UPOV

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ARGENTINE EXPERIENCE USING GAIA SOFTWARE

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The Annex to this document contains a copy of a presentation "Argentine Experience Using GAIA Software" made at the thirty-fifth session of the Technical Working Party on Automation and Computer Programs (TWC).

[Annex follows]

ARGENTINE EXPERIENCE USING GAIA SOFTWARE

Argentine PVP Office
INASE

BACKGROUND

- 2012 - 2015 Threshold calibration trial for molecular markers based on the example of parent lines in Maize from France.

- 2015 Training session on GAIA for Argentine examiners, led by Christophe Chevalier and Christelle Guitouni.

- Nowadays, we are working on GAIA thresholds to check distinctness in soybean, wheat, grapevine and sunflower.

INASE SOFTWARE FOR DISTINCTNESS: *DIF* SOFTWARE

- Developed in Argentina - 1994.

- Used to distinguish varieties by considering QL and QN characteristics.

- Usefull to provide a variety description.

The near future:
Add molecular markers analysis for the distinctness examination of soybean varieties.

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GAIA

SOYBEAN

Importance of GAIA software

- Average number of aplications per year: 150 varieties. (Number of registered varieties: 950)
- Few number of characteristics to be used for distinctness.

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The list of most similar varieties is extensive

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Therefore, a big amount of varieties should be tested on the field.

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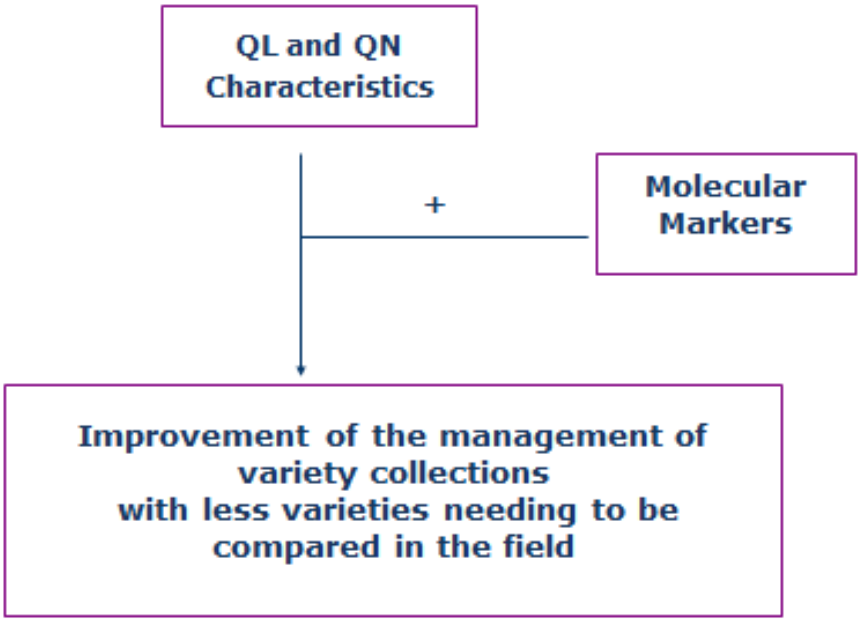
This methodology represents high costs and less efficiency



SOYBEAN TRIALS FIELD

- This field trial were made to be compared with molecular markers results, if both match then were the best finding selection.

- Design: 6 candidates and 11 varieties to be compared per each candidate.

- Test years: 2012-2013, 2013-2014 and 2014-2015.

- Methodology: evaluation made on set of pairs and classification according to the Geves Maize Model.

- The comparison was made by experts of the PVP Office and Breeders.

DESK WORK

- Selection of relevant characteristics for the distinctness of varieties
- Group characteristics in 3 levels: least reliable, reliable and most reliable
- Assign weightings to each characteristic
- Process the molecular data to select the molecular markers
- Comparison between molecular genotypes analysis and phenotipical results
- Selection of the morphological and molecular thresholds

Launch GAIA for comparison

WEIGHT ASSIGNMENT IN A CHARACTERÍSTIC

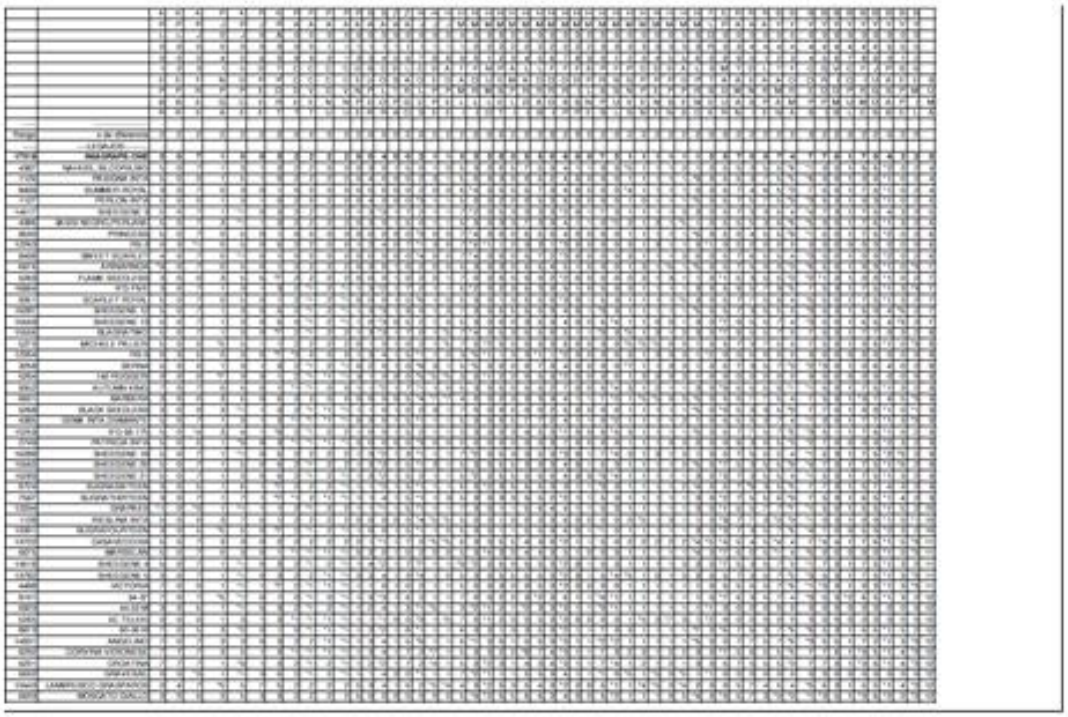
- Growth type:
  - 1 = Determinate
  - 2 = Semideterminate
  - 3 = Indeterminate

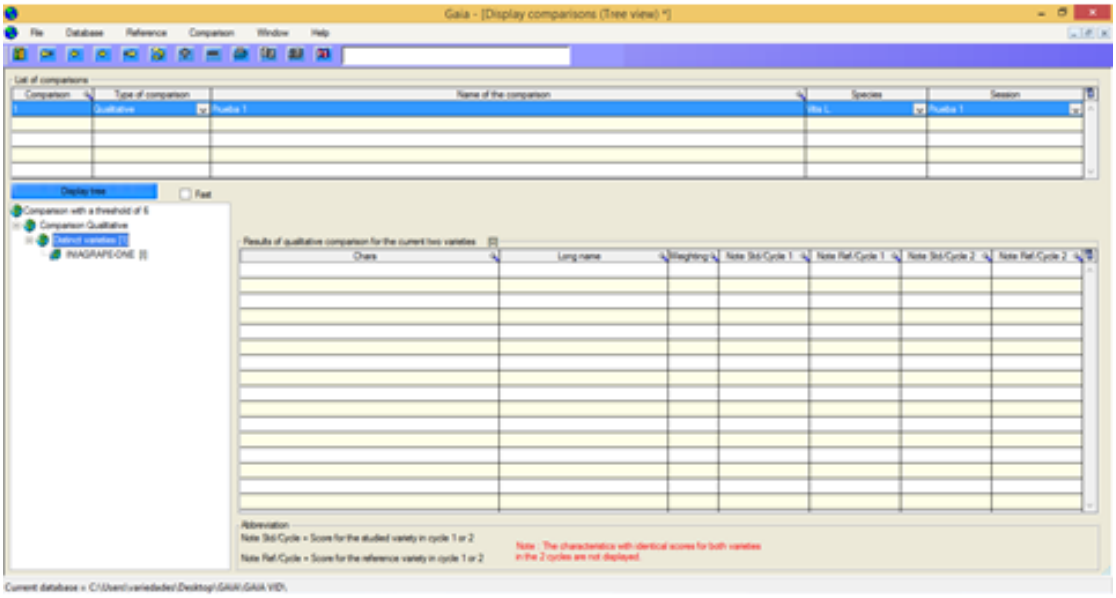
•The experts add a weight to the comparisons of the levels of expression

Comparison of notes with their weights		
	Diference	Weight
Determinate (1) vs. Determinate (1)	0	0
Determinate (1) vs. Semideterminate (2)	1	0
Determinate (1) vs. Indeterminate (3)	2	9
Semideterminate (2) vs. Semideterminate (2)	0	0
Semideterminate (2) vs. Indeterminate (3)	1	3
Indeterminate (3) vs. Indeterminate (3)	0	0

EXPERIENCE ON GRAPEVINE DIFERENCIATION WITH GAIA AND *DIF*

- With the *DIF* information we prepared the GAIA database for grapevine.
- Prepared the matrix weight per each characteristic.
- Launch the GAIA and *DIF* comparison simultaneously.
- Compared the comparisons of both softwares.
- Adjust the weights to generate more precision on GAIA Software.




Gaia - [Display comparisons (Tree view) *]
File
Database
Reference
Comparison
Window
Help
List of comparisons
Comparison
Type of comparison
Name of the comparison
Species
Session
Qualitative
Prueba 1
Vitis L.
Display tree
Fast
Comparison with a threshold of 6
Comparison Qualitative
Distinct varieties [1]
INIAGRAPE-ONE [i]
Results of qualitative comparison for the current two varieties
Charac
Long name
Weighting
Note Std./Cycle 1
Note Ref./Cycle 1
Note Std./Cycle 2
Note Ref./Cycle 2
Abbreviation
Note Std./Cycle = Score for the studied variety in cycle 1 or 2
Note Ref./Cycle = Score for the reference variety in cycle 1 or 2
Note : The characteristics with identical scores for both varieties in the 2 cycles are not displayed.
Current database = C:\Users\variedades\Desktop\GAIA\GAIA VID\

FINAL THOUGHTS...

- Year 2018-2019, biomolecular distances could be use for the distincness exam in soybean.

- Continue using GAIA software for phenotipical distinguish in other species.

- For future, extend the use of GAIA with molecular distances in other species.

THANKS FOR YOUR ATTENTION

The PVP Office staff

[End of Annex and of document]