

Management of variety collections

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How we use molecular techniques in France

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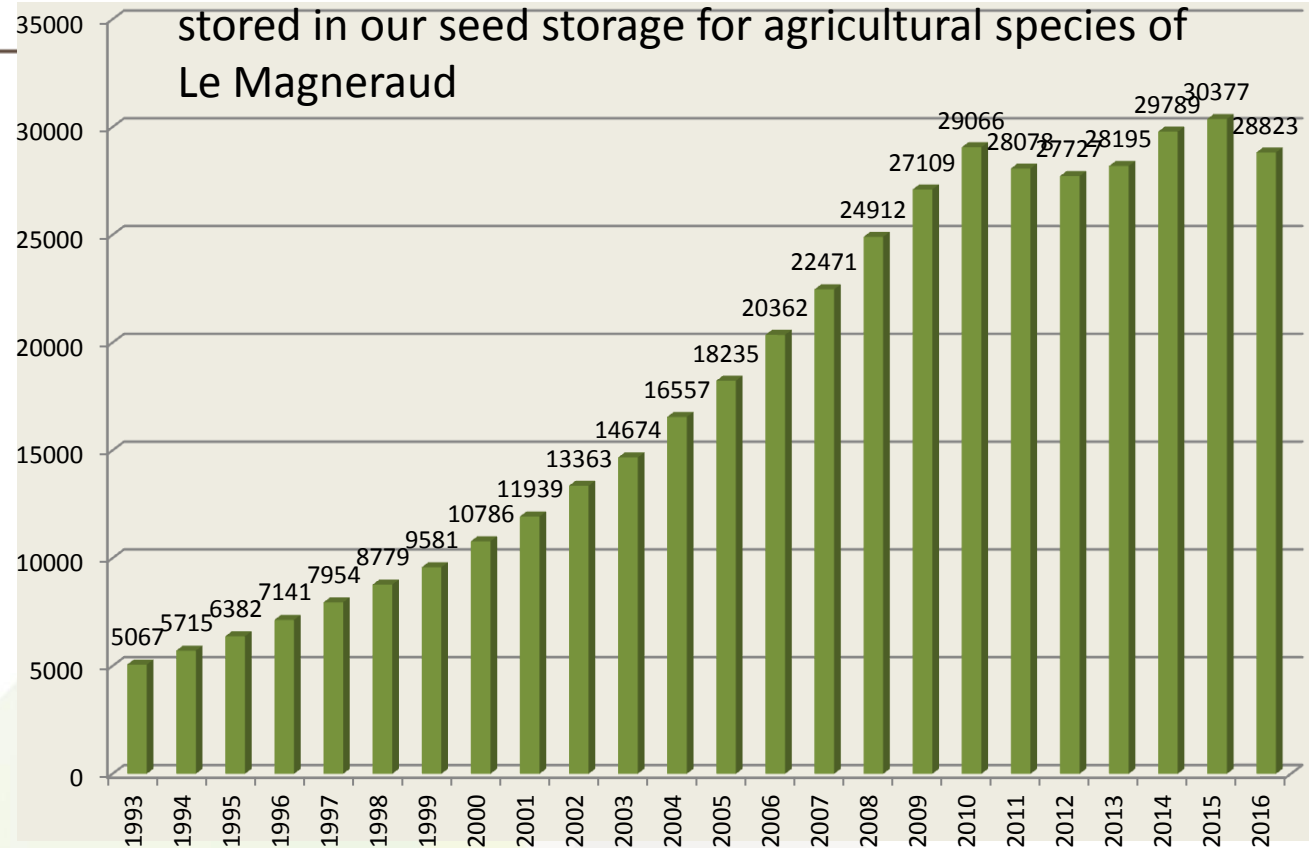
Need for a more efficient management of variety collections

- **Increasing size of the variety collections :**

=> Need to improve the management of the collections

=> Need to develop new tools and procedures

Example of the evolution of the number of varieties stored in our seed storage for agricultural species of Le Magneraud



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One possible option is the use of molecular markers

- Following UPOV guidance TGP/15/1
- The objective is to develop an efficient tool, based on a **combination of phenotypic and molecular distances**, to identify within the variety collection, those varieties which need to be compared with candidate varieties in order to improve the selection of “distinct plus” varieties and so to limit the workload without decreasing the quality of the test. The challenge is to develop a secure system that:
 - (a) only selects varieties which are similar to the candidate varieties; and
 - (b) limits the risk of not selecting a variety in the variety collection which needs to be compared in the field, especially when there is a large or expensive variety collection.



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Combination of morphological distance and genetic distance for the management of reference collection

- Used in routine in GEVES for maize and spring barley
 - On-going projects in GEVES to develop the use on sorghum and wheat
 - Future possible collaborative projects on oilseed rape, durum wheat
- > Mainly used for agricultural species, with large variety collections, with a 2-year DUS test, with 2 testing locations per year in France



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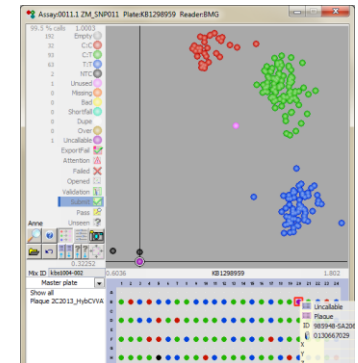
How we use molecular techniques in France for the management of variety collections

First DUS cycle

Description in the field



Description in our lab BIOGEVES



Comparison of the description with our database :

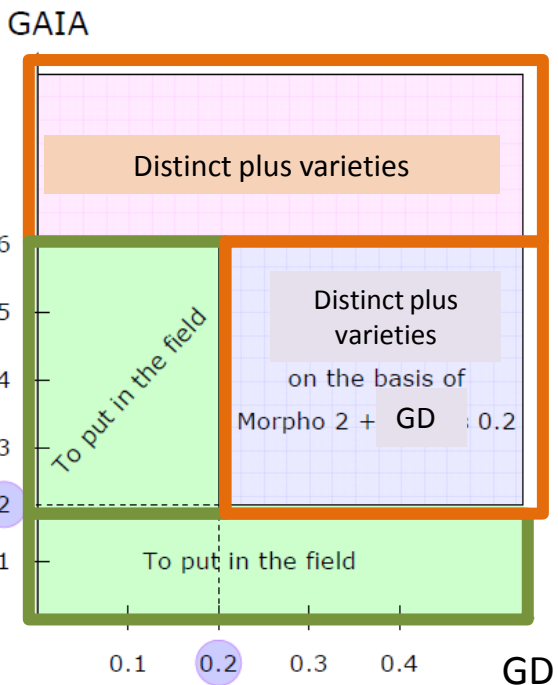
- calculation of morphological distance for each pair of varieties
- calculation of genetic distance for each pair of varieties

Combination of morphological distance and genetic distance in order to decide which pairs of varieties should be compared side by side in the field during second DUS cycle

Combination of morphological distance and genetic distance for the management of reference collection

● 2 steps:

1. Comparison of **Morphological Distances** (notes from 1 to 9)



If MD ≥ 6 Distinct plus varieties

If MD < 2 To put in the field

2. For all pairs with MD between 2 and 6, we look at the **Genetic Distance**

If GD < threshold To put in the field

If GD ≥ threshold Distinct plus varieties

Threshold for morphological data →

↑ Threshold for molecular distances

Exemple of efficiency. Maize inbred lines DUS trial in 2013 :

274 candidate inbred lines ; 3741 inbred lines in the reference collection of GEVES
= **more than 1 million** pairs of lines to compare side by side in the field

With GAIA only morphological data
5266 pairs grown side by side

Reduction in the
number of plots and
varieties grown side
by side in field

With GAIA morphological + isoenzymes data
905 pairs grown side by side

With GAIA morphological + genetic distances
647 pairs grown side by side

An additional reduction of 28 % of
plots grown side by side by switching
from isoenzymes to genetic distances
calculated from SNP markers



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● Conclusion :

- Molecular markers can be an efficient tool to manage variety collections

- Our experience shows efficiency in a 2 year DUS test

Is there an opportunity for a one year DUS test for Distinct + varieties?

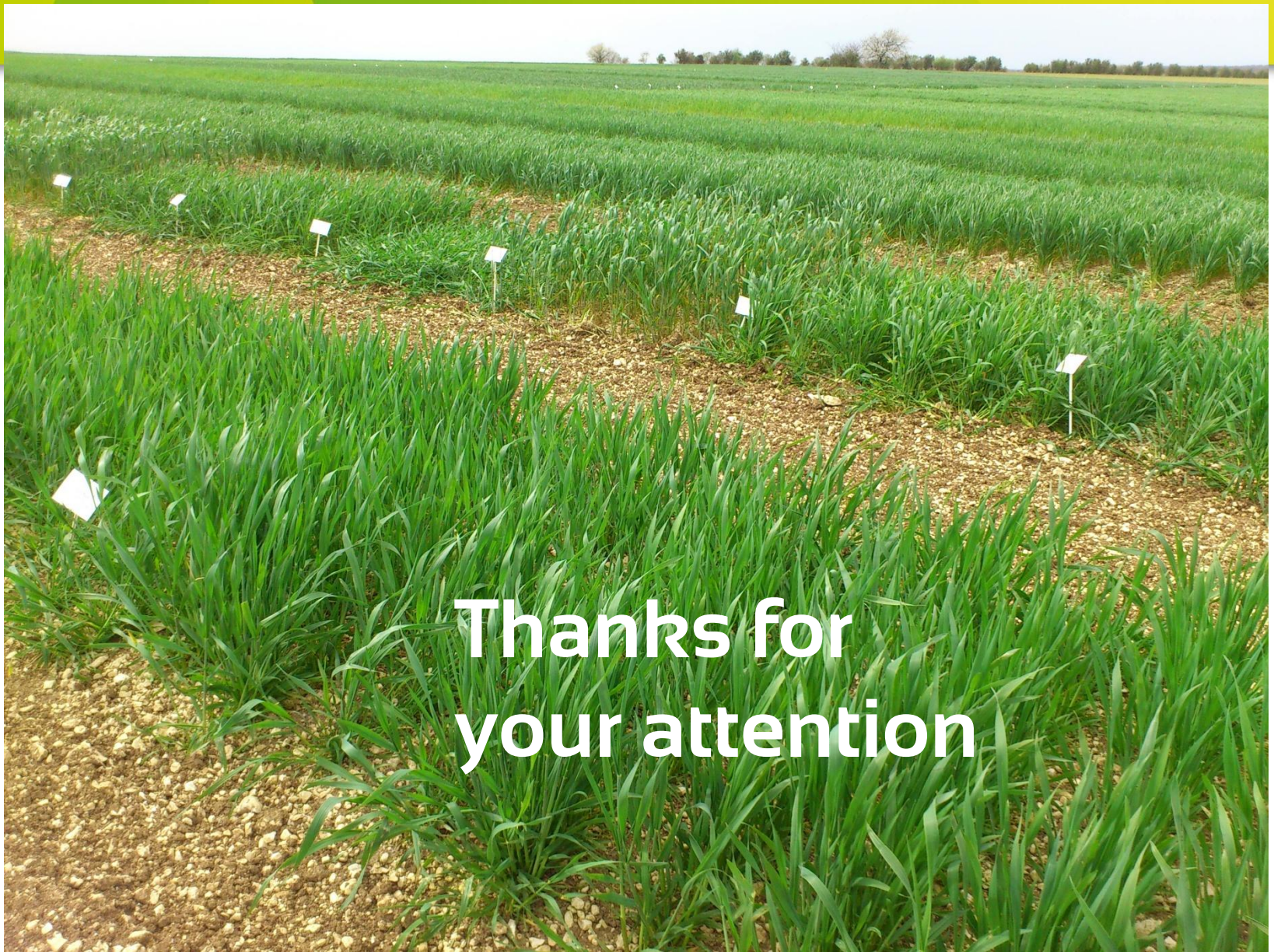
- Other options to consider to better manage variety collections, for example better use of TQ

- Molecular markers also used for other uses , such as hybrid conformity, or sample identity control



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**Thanks for
your attention**



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