

**Working Group on Biochemical and Molecular Techniques
and DNA-Profiling in Particular****BMT/16/9****Sixteenth Session
La Rochelle, France, November 7 to 10, 2017****Original:** English
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THE USE OF MOLECULAR DISTANCE AS A CHARACTERISTIC? ASSESSMENT OF THE REFERENCE VARIETY MODEL BASED ON GEVES SNP MAIZE DATA*Document prepared by an expert from France**Disclaimer: this document does not represent UPOV policies or guidance*

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]

Report of work on molecular techniques in relation to DUS examination

"The use of molecular distance as a characteristic?
Assessment of the reference variety model based on GEVES SNP maize data"

Experts from France

BMT 2017



« 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 and S4 in the exemple below)
- Integrate GD like all other morphological characteristics



« 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."

- Code the GD and same treatment as QN, MG

Comparison between the 3 applications

Application of the normal SNP rules possible?

SNP	USA	EU	Japan
1	1	1	1
2	1	1	1
3	1	1	1
4	1	1	1
5	1	1	1
6	1	1	1
7	1	1	1
8	1	1	1
9	1	1	1
10	1	1	1
11	1	1	1
12	1	1	1
13	1	1	1
14	1	1	1
15	1	1	1
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95	1	1	1
96	1	1	1
97	1	1	1
98	1	1	1
99	1	1	1
100	1	1	1



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Approach assesment

- Using SNP data already available on Maize

=> But first of all ...

1. How to make it work ?
2. Which parameters can affect results ?
3. How to evaluate and test the approach?

=> And then first simulations

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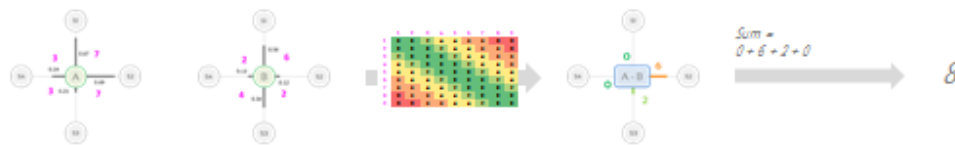
How to make it work ?

- Different approach possibles :

- **Approach 1** : calculate sum of the differences of the genetic distances ($\sum \Delta GD$)



- **Approach 2** : create classes of genetic distance then sum of the weight matrix ($\sum GW$)



- Other Approach: Fingerprinting? Calculate the ΔGD then transform it into weight?

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Which parameters can affect 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 coding and weight matrix: (Approach 2)
 - Resolution
 - Sensitivity
- –



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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
 - In number of pairs to sow
 - Take care to not exclude close pairs
- ...

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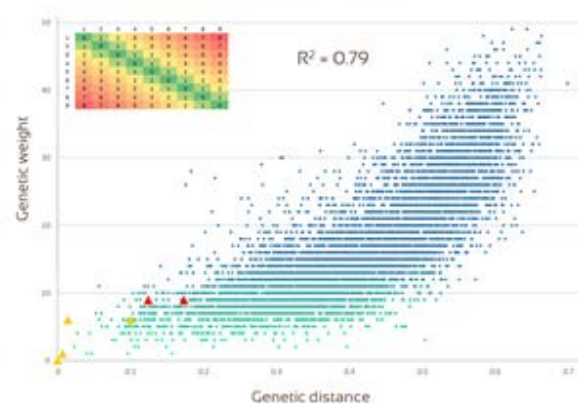
First simulations

- Correlation between the data and the genetic distances (2013 data)

- Approach 1: $\Sigma \Delta DGs$



- Approach 2: weight matrix

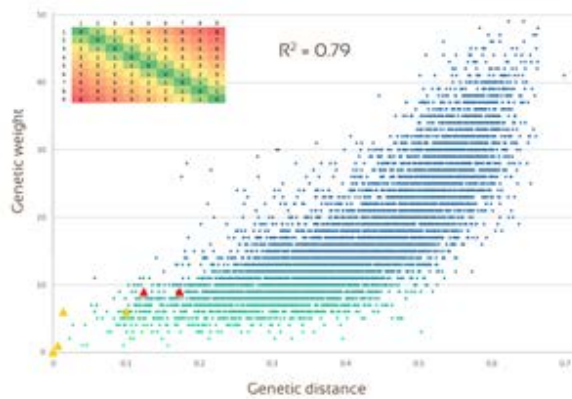


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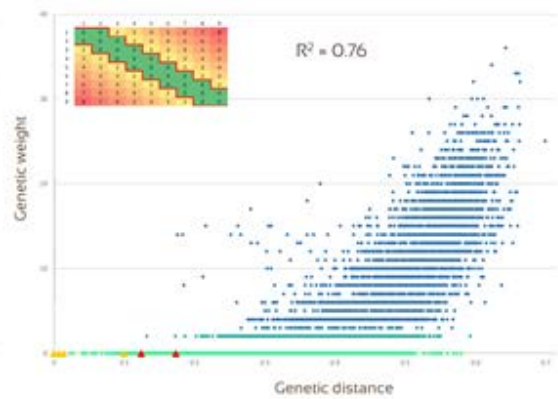
First simulations

- Incidence of the matrix resolution (2013 data)

- Approach 2 : weight matrix (sensitivity +)



- Approach 2 : weight matrix (sensitivity -)



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Conclusion and ongoings

- 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 depend on parameters settings



Need for more simulations on different marker set/
species/parameter settings

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Thank you

[End of Annex and of document]