UPOV

International Union for the Protection of New Varieties of Plants

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Technical Working Party on Testing Methods and Techniques
Fourth Session
Cambridge, United Kingdom, June 2 to 5, 2026

Technical Working Party for Agricultural Crops
Fifty-fifth Session
Seoul, Republic of Korea, June 15 to 18, 2026

TWM/4/24-TWA/55/8

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EXPLORING THE POTENTIAL USE OF UPOV MODEL COMBINING PHENOTYPIC AND MOLECULAR DISTANCES IN THE MANAGEMENT OF VARIETY COLLECTIONS FOR BREAD WHEAT IN FRANCE

Document prepared by an expert from France

The annex to this document contains a presentation “Exploring the potential use of UPOV model Combining Phenotypic and Molecular Distances in the Management of Variety Collections for Bread wheat in France”, to be made by an expert from France, at the fourth session of the TWM and the fifty-fifth session of the TWA.

[Annex follows]

ANNEX

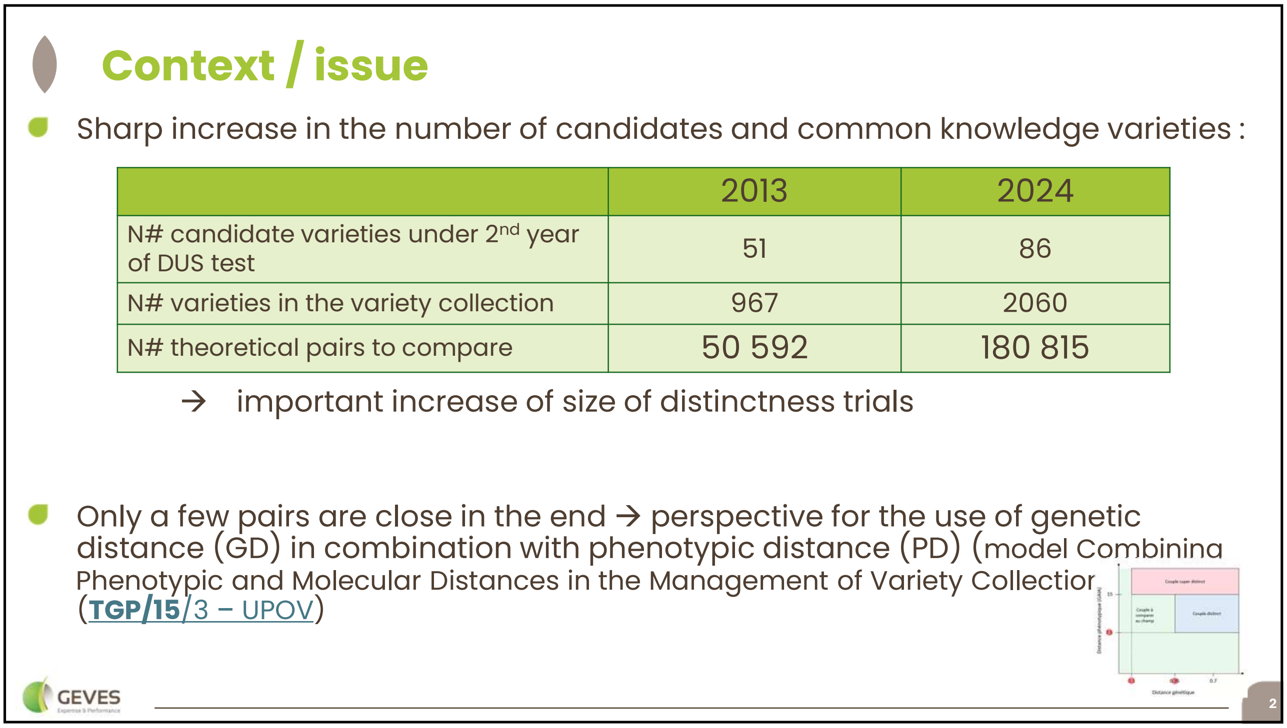
GEVES
Expertise & Performance
Groupe d'Étude et de contrôle des Variétés Et des Semences

Exploring the potential use of UPOV model Combining Phenotypic and Molecular Distances in the Management of Variety Collections for Bread wheat in France

TWM 4, 2-5 June 2026
TWA 55, 15-18 June 2026

invite

This project has received funding from the European Union's Horizon 2020 Research and Innovation programme under Grant Agreement No 817970.
www.h2020-invite.eu



Context / issue

- Sharp increase in the number of candidates and common knowledge varieties :

	2013	2024
N# candidate varieties under 2^{nd} year of DUS test	51	86
N# varieties in the variety collection	967	2060
N# theoretical pairs to compare	50 592	180 815

→ important increase of size of distinctness trials

- Only a few pairs are close in the end → perspective for the use of genetic distance (GD) in combination with phenotypic distance (PD) (model Combining Phenotypic and Molecular Distances in the Management of Variety Collection (**TGP/15**/3 – UPOV)

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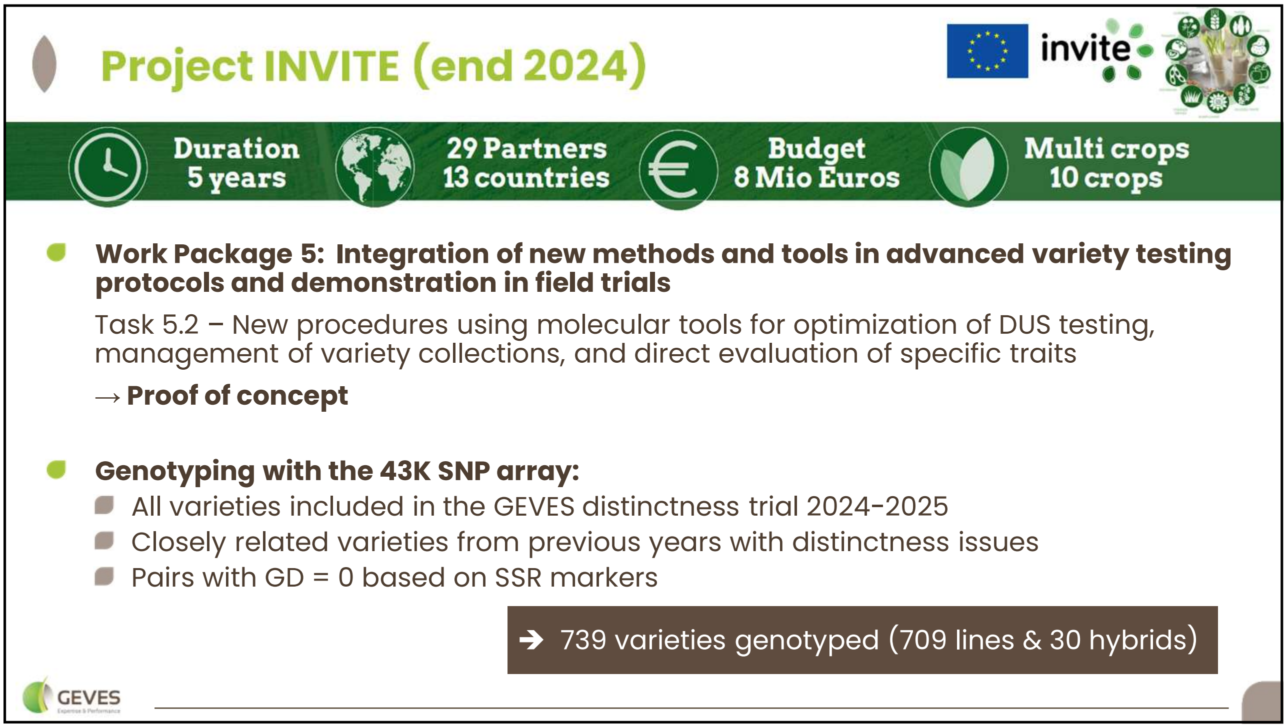


Project INVITE (end 2024)

Duration
5 years

29 Partners
13 countries

Budget
8 Mio Euros

Multi crops
10 crops

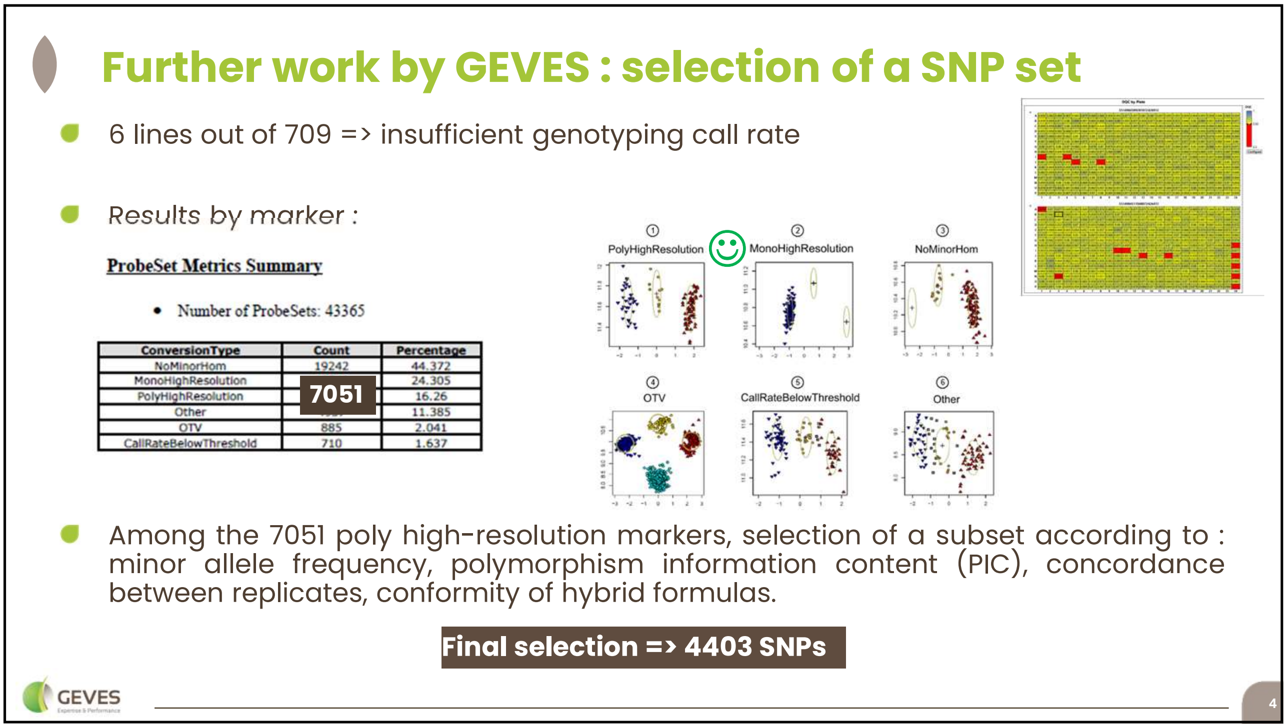
- **Work Package 5: Integration of new methods and tools in advanced variety testing protocols and demonstration in field trials**

  Task 5.2 – New procedures using molecular tools for optimization of DUS testing, management of variety collections, and direct evaluation of specific traits

  → **Proof of concept**

- **Genotyping with the 43K SNP array:**
  - All varieties included in the GEVES distinctness trial 2024-2025
  - Closely related varieties from previous years with distinctness issues
  - Pairs with GD = 0 based on SSR markers

➔ 739 varieties genotyped (709 lines & 30 hybrids)



Further work by GEVES : selection of a SNP set

- 6 lines out of 709 => insufficient genotyping call rate

- *Results by marker :*

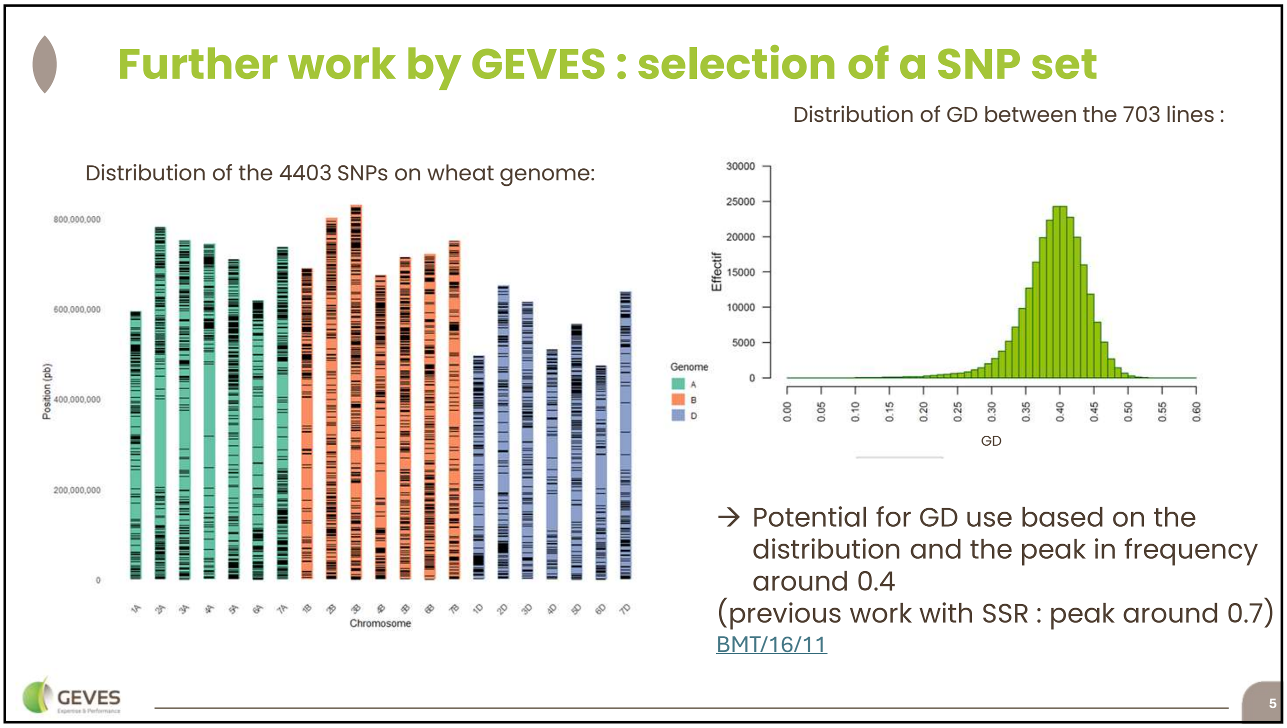
ProbeSet Metrics Summary

- Number of ProbeSets: 43365

ConversionType	Count	Percentage
NoMinorHom	19242	44.372
MonoHighResolution	[illegible]	24.305
PolyHighResolution	7051	16.26
Other	[illegible]	11.385
OTV	885	2.041
CallRateBelowThreshold	710	1.637

- Among the 7051 poly high-resolution markers, selection of a subset according to : minor allele frequency, polymorphism information content (PIC), concordance between replicates, conformity of hybrid formulas.

Final selection => 4403 SNPs



Further work by GEVES : selection of a SNP set

Distribution of the 4403 SNPs on wheat genome:

Distribution of GD between the 703 lines :

→ Potential for GD use based on the distribution and the peak in frequency around 0.4

(previous work with SSR : peak around 0.7) BMT/16/11

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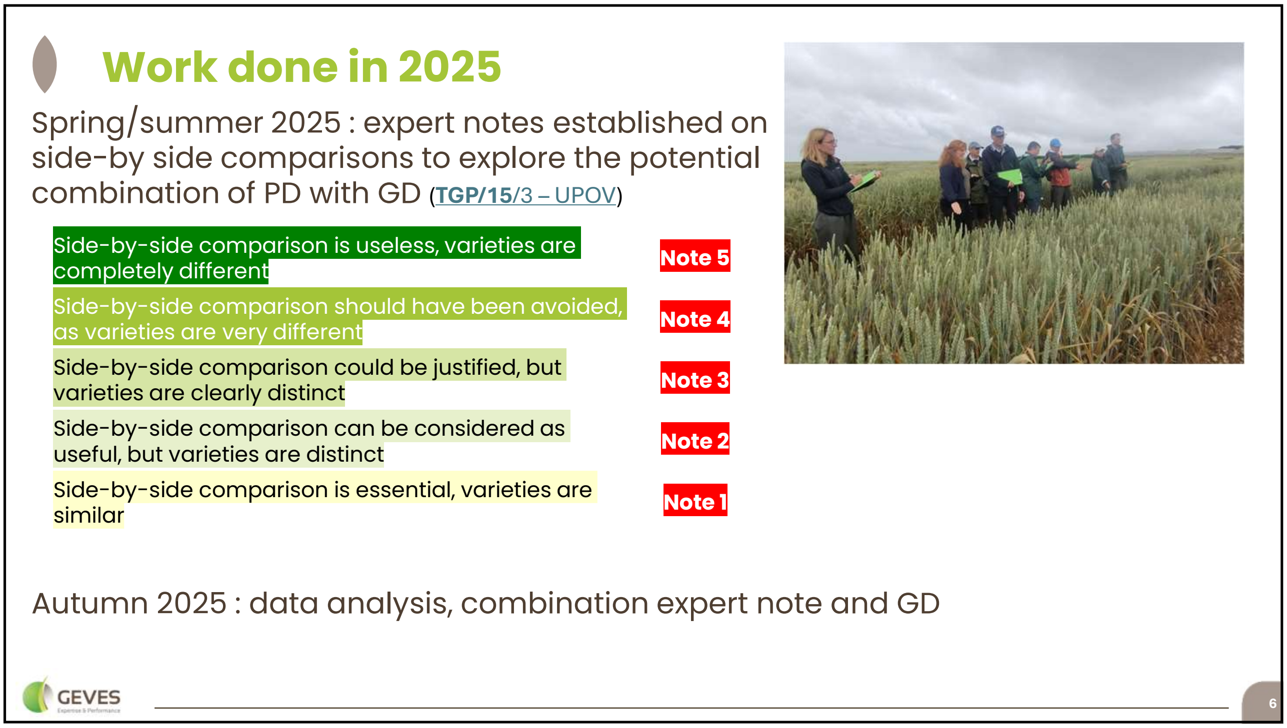

Work done in 2025

Spring/summer 2025 : expert notes established on side-by side comparisons to explore the potential combination of PD with GD (TGP/15/3 – UPOV)

Side-by-side comparison is useless, varieties are completely different	Note 5
Side-by-side comparison should have been avoided, as varieties are very different	Note 4
Side-by-side comparison could be justified, but varieties are clearly distinct	Note 3
Side-by-side comparison can be considered as useful, but varieties are distinct	Note 2
Side-by-side comparison is essential, varieties are similar	Note 1

Autumn 2025 : data analysis, combination expert note and GD

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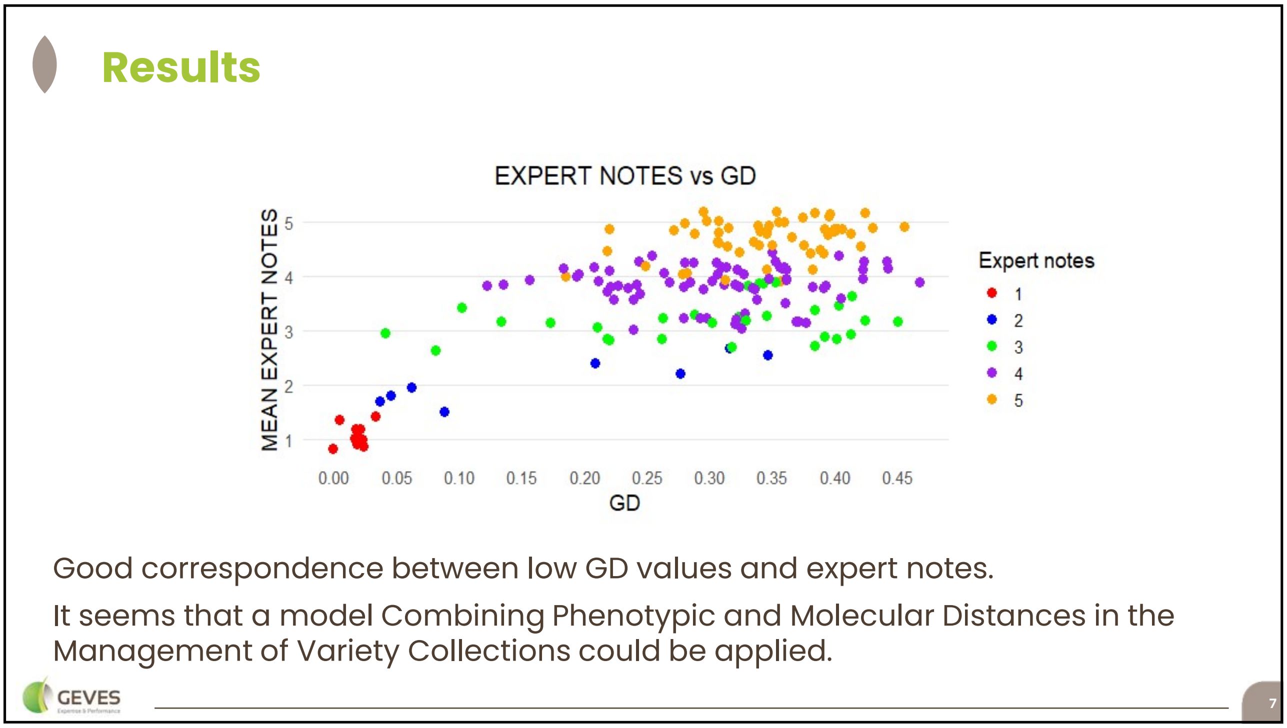
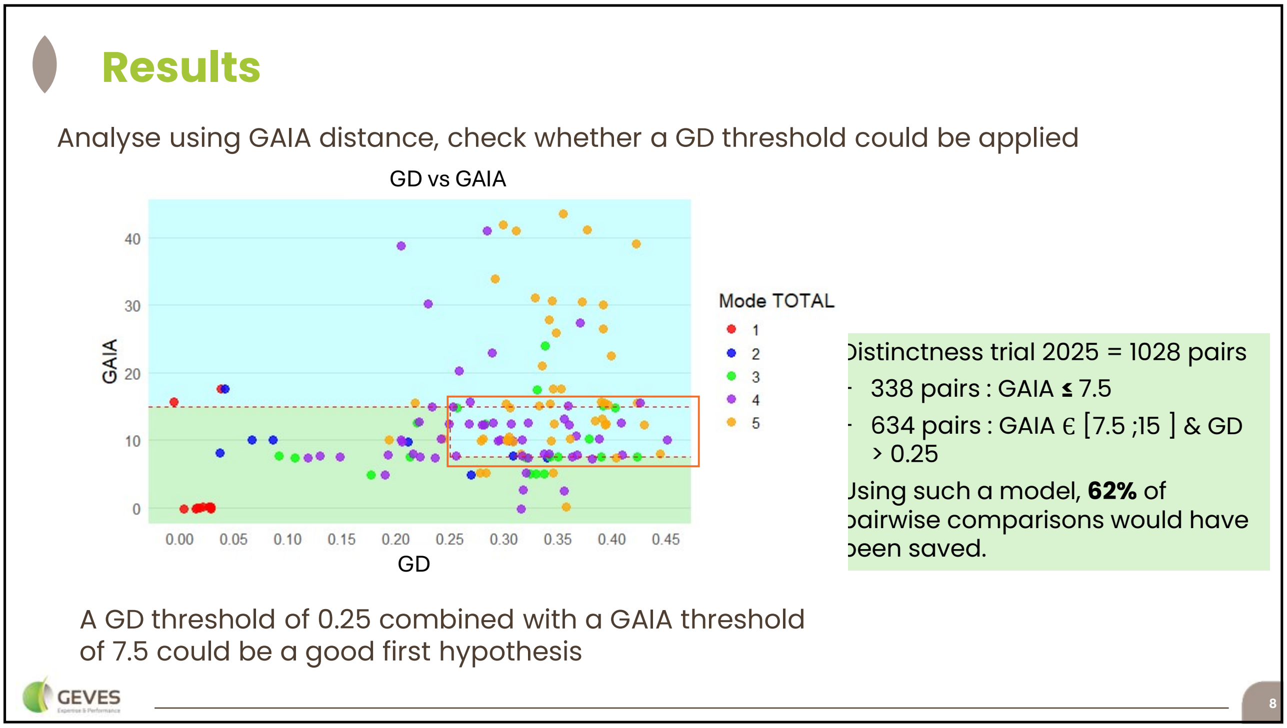


Results

Good correspondence between low GD values and expert notes.

It seems that a model Combining Phenotypic and Molecular Distances in the Management of Variety Collections could be applied.



Results

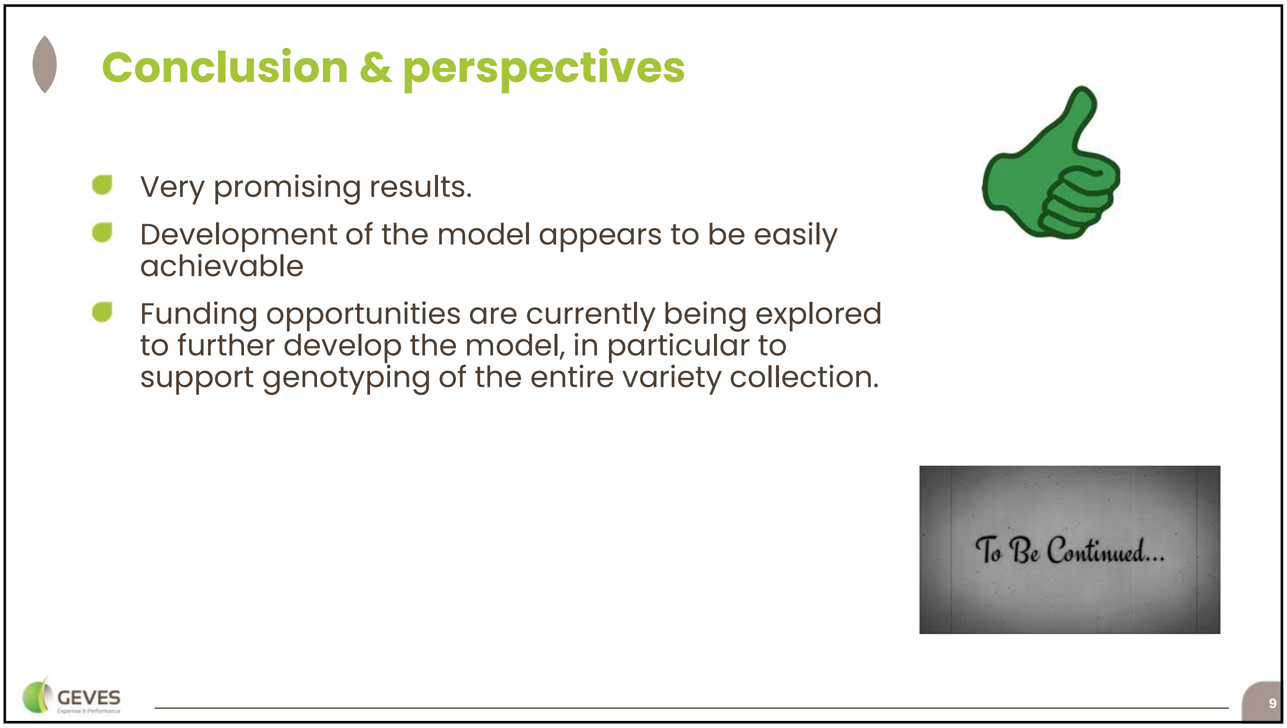
Analyse using GAIA distance, check whether a GD threshold could be applied

istinctness trial 2025 = 1028 pairs

- 338 pairs : GAIA ≤ 7.5
- 634 pairs : GAIA ∈ [7.5 ;15] & GD > 0.25

sing such a model, **62%** of airwise comparisons would have een saved.

A GD threshold of 0.25 combined with a GAIA threshold of 7.5 could be a good first hypothesis



Conclusion & perspectives

- Very promising results.
- Development of the model appears to be easily achievable
- Funding opportunities are currently being explored to further develop the model, in particular to support genotyping of the entire variety collection.

To Be Continued...

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Thank you for your attention

[End of Annex and of document]