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

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AN ATTEMPT TO USE MOLECULAR MARKERS FOR WINTER WHEAT REFERENCE COLLECTION MANAGEMENT

Document prepared by an expert from France

1. Some years ago, a set of SSR markers was selected by GEVES in the framework of varietal control. Considering the availability of this set and the large size of the reference collection of winter wheat to manage, GEVES decided to look at the possibility to combine phenotypic and genetic distances for the management of its reference collection. This method had already been developed in France for Spring barley.

2. The results of this study show that, with the current set of markers, the use of genetic distance does not enable the size of field trials to be significantly reduced.

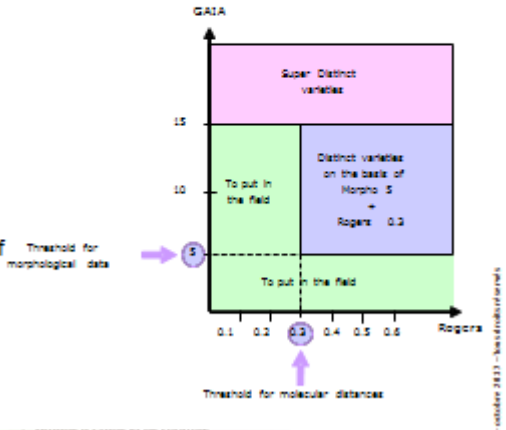
[Annex follows]

An attempt to use molecular markers for winter wheat reference collection management

GEVES
Expertise & Performance

Background on spring barley

- UPOV model 2 already used for spring barley in GEVES since 2013
- 30 SSR markers
- Use of Gaia software
- Add a reduction by 40% (in average) of the number of pairs to grow in the field compared



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Background on spring barley – Example in 2017

12 candidate varieties; 608 varieties in reference collection
= 7218 theorical pairs of varieties to compare side by side on the field.

With morphological data
311 pairs to grow side by side

Decrease of the number of plots and varieties to grow side by side

With morphological + genetic distances
214 pairs to grow side by side

Additional saving of 31% of plots

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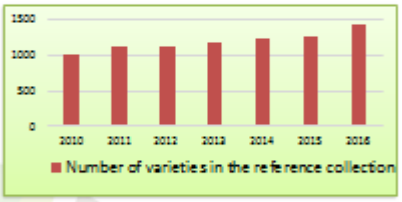
Study on winter wheat

- ✓ High number of varieties in the reference collection, nonstop increasing
- ✓ Increased workload and need for more space to conduct the trials
- ✓ Availability of SSR markers on winter wheat in GEVES

→ Attempt to apply UPOV model 2 on winter wheat



SSR markers set

- Development of a set of 20 SSR markers in GEVES (2002-2006)
- Original aim: Identity control
  → discrimination of all the varieties of the French national list

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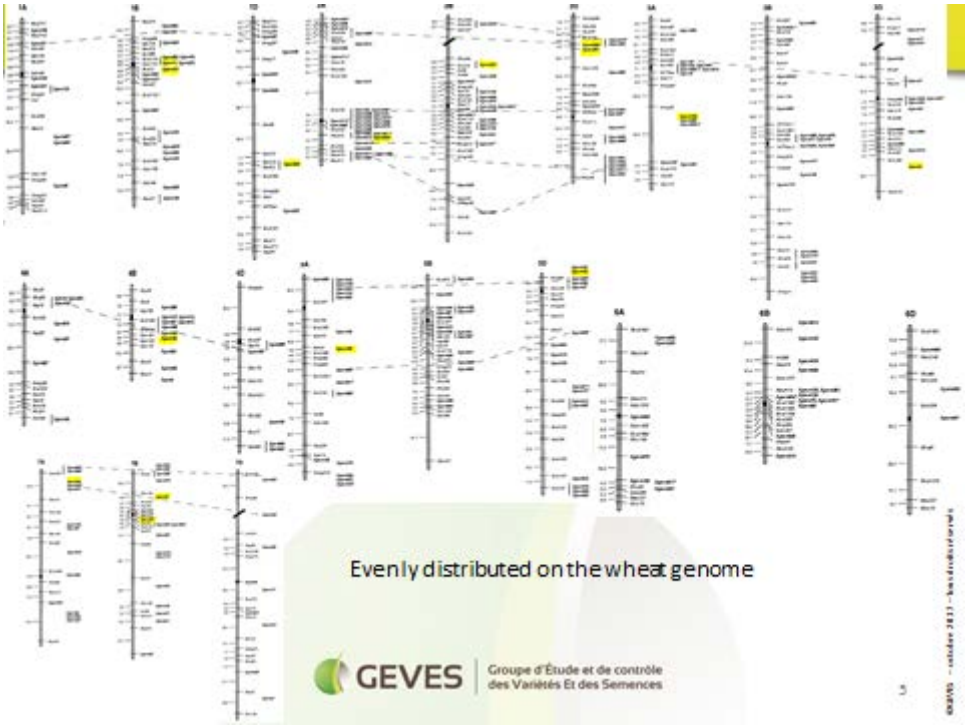
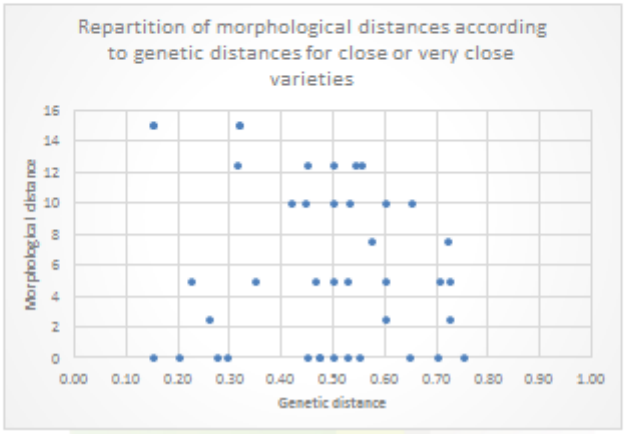


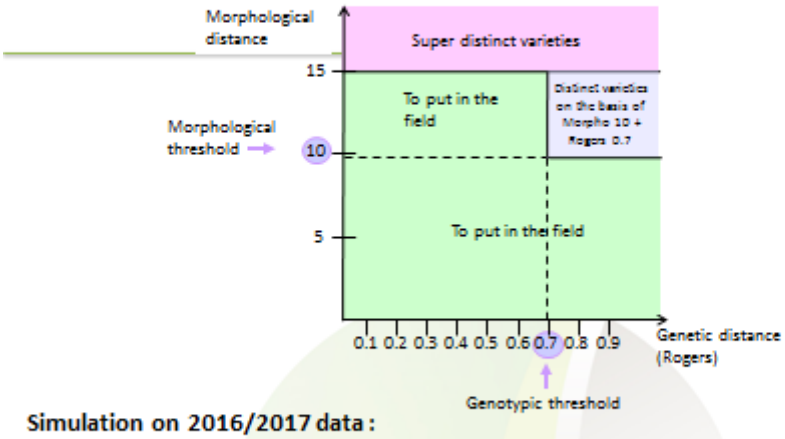
Methodological study

- Aim: to define a genetic distance threshold beyond which no pair of varieties are similar or very close

- Use of rogers genetic distance



Proposal for decisions rules



Simulation on 2016/2017 data :

→ reduction of only 7% of comparisons (out of 1915 comparisons)

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Conclusions

- ✓ Low efficiency compared to the use on spring barley (7% vs 31% in 2017)
  - ➢ Due to the genetic of the specie ?
  - ➢ Due to the current markers set ?
  - ➢ Due to the calibration ?
- ✓ Potential follow-up:
  - ➢ Optimization of the calibration (more data)
  - ➢ Modification of the set (increase the number of SSR markers)
  - ➢ Development and test of SNPs

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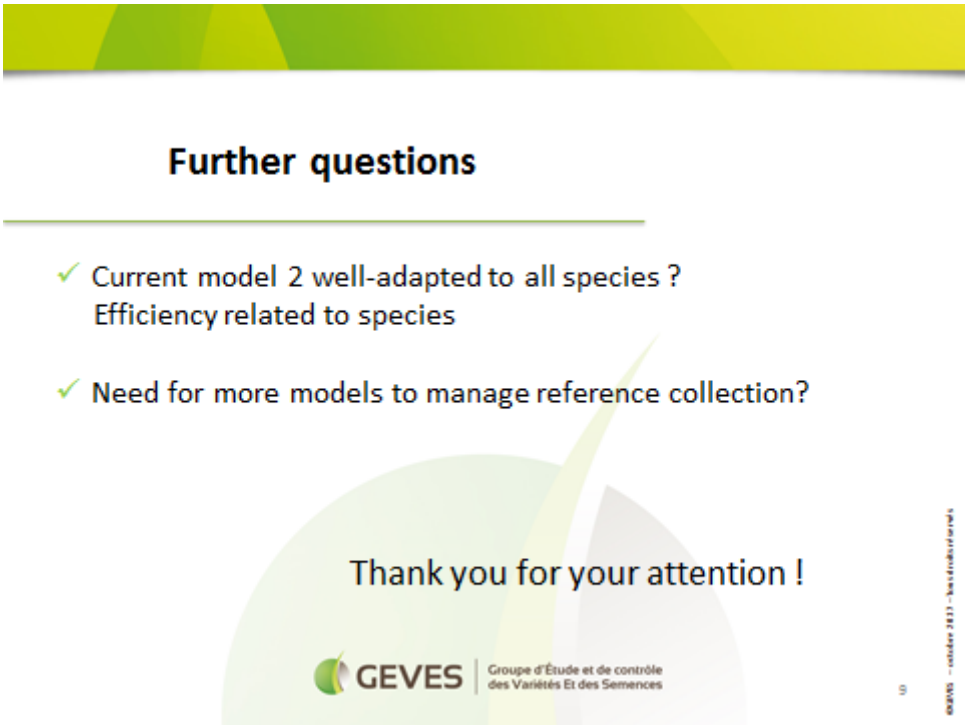

[End of Annex and of document]