UPOV

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SOYBEAN EDV THRESHOLD DEVELOPMENT

Document prepared by an expert from the International Seed Federation (ISF)

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The annex to this document contains a copy of a presentation “Soybean EDV Threshold Development”, to be made by an expert from the International Seed Federation (ISF), at the third session of the TWM.

[Annex follows]

Soybean EDV Threshold Development

Barry Nelson – ASTA (American Seed Trade Association) Molecular Marker Working Group Chair *on behalf of ASTA and Seed Association of the Americas (SAA)members*

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Outline

- Project Objective
- Organizations Involved
- Technical Approach
  - The Maize Model for EDV Thresholds
  - Soybean Backcross Similarity Evaluation
- Summary and Next Steps

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Project Objective

Objective

- Establish data driven marker similarity threshold(s) to serve as trigger point(s) in EDV determination.

- UPOV/EXN/EDV
  - (b) Varieties involving the use of two or more parents ("multi-parental" varieties) may be predominantly derived from one parent (the initial variety) by selectively retaining the genome of the initial variety, for example through repeated backcrossing. In this case, **crop-specific genetic similarity thresholds might be defined in order to determine predominant derivation.**

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Organizations Involved

ASTA
SAA Seed Association of the Americas
ICIA Indiana Crop Improvement Association
University of Buenos Aires
BASF We create chemistry
BAYER
CORTEVA agriscience
GDM
syngenta

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Technical Approach

THE RIGHTS OF THE BREEDER

Article 14

Scope of the Breeder's Right

[…]

(5) [*Essentially derived and certain other varieties*] *(a)* The provisions of paragraphs (1) to (4)* shall also apply in relation to

(i) varieties which are essentially derived from the protected variety, where the protected variety is not itself an essentially derived variety,

(ii) varieties which are not clearly distinguishable in accordance with Article 7 from the protected variety and

(iii) varieties whose production requires the repeated use of the protected variety.

(b) For the purposes of subparagraph *(a)*(i), a variety shall be deemed to be essentially derived from another variety ("the initial variety") when

(i) it is predominantly derived from the initial variety, or from a variety that is itself predominantly derived from the initial variety, while retaining the expression of the essential characteristics that result from the genotype or combination of genotypes of the initial variety,

(ii) it is clearly distinguishable from the initial variety and

(iii) except for the differences which result from the act of derivation, it conforms to the initial variety in the expression of the essential characteristics that result from the genotype or combination of genotypes of the initial variety.

(c) Essentially derived varieties may be obtained for example by the selection of a natural or induced mutant, or of a somaclonal variant, the selection of a variant individual from plants of the initial variety, backcrossing, or transformation by genetic engineering.

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Technical Approach – The Maize Model

- Focus on the backcrossing as an example of how and EDV may be obtained
- Based on the model used to establish maize EDV thresholds
  - Heckenberger M., Bohn M. and Melchinger A.E. 2005c. Identification of essentially derived varieties obtained from **biparental crosses of homozygous lines**. I. SSR data from maize inbreds. Crop Sci. 45: 1120–1131.
    - This work was based on 66 parent biparental crosses.
- EDV thresholds for maize serve as 'trigger points' for determination of predominant derivation

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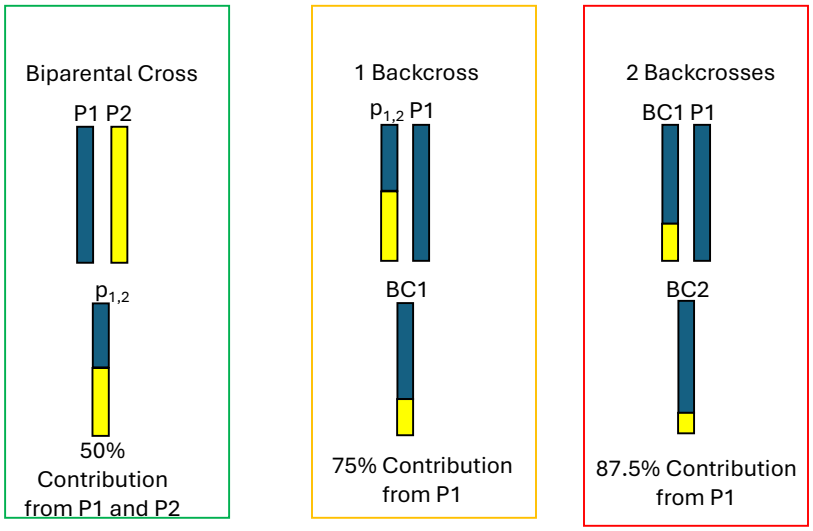
Technical Approach – The Maize Model



*Heckenberger, M., M. Bohn, and A.E. Melchinger. 2005. Identification of Essentially Derived Varieties Obtained from Biparental Crosses of Homozygous Lines: I. Simple Sequence Repeat Data from Maize Inbreds. Crop Sci. 45:1120–1131.

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Technical Approach

- Soybean Backcross Similarity Evaluation

Soybean Varieties

- Public & Ex PVP
  - Avoids varieties encumbered by PVP or Patents in force

Marker Set

- BARCSoySNP6K
  - Qijian Song, Long Yan, Charles Quigley, Edward Fickus, He Wei, Linfeng Chen, Faming Dong, Susan Araya, Jinlong Liu, David Hyten, Vincent Pantalone, and Randall L. Nelson. 2020. Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. The Plant Journal 104, 800-811.
  - 6000 SNP whole genome panel
    - Used in previous work on Soy Distinctness Threshold

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Technical Approach

- Soybean Backcross Similarity Evaluation

The Task

- Evaluate Ex PVP and Public Varieties for BC2 Pedigrees

The Problem

- Not enough BC2 pedigrees to compute similarities!

The Solution

- Focus on Bi-Parental Cross and Compute Similarities of:
  - Bi-Parental Cross
  - BC1 Similarity(computed)
  - BC2 Similarity(computed)

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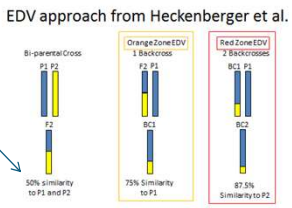
Technical Approach

- Soybean Backcross Similarity Evaluation

Bi-Parental Cross Similarity

- For example:
  - A3127 = Essex/Williams
    - Compute similarity of parents, ie. Essex to Williams
      - Similarity of Essex to Williams = 56%



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Technical Approach
- Soybean Backcross Similarity Evaluation of A3127

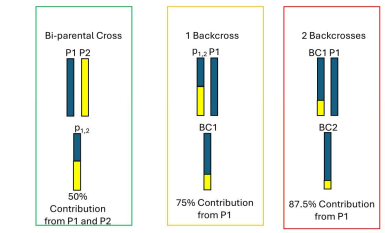
BC1 Similarity (*Computed)*

- BC1 Sim = ((100%-BP Sim)/2) + BP Sim
- BC1 Sim = (100%-56%/2) + 56% = 78%

BC2 Similarity (*Computed)*

- BC2 Sim = ((1-BC1 Sim)/2) + BC1 Sim
- BC2 Sim = (100%-78%/2) + 78% = 89%

Technical Approach – Parent Contribution



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Technical Approach
- Soybean Backcross Similarity Evaluation

Variety #	Variety Name	Parent 1	Parent 2	Bi-Parental?
1	Coles	HARK	PROVAR X DISOY X MAGNA	N
2	Marion	AMSOY	PROVAR X DISOY X MAGNA	N
3	Cumberland	CORSOY	WILLIAMS	Y
4	Oakland	L66L-137	CALLAND	Y
5	Vinton	HARK	PROVAR X DISOY X MAGNA	N
6	Sloan	M59-120X	IVR EX4731	Y
7	Vickery	CORSOY	ANOKA X MACK	N
8	Weber	C1453	SWIFT	Y
~1700				

- Biparental pedigrees only!
- >1700 varieties evaluated
- We currently have >800 varieties derived from biparental crosses

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Summary

- The process to establish EDV thresholds in maize were based on backcrossing and was successfully implemented and adopted by ISF.
- A similar model is being explored for soybeans.

Next Steps

- Generate public 6k SNP data where needed
- Compute biparental similarities, BC1's, and BC2's
- Breeder validation among stakeholders
- Socialize / agreement among seed associations

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Thank You!

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[End of Annex and of document]