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

BMT/18/17 Add.

Eighteenth Session
Hangzhou, China, October 16 to 18, 2019

Original: English
Date: November 7, 2019

ADDENDUM TO
USE OF MOLECULAR MARKERS FOR PROTECTION AND VARIETAL IDENTIFICATION: STATE OF THE ART IN ARGENTINA

Document prepared by an expert from Argentina

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The annex to this document contains a copy of a presentation on “Use of molecular markers for protection and varietal identification: state of the art in Argentina”, made at the eighteenth session of the BMT.

[Annex follows]

ANNEX

Use of molecular markers for protection and varietal identification: state of the art in Argentina

This work was prepared by experts from Argentina

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18th session of BMT
Hangzhou, China
Oct.16-18, 2019

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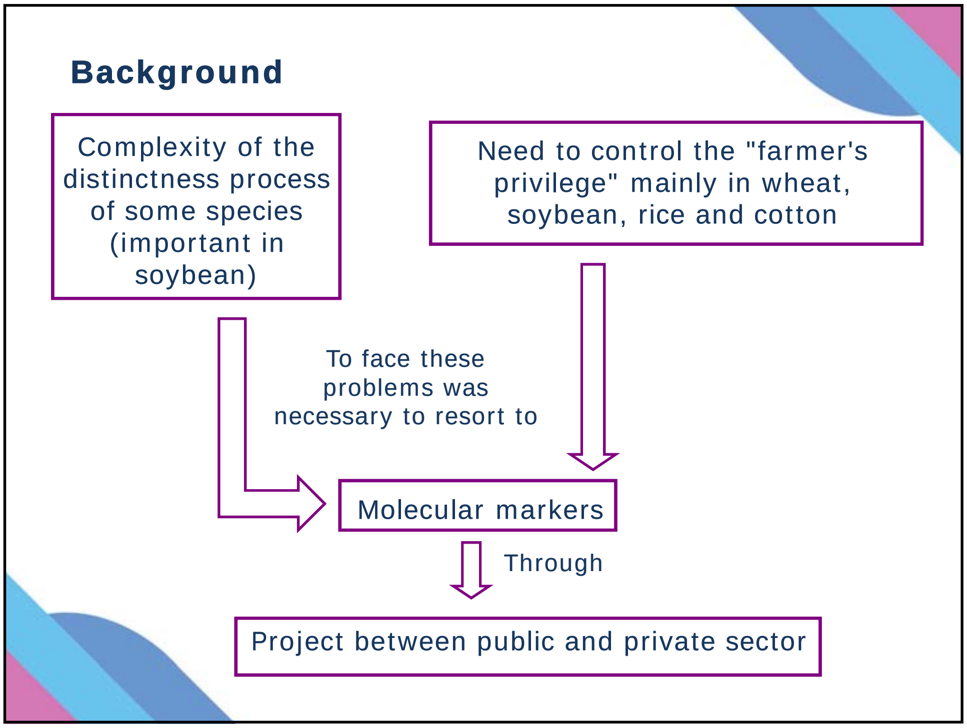


Background

Complexity of the distinctness process of some species (important in soybean)

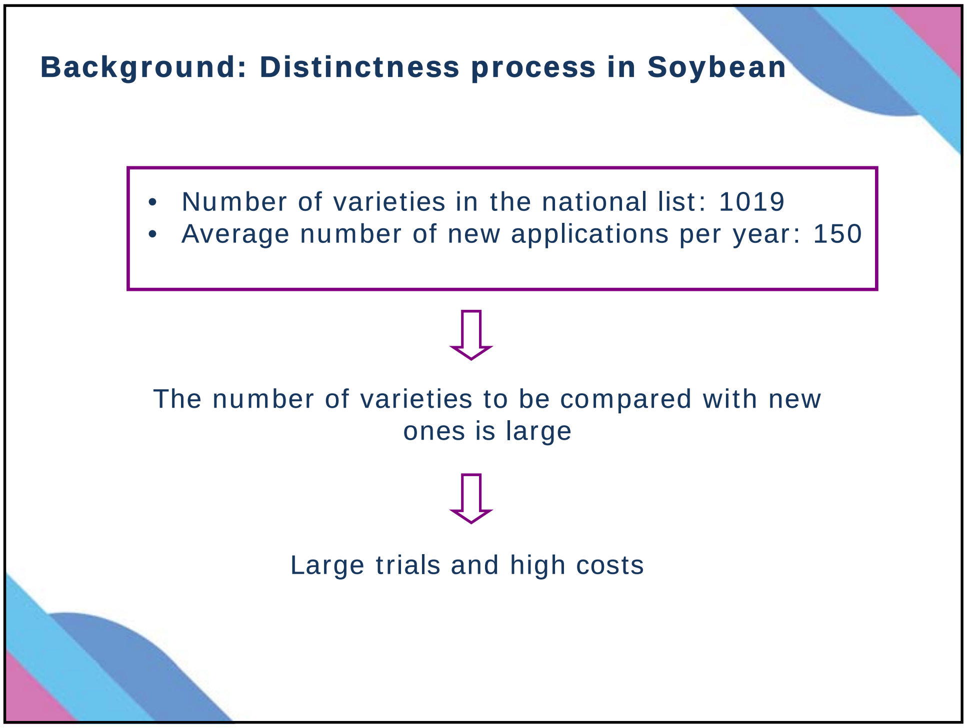
Need to control the "farmer's privilege" mainly in wheat, soybean, rice and cotton

To face these problems was necessary to resort to

Molecular markers

Through

Project between public and private sector



Background: Distinctness process in Soybean

- Number of varieties in the national list: 1019
- Average number of new applications per year: 150

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The number of varieties to be compared with new ones is large

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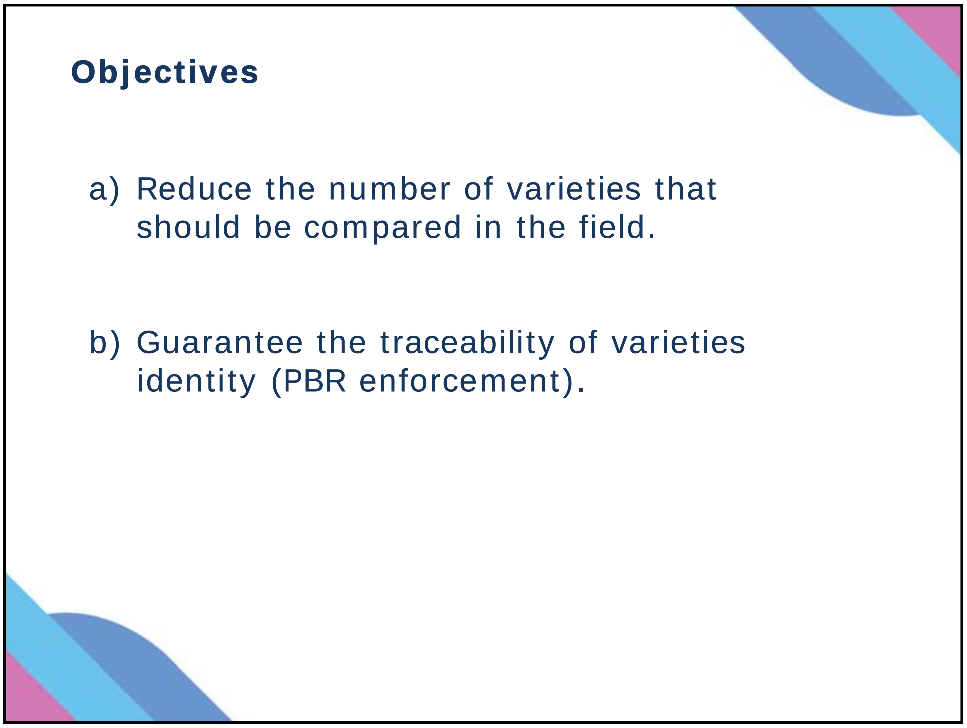
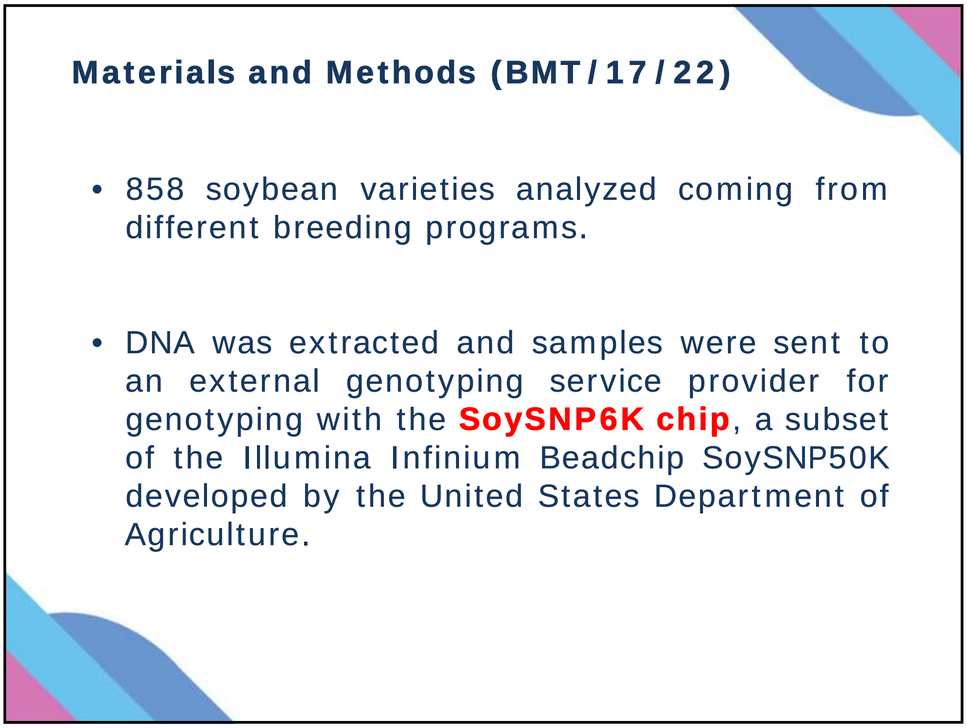
Large trials and high costs



Objectives

a) Reduce the number of varieties that should be compared in the field.

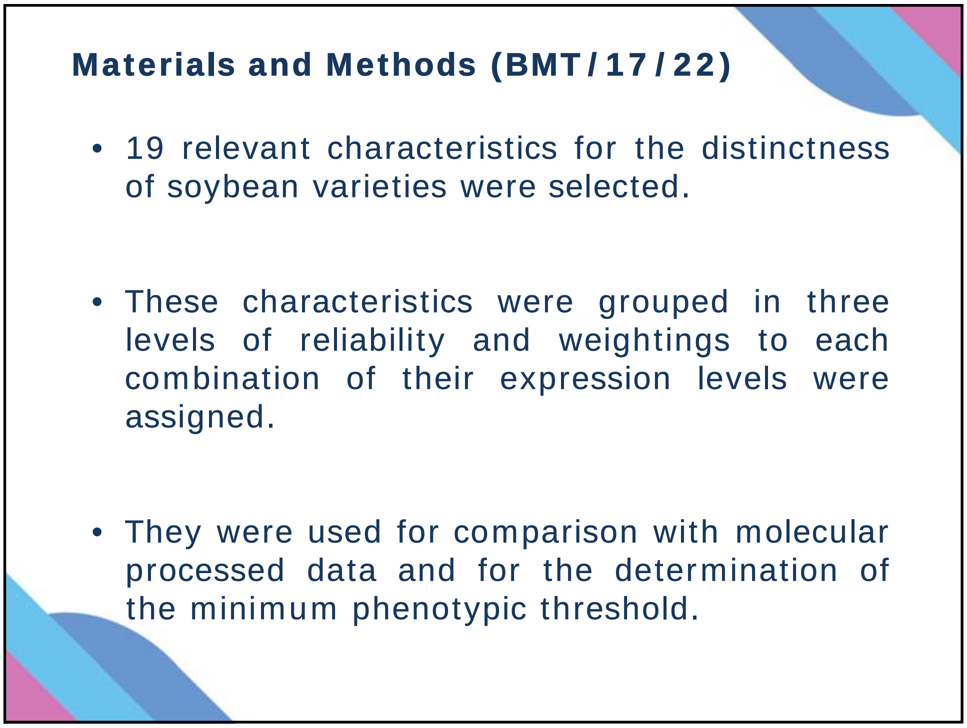
b) Guarantee the traceability of varieties identity (PBR enforcement).



Materials and Methods (BMT/17/22)

- 858 soybean varieties analyzed coming from different breeding programs.

- DNA was extracted and samples were sent to an external genotyping service provider for genotyping with the **SoySNP6K chip**, a subset of the Illumina Infinium Beadchip SoySNP50K developed by the United States Department of Agriculture.



Materials and Methods (BMT/17/22)

- 19 relevant characteristics for the distinctness of soybean varieties were selected.

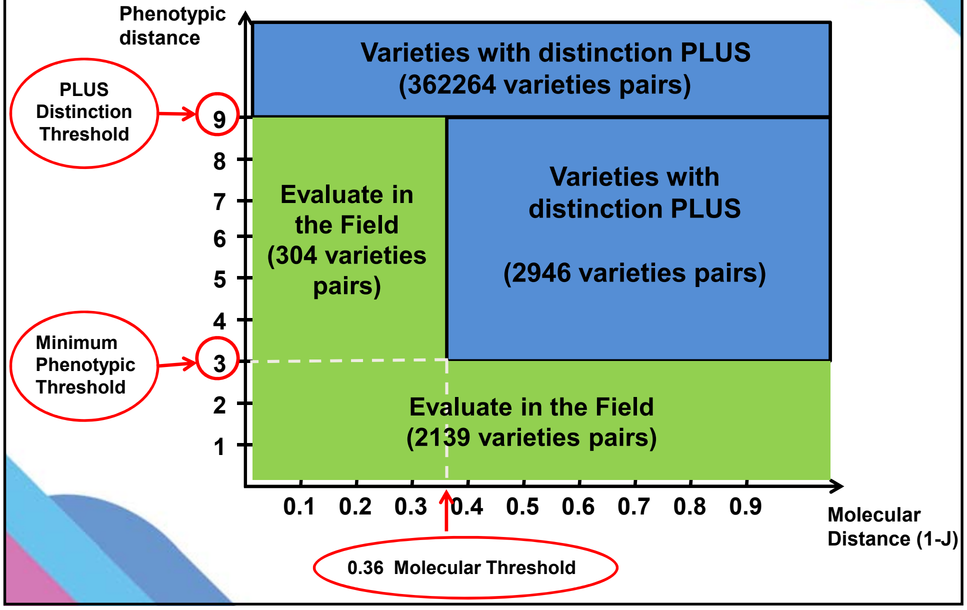
- These characteristics were grouped in three levels of reliability and weightings to each combination of their expression levels were assigned.

- They were used for comparison with molecular processed data and for the determination of the minimum phenotypic threshold.

Results in relation to objective a) (BMT/17/22)

- We select a set of 4004 SNPs markers distributed in the genome that represent the genetic background and produce efficient discrimination power.
- We determine the molecular distance threshold and the minimum phenotypical distance threshold, based on 3 years field trials (necessary for UPOV model 2).

Results in relation to objective a) (BMT/17/22)

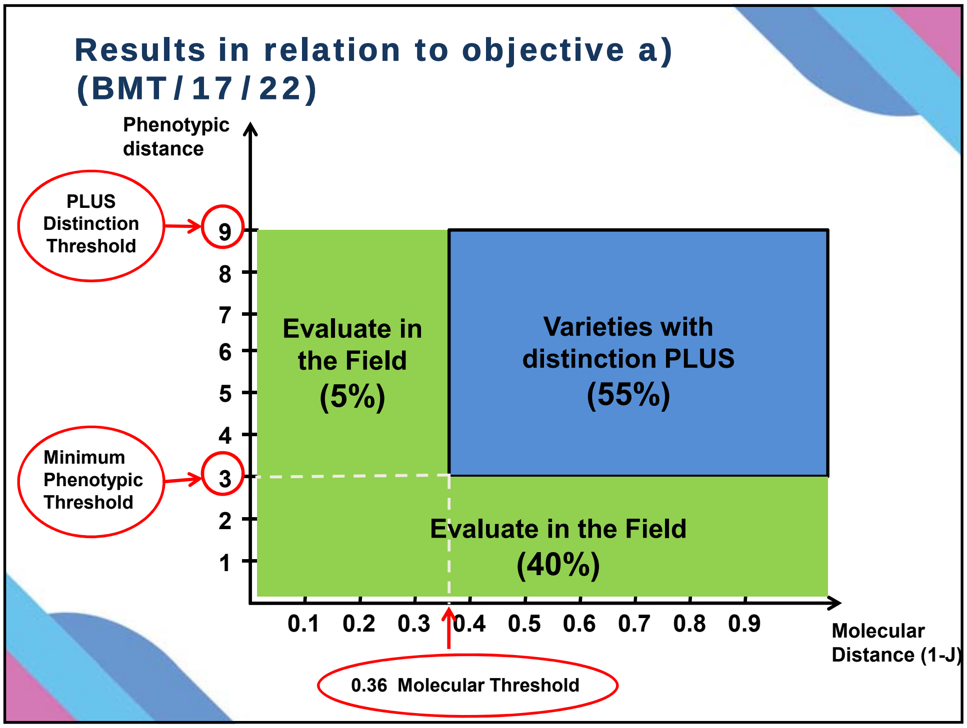


Varieties with distinction PLUS (362264 varieties pairs)

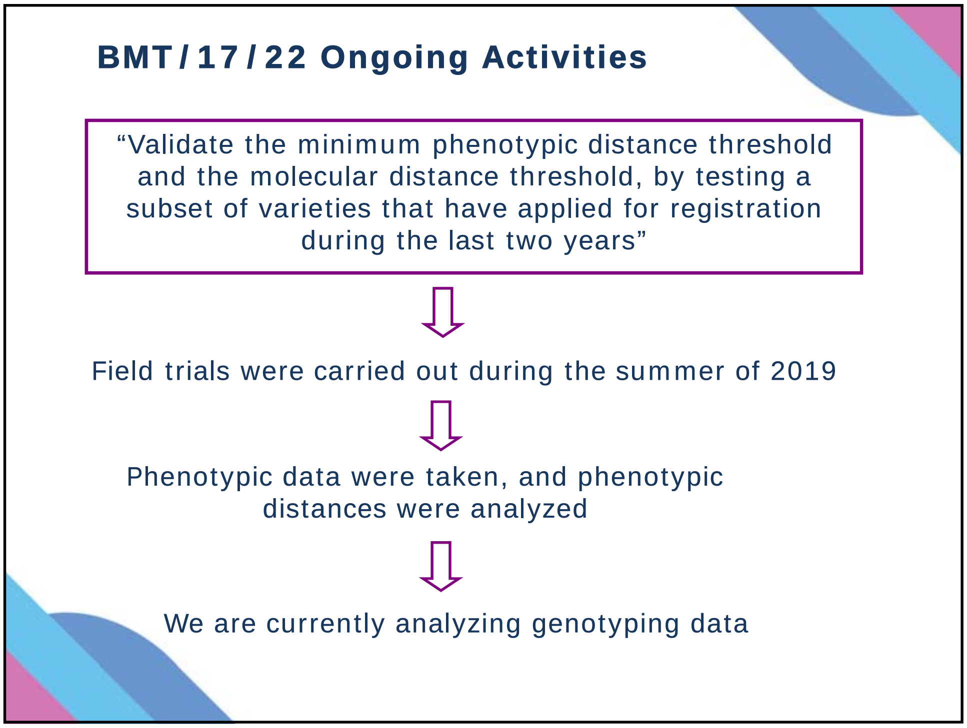
Evaluate in the Field (304 varieties pairs)

Varieties with distinction PLUS (2946 varieties pairs)

Evaluate in the Field (2139 varieties pairs)



Results in relation to objective a) (BMT/17/22)



BMT/17/22 Ongoing Activities

“Validate the minimum phenotypic distance threshold and the molecular distance threshold, by testing a subset of varieties that have applied for registration during the last two years”

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Field trials were carried out during the summer of 2019

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Phenotypic data were taken, and phenotypic distances were analyzed

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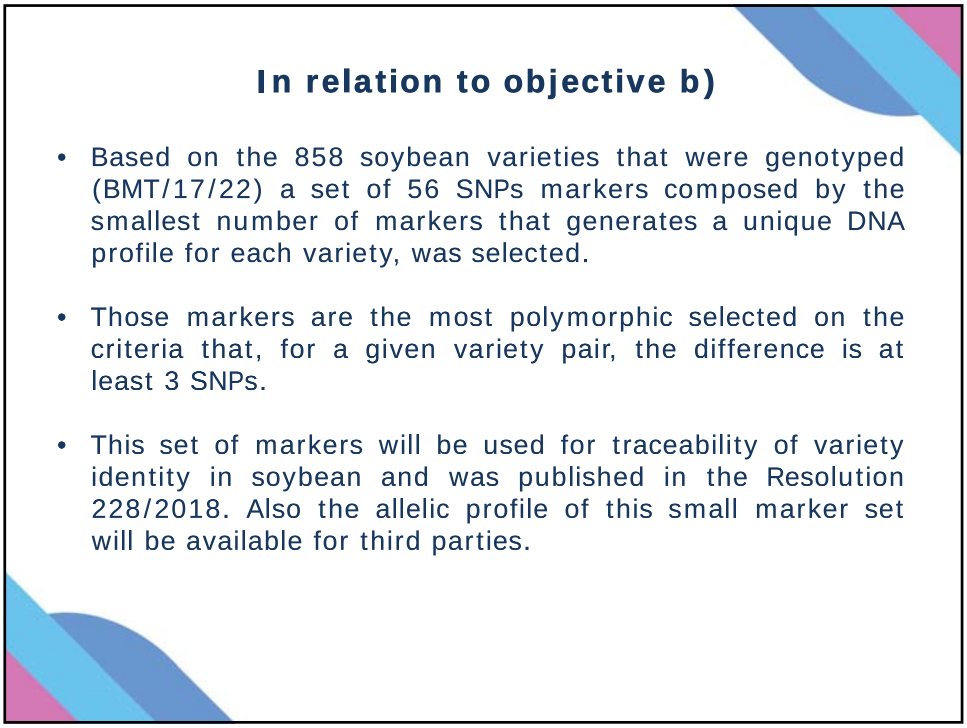
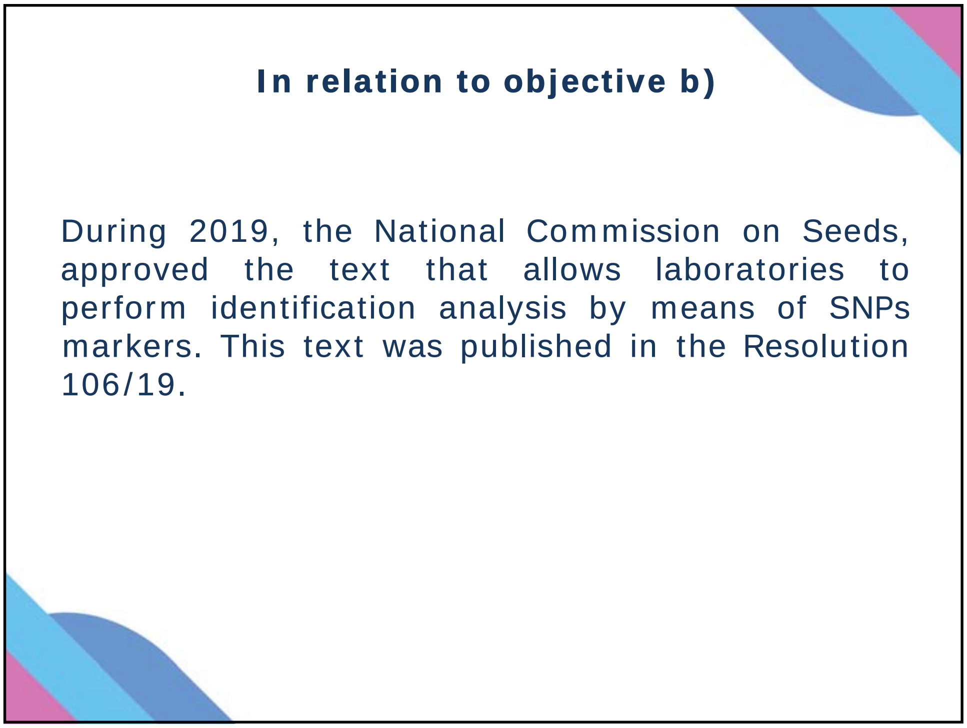
We are currently analyzing genotyping data



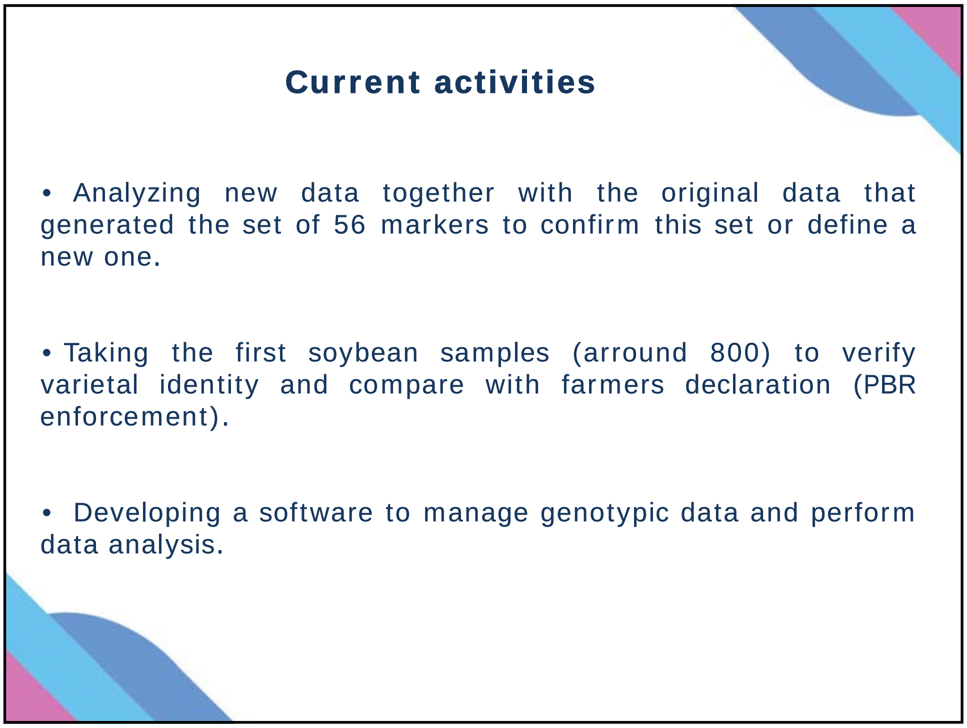
In relation to objective b)

- Based on the 858 soybean varieties that were genotyped (BMT/17/22) a set of 56 SNPs markers composed by the smallest number of markers that generates a unique DNA profile for each variety, was selected.
- Those markers are the most polymorphic selected on the criteria that, for a given variety pair, the difference is at least 3 SNPs.
- This set of markers will be used for traceability of variety identity in soybean and was published in the Resolution 228/2018. Also the allelic profile of this small marker set will be available for third parties.



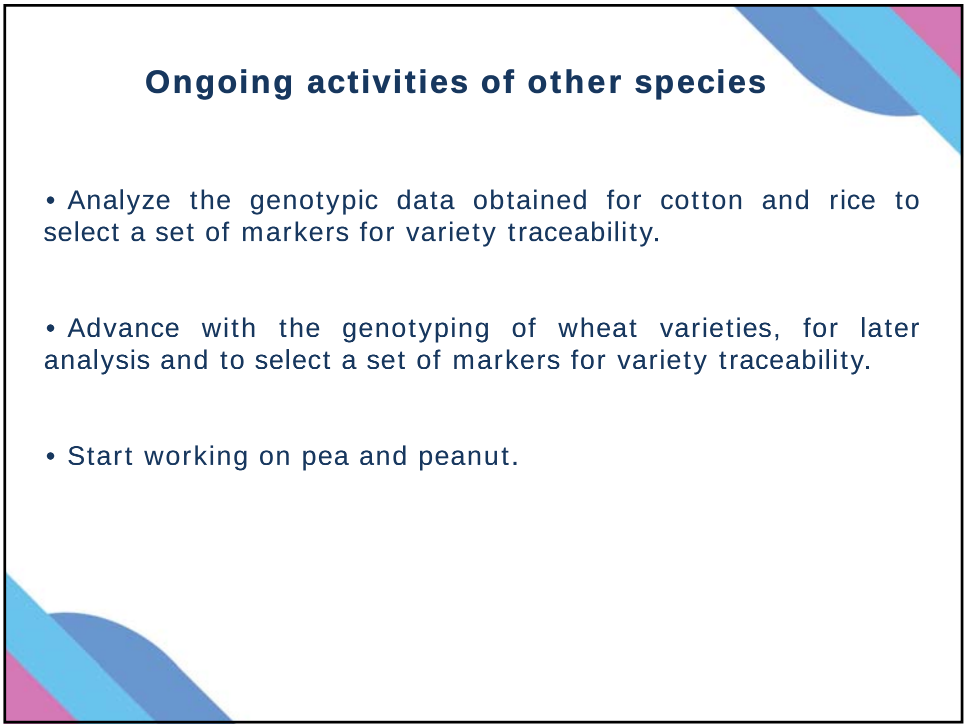
In relation to objective b)

During 2019, the National Commission on Seeds, approved the text that allows laboratories to perform identification analysis by means of SNPs markers. This text was published in the Resolution 106/19.



Current activities

- Analyzing new data together with the original data that generated the set of 56 markers to confirm this set or define a new one.
- Taking the first soybean samples (arround 800) to verify varietal identity and compare with farmers declaration (PBR enforcement).
- Developing a software to manage genotypic data and perform data analysis.



Ongoing activities of other species

- Analyze the genotypic data obtained for cotton and rice to select a set of markers for variety traceability.
- Advance with the genotyping of wheat varieties, for later analysis and to select a set of markers for variety traceability.
- Start working on pea and peanut.

Acknowledgment

Experts from INASE and FCEyN-UBA

Maria Fernanda Dalmau- INASE
Maria Alicia Loray – INASE
Mariano Alejandro Mangieri – INASE
Ana Laura Vicario – INASE
Marcelo Marti – FCEyN-UBA
German F Burguener – FCEyN-UBA
Jonathan Javier Zaiat – FCEyN-UBA
Raimundo Lavignolle – INASE
Hernando Pecci – INASE
Ignacio Aranciaga - INASE

Experts from Argentine Seed Association (ASA)

Mirta Antongiovanni
Gaspar Malone
Edgardo Gabriel Bresso
Roberto Oscar Enriquez
Claudia Karina Herrmann
Maria Eva González
Andrés Pereyra
Mauro Meier
Gustavo Abratti
Julieta Alloatti
Carlos Dezar
Mariana Gallo
Alberto Javier Salvador
Alfredo Paseyro
Juan Erdmann

Thanks for your attention!!!

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