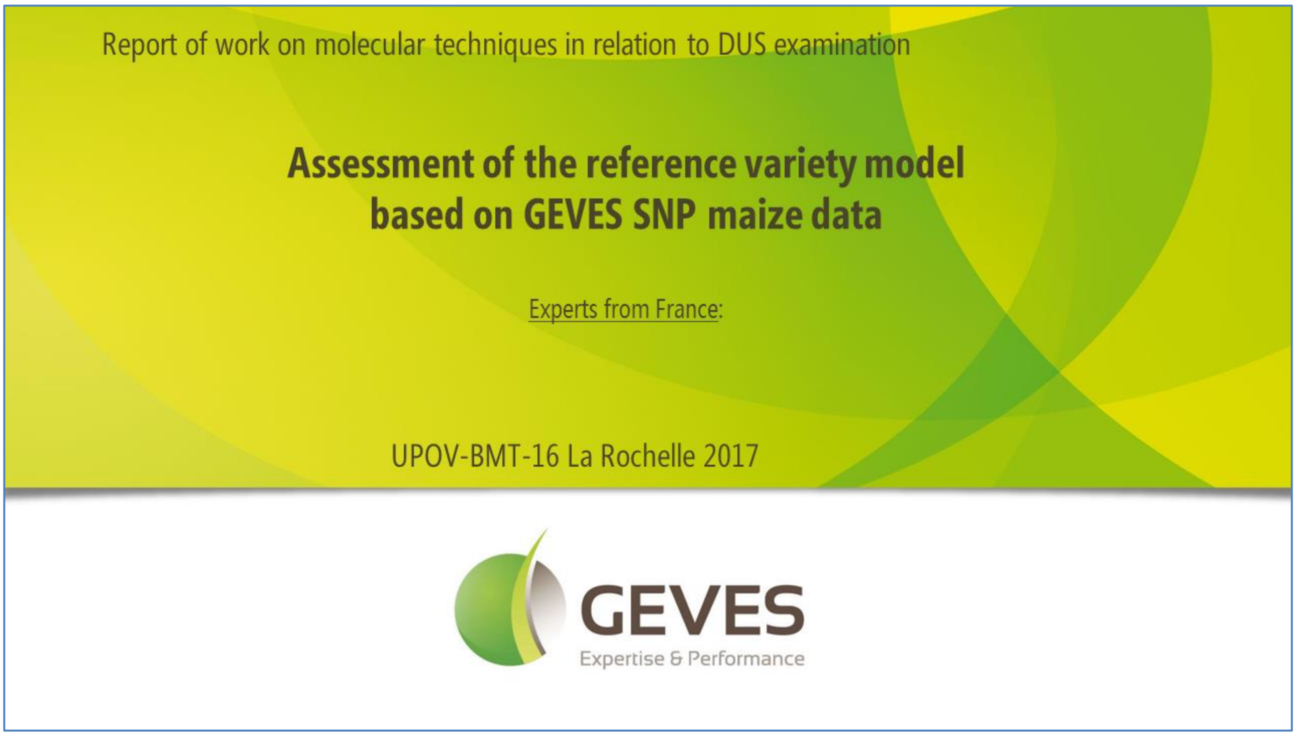
As a follow up to the previous presentations by the American Seed Trade Association (ASTA) (document BMT/14/5 “The Use of Reference Varieties in Varietal Distinction: an Approach under Investigation in the US for Potential Application in Plant Variety Protection”), and the Netherlands (document BMT/15/22 Rev “Can Molecular Distance be used as Characteristic?”), we are testing this new concept based on genetic distances to so called “reference” varieties. Our study explores different calculations to transform genetic distances into characteristics and highlights some consequences of the potential use of this approach in DUS examination.

[Annex follows]

ANNEX

THE USE OF MOLECULAR DISTANCE AS A CHARACTERISTIC? ASSESSMENT OF THE REFERENCE VARIETY MODEL BASED ON GEVES SNP MAIZE DATA

Presentation prepared by experts from France



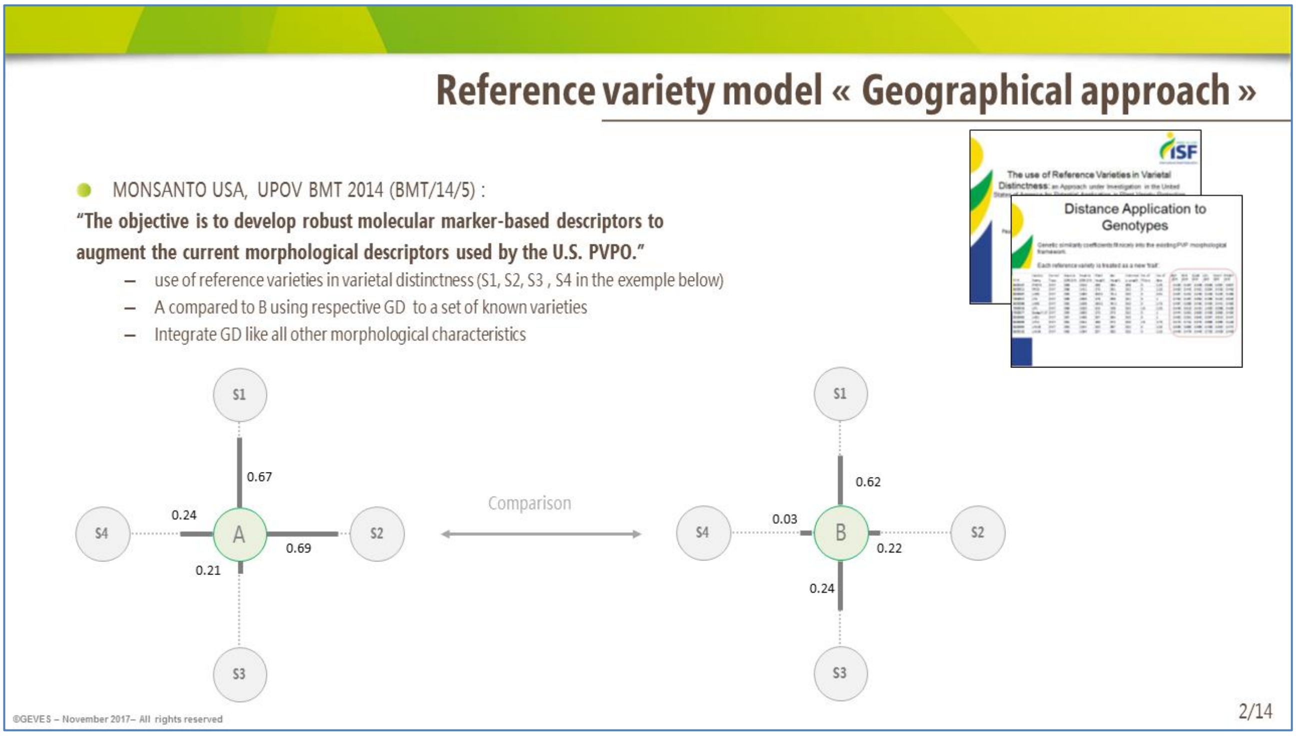
Report of work on molecular techniques in relation to DUS examination

Assessment of the reference variety model based on GEVES SNP maize data

Experts from France:

UPOV-BMT-16 La Rochelle 2017

GEVES
Expertise & Performance



Reference variety model « Geographical approach »

- MONSANTO USA, UPOV BMT 2014 (BMT/14/5) :

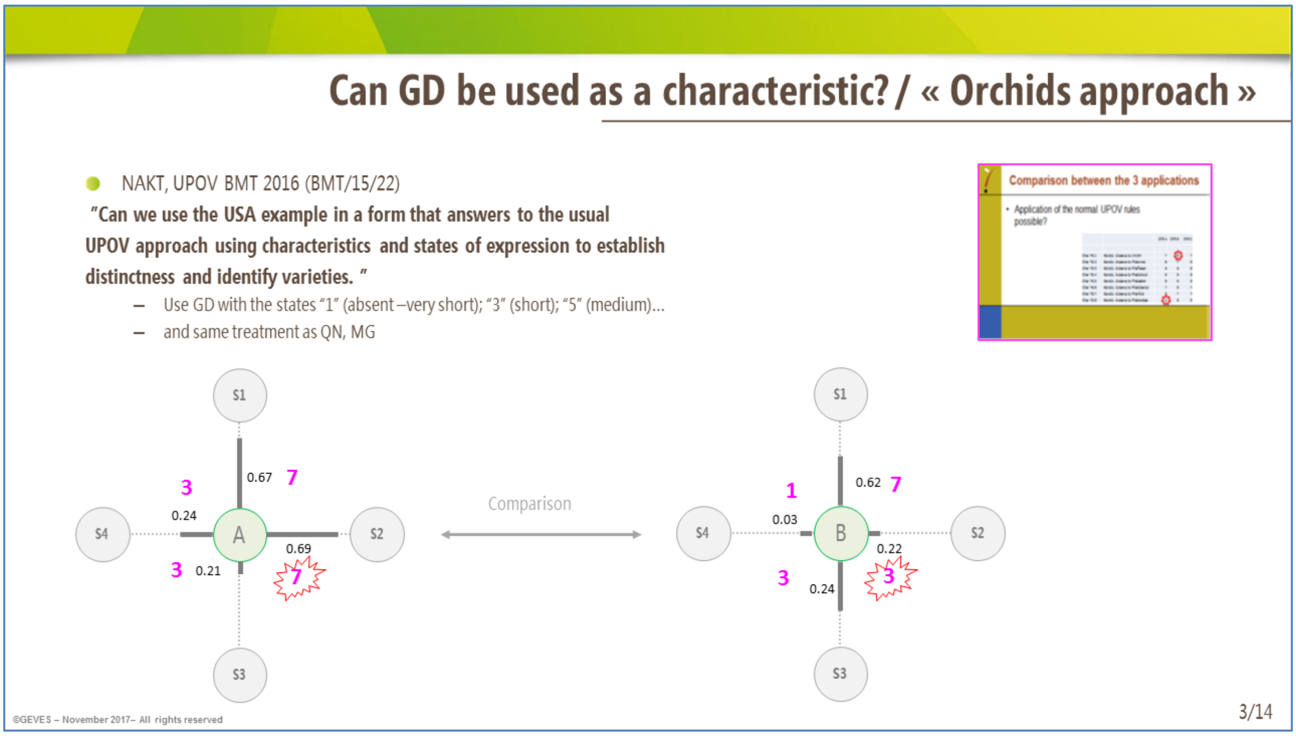
“The objective is to develop robust molecular marker-based descriptors to augment the current morphological descriptors used by the U.S. PVPO.”

  - use of reference varieties in varietal distinctness (S1, S2, S3 , S4 in the exemple below)
  - A compared to B using respective GD to a set of known varieties
  - Integrate GD like all other morphological characteristics

ISF

The use of Reference Varieties in Varietal Distinctness: an Approach under Investigation in the United

Distance Application to Genotypes



Can GD be used as a characteristic? / « Orchids approach »

- NAKT, UPOV BMT 2016 (BMT/15/22)

"Can we use the USA example in a form that answers to the usual UPOV approach using characteristics and states of expression to establish distinctness and identify varieties. "

- Use GD with the states "1" (absent –very short); "3" (short); "5" (medium)…
- and same treatment as QN, MG

Comparison between the 3 applications

- Application of the normal UPOV rules possible?

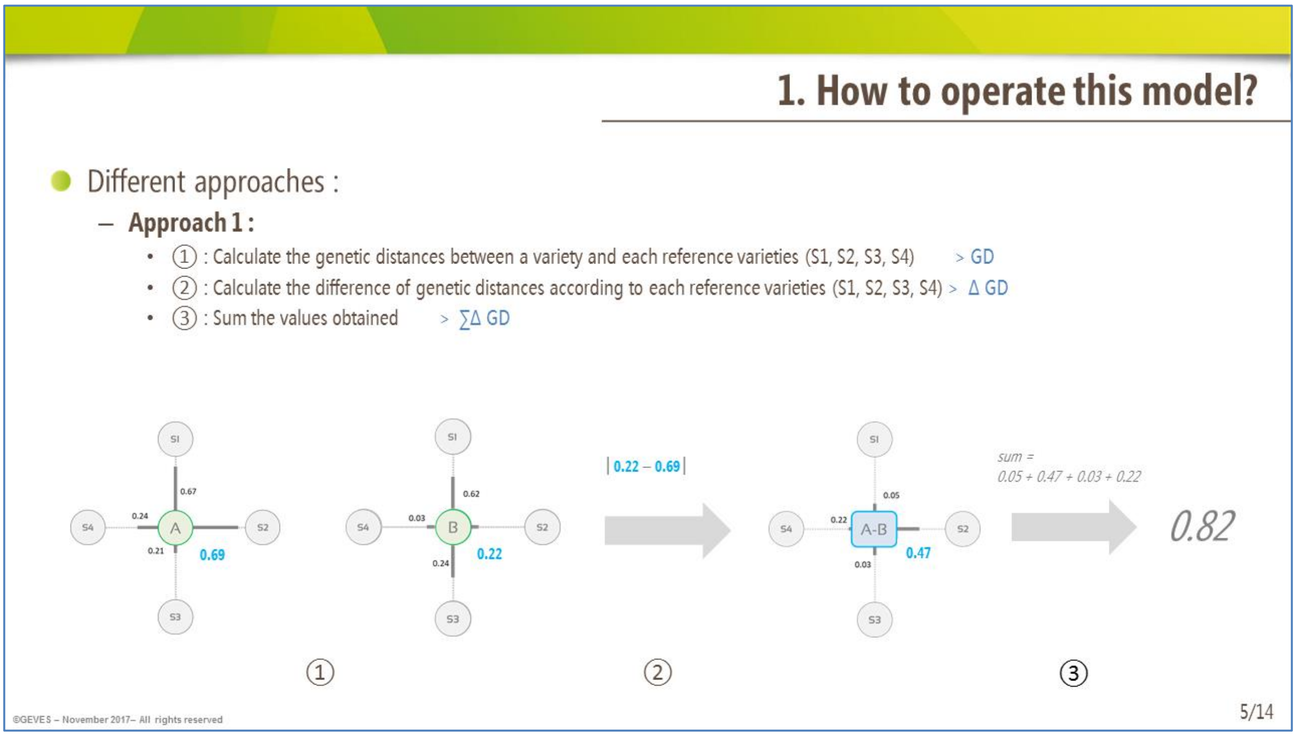
Approach assessment

- Using GEVES SNP data already available on Maize

> First of all :

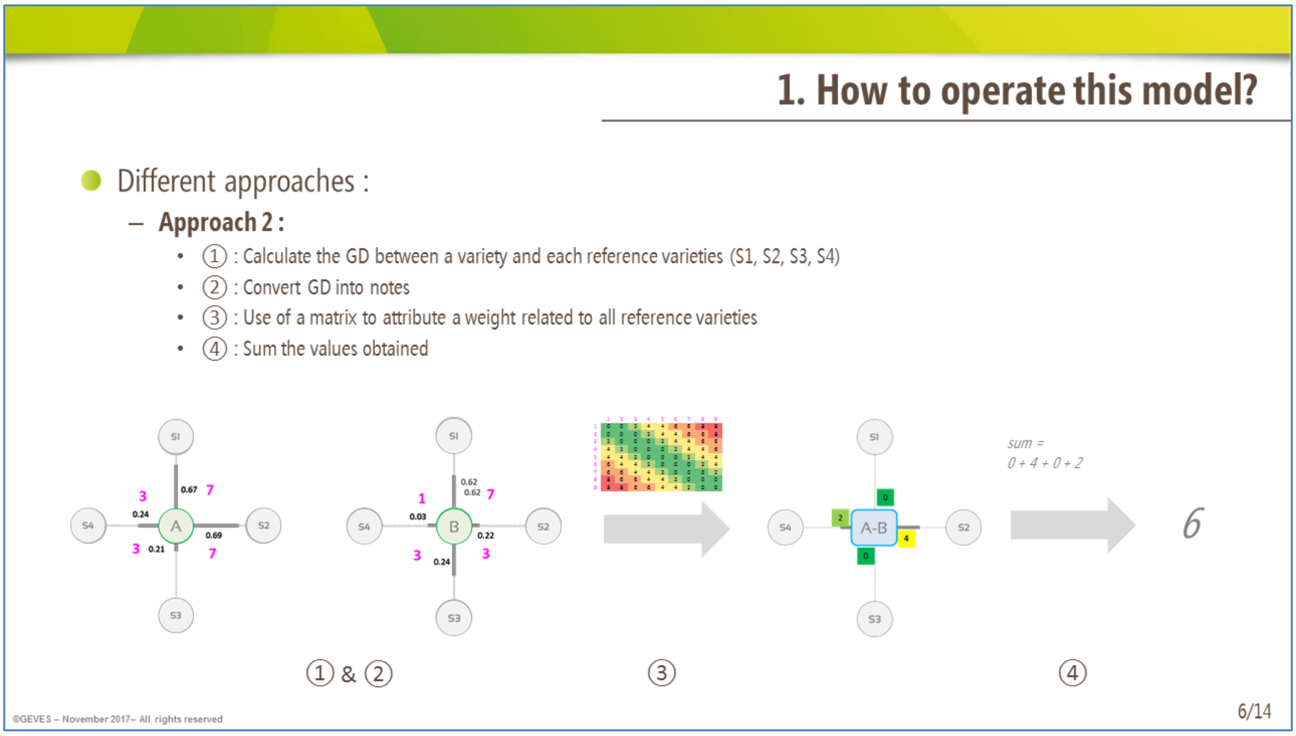
1. How to operate this model?
2. Which parameters may have an impact on the results ?
3. How to evaluate and test the approach?

➡ Then first simulations …



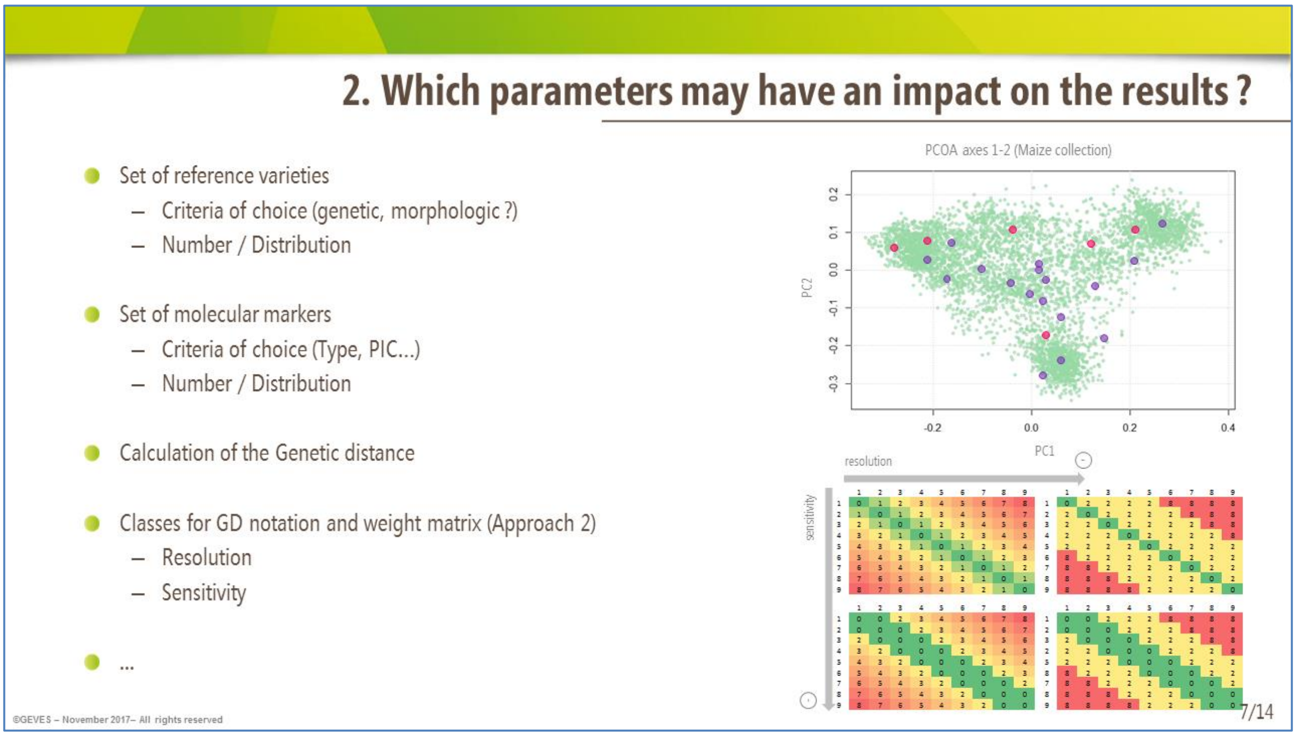
1. How to operate this model?

- Different approaches :
  - **Approach 1 :**
    - ① : Calculate the genetic distances between a variety and each reference varieties (S1, S2, S3, S4) > GD
    - ② : Calculate the difference of genetic distances according to each reference varieties (S1, S2, S3, S4) > Δ GD
    - ③ : Sum the values obtained > ∑Δ GD



1. How to operate this model?

- Different approaches :
  - **Approach 2 :**
    - ① : Calculate the GD between a variety and each reference varieties (S1, S2, S3, S4)
    - ② : Convert GD into notes
    - ③ : Use of a matrix to attribute a weight related to all reference varieties
    - ④ : Sum the values obtained



2. Which parameters may have an impact on the results ?

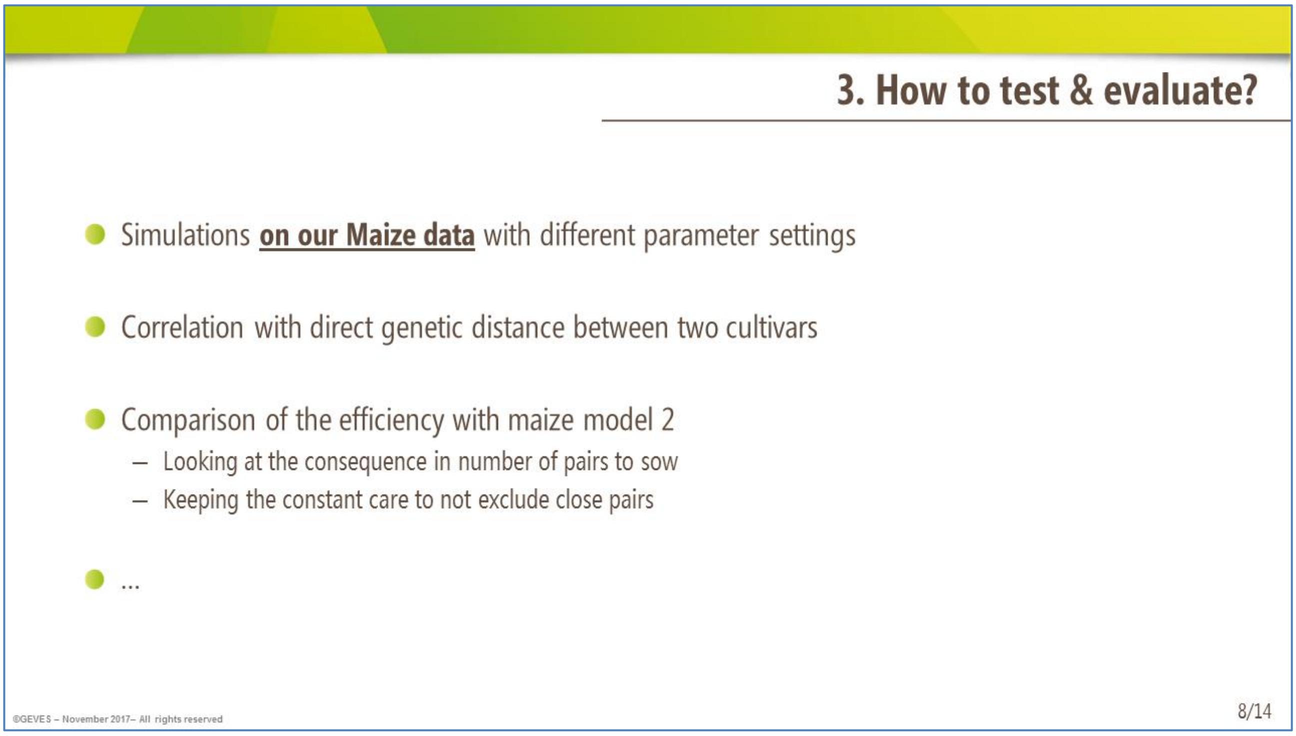
- Set of reference varieties
  - Criteria of choice (genetic, morphologic ?)
  - Number / Distribution
- Set of molecular markers
  - Criteria of choice (Type, PIC…)
  - Number / Distribution
- Calculation of the Genetic distance
- Classes for GD notation and weight matrix (Approach 2)
  - Resolution
  - Sensitivity
- …

	1	2	3	4	5	6	7	8	9
1	0	1	2	3	4	5	6	7	8
2	1	0	1	2	3	4	5	6	7
3	2	1	0	1	2	3	4	5	6
4	3	2	1	0	1	2	3	4	5
5	4	3	2	1	0	1	2	3	4
6	5	4	3	2	1	0	1	2	3
7	6	5	4	3	2	1	0	1	2
8	7	6	5	4	3	2	1	0	1
9	8	7	6	5	4	3	2	1	0

	1	2	3	4	5	6	7	8	9
1	0	2	2	2	2	8	8	8	8
2	2	0	2	2	2	2	8	8	8
3	2	2	0	2	2	2	2	8	8
4	2	2	2	0	2	2	2	2	8
5	2	2	2	2	0	2	2	2	2
6	8	2	2	2	2	0	2	2	2
7	8	8	2	2	2	2	0	2	2
8	8	8	8	2	2	2	2	0	2
9	8	8	8	8	2	2	2	2	0

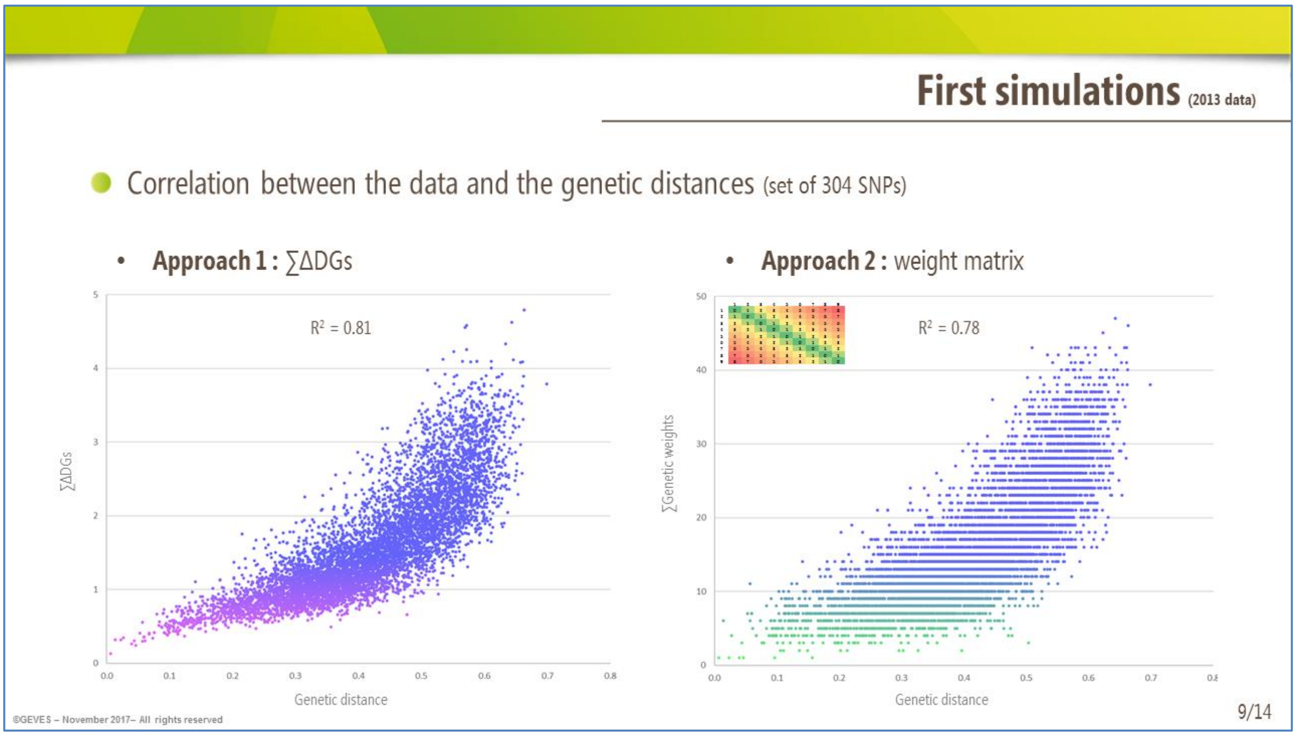
	1	2	3	4	5	6	7	8	9
1	0	0	2	3	4	5	6	7	8
2	0	0	0	2	3	4	5	6	7
3	2	0	0	0	2	3	4	5	6
4	3	2	0	0	0	2	3	4	5
5	4	3	2	0	0	0	2	3	4
6	5	4	3	2	0	0	0	2	3
7	6	5	4	3	2	0	0	0	2
8	7	6	5	4	3	2	0	0	0
9	8	7	6	5	4	3	2	0	0

	1	2	3	4	5	6	7	8	9
1	0	0	2	2	2	8	8	8	8
2	0	0	0	2	2	2	8	8	8
3	2	0	0	0	2	2	2	8	8
2	2	2	0	0	0	2	2	2	8
5	2	2	2	0	0	0	2	2	2
8	8	2	2	2	0	0	0	2	2
7	8	8	2	2	2	0	0	0	2
8	8	8	8	2	2	2	0	0	0
9	8	8	8	8	2	2	2	0	0



3. How to test & evaluate?

- Simulations **on our Maize data** with different parameter settings
- Correlation with direct genetic distance between two cultivars
- Comparison of the efficiency with maize model 2
  - Looking at the consequence in number of pairs to sow
  - Keeping the constant care to not exclude close pairs
- …

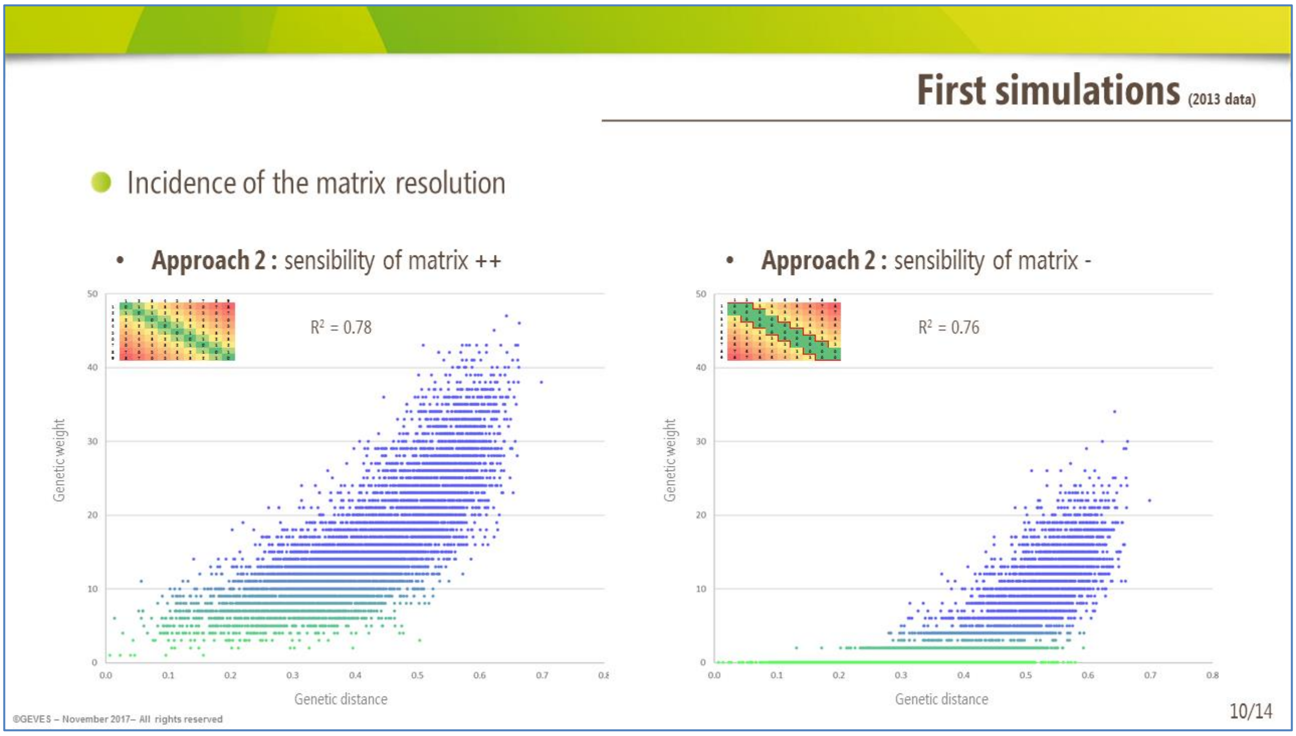


First simulations (2013 data)

- Correlation between the data and the genetic distances (set of 304 SNPs)
  - **Approach 1 :** ∑ΔDGs
  - **Approach 2 :** weight matrix

©GEVES – November 2017– All rights reserved

9/14



First simulations (2013 data)

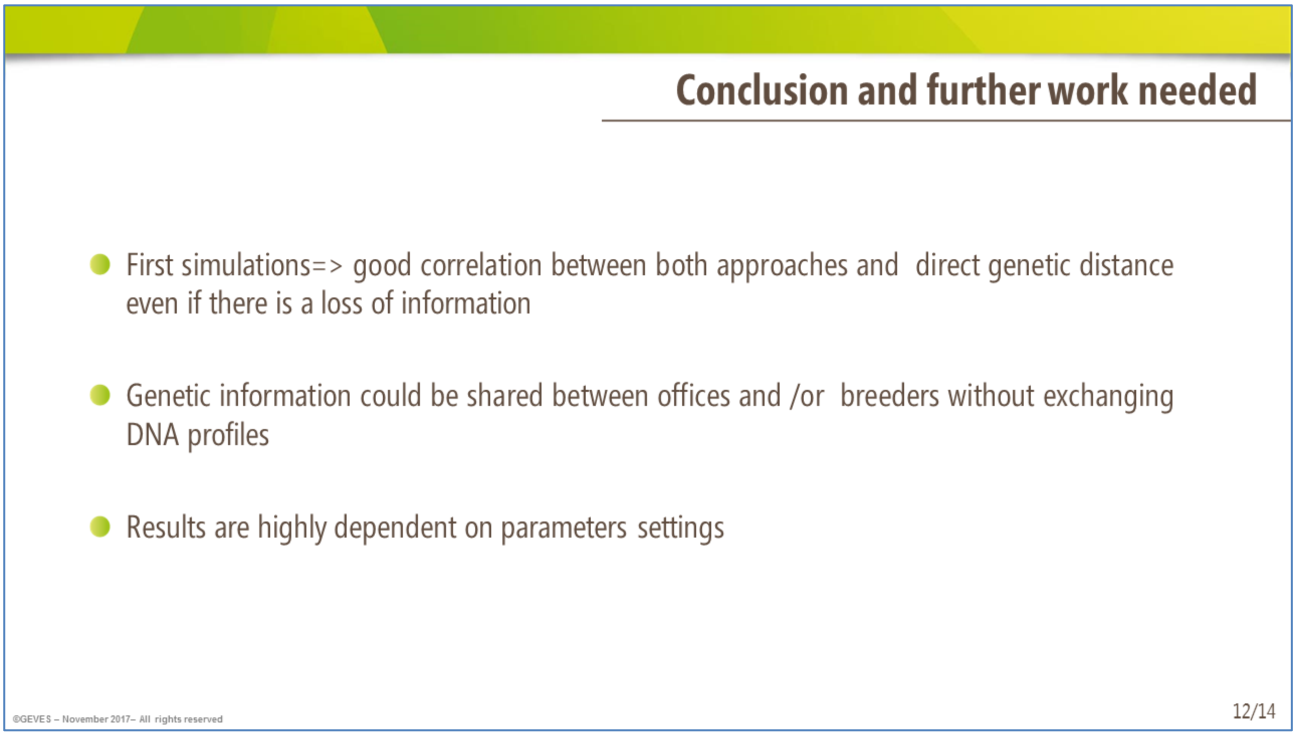
- Incidence of the matrix resolution
  - **Approach 2 :** sensibility of matrix ++
  - **Approach 2 :** sensibility of matrix -

©GEVES – November 2017– All rights reserved

10/14

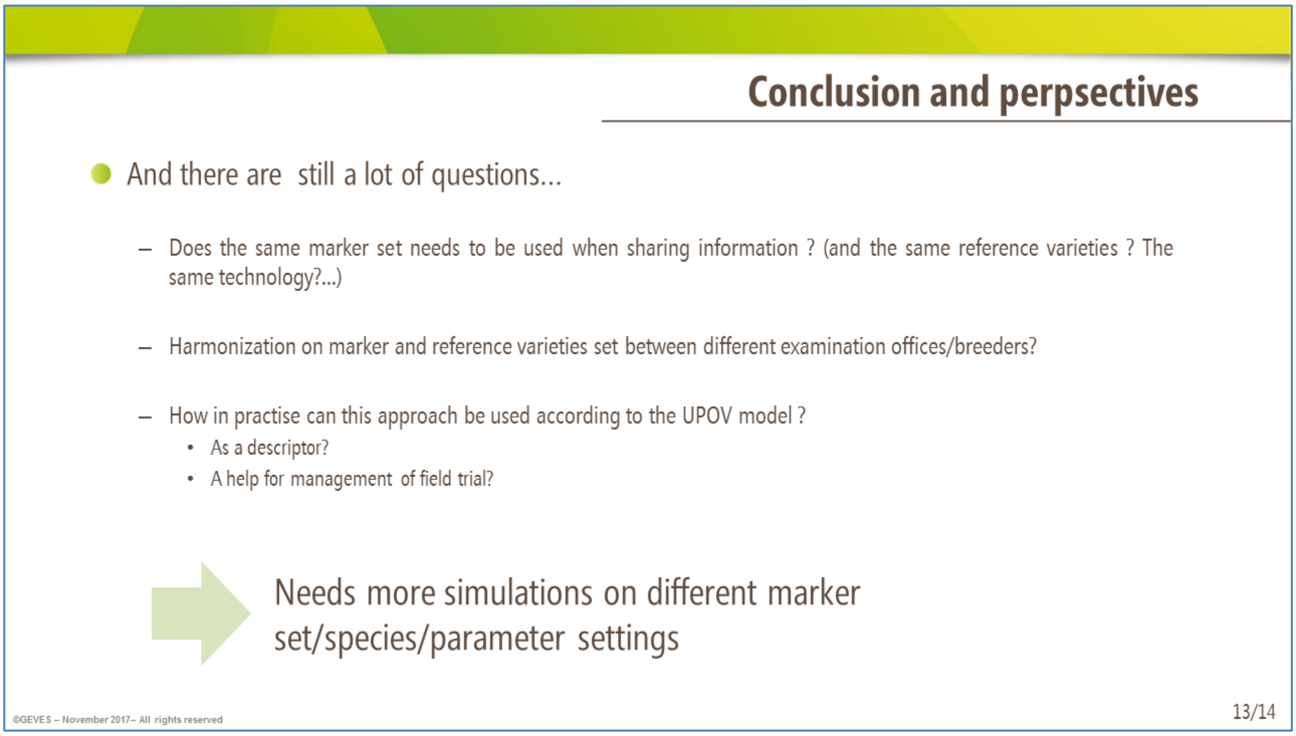
First simulations (2013 data)

- Incidence of the marker set



Conclusion and further work needed

- First simulations=> good correlation between both approaches and direct genetic distance even if there is a loss of information
- Genetic information could be shared between offices and /or breeders without exchanging DNA profiles
- Results are highly dependent on parameters settings



Conclusion and perpsectives

- And there are still a lot of questions…
  - Does the same marker set needs to be used when sharing information ? (and the same reference varieties ? The same technology?...)
  - Harmonization on marker and reference varieties set between different examination offices/breeders?
  - How in practise can this approach be used according to the UPOV model ?
    - As a descriptor?
    - A help for management of field trial?

Needs more simulations on different marker set/species/parameter settings

Many thanks to:

Jehan-Babtiste MAUROUX
Muriel THOMASSET
Anne BERNOLE
Arnaud REMAY
Clarisse LECLAIR

Thank you

GEVES
Expertise & Performance

[End of Annex and of document]