

Conservation and Sustainability Use of Genetic Resources for Food and Agriculture



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Jean-Marcel Ribaut
GCP, Mexico

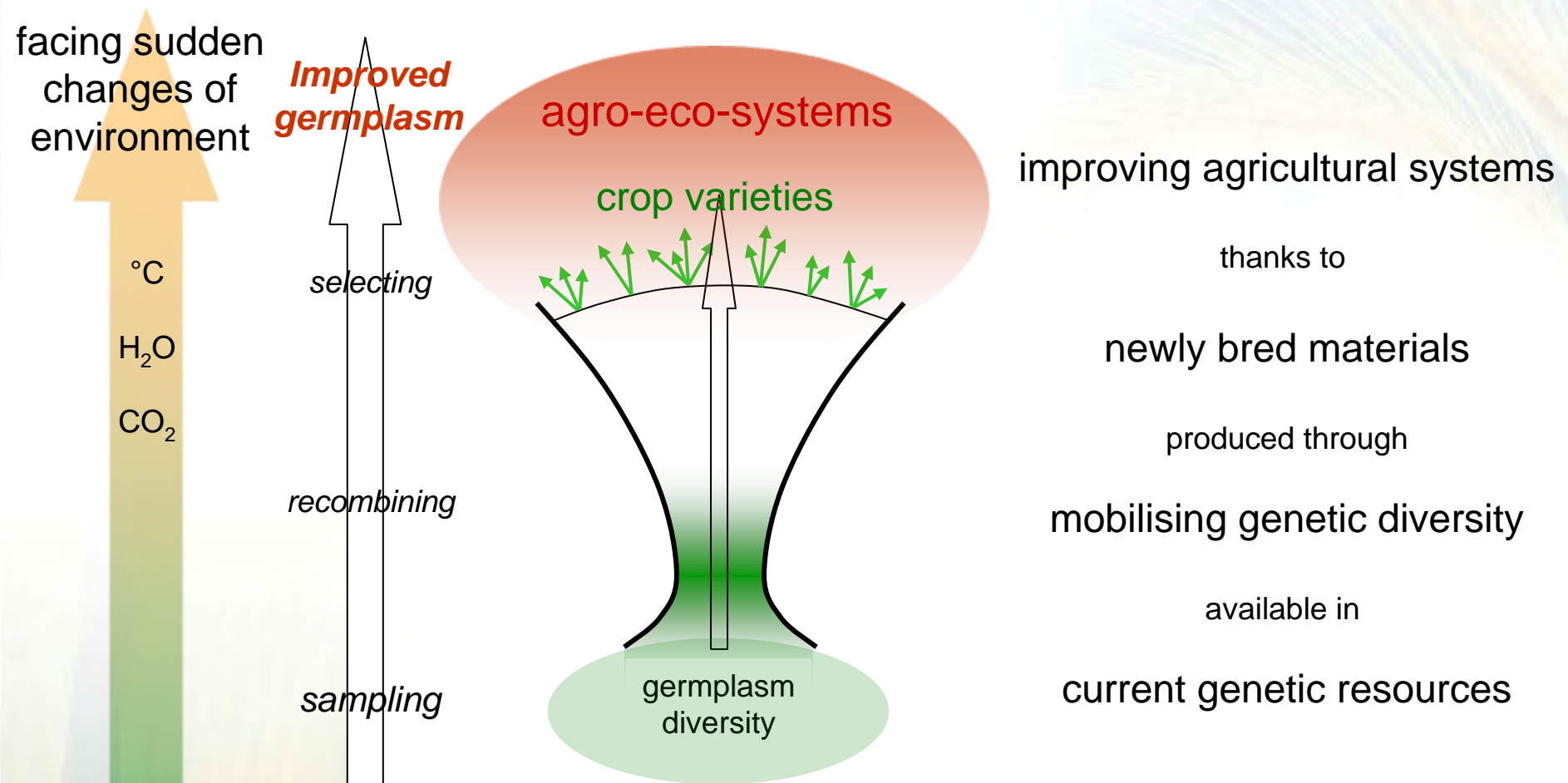
Jean Christophe Glaszmann
CIRAD, France and GCP, Mexico

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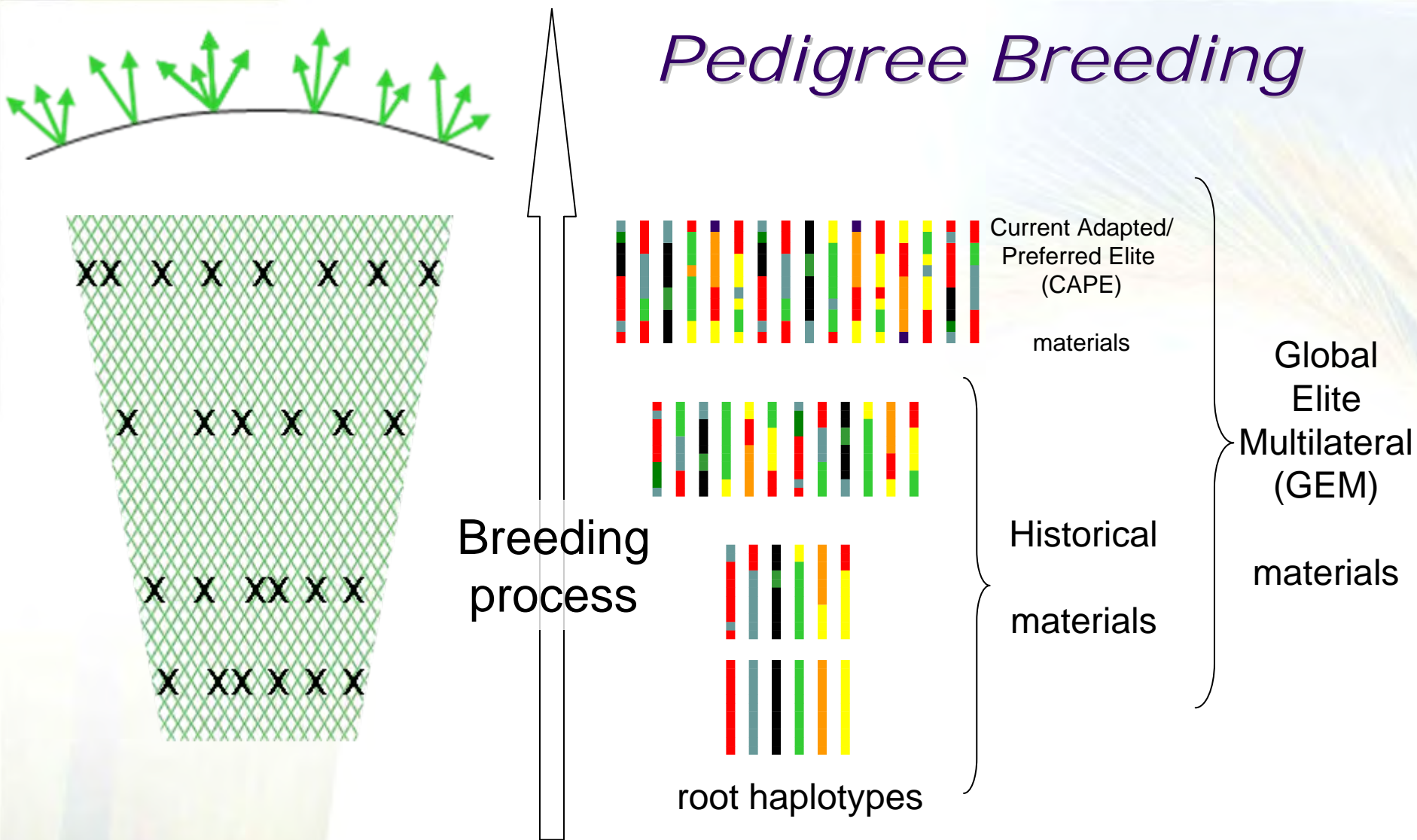
*Generation Challenge Programme Mission: Using
genetic diversity and advanced plant science to
improve crops for greater food security in the
developing world*

Genetic Resources and Plant Breeding



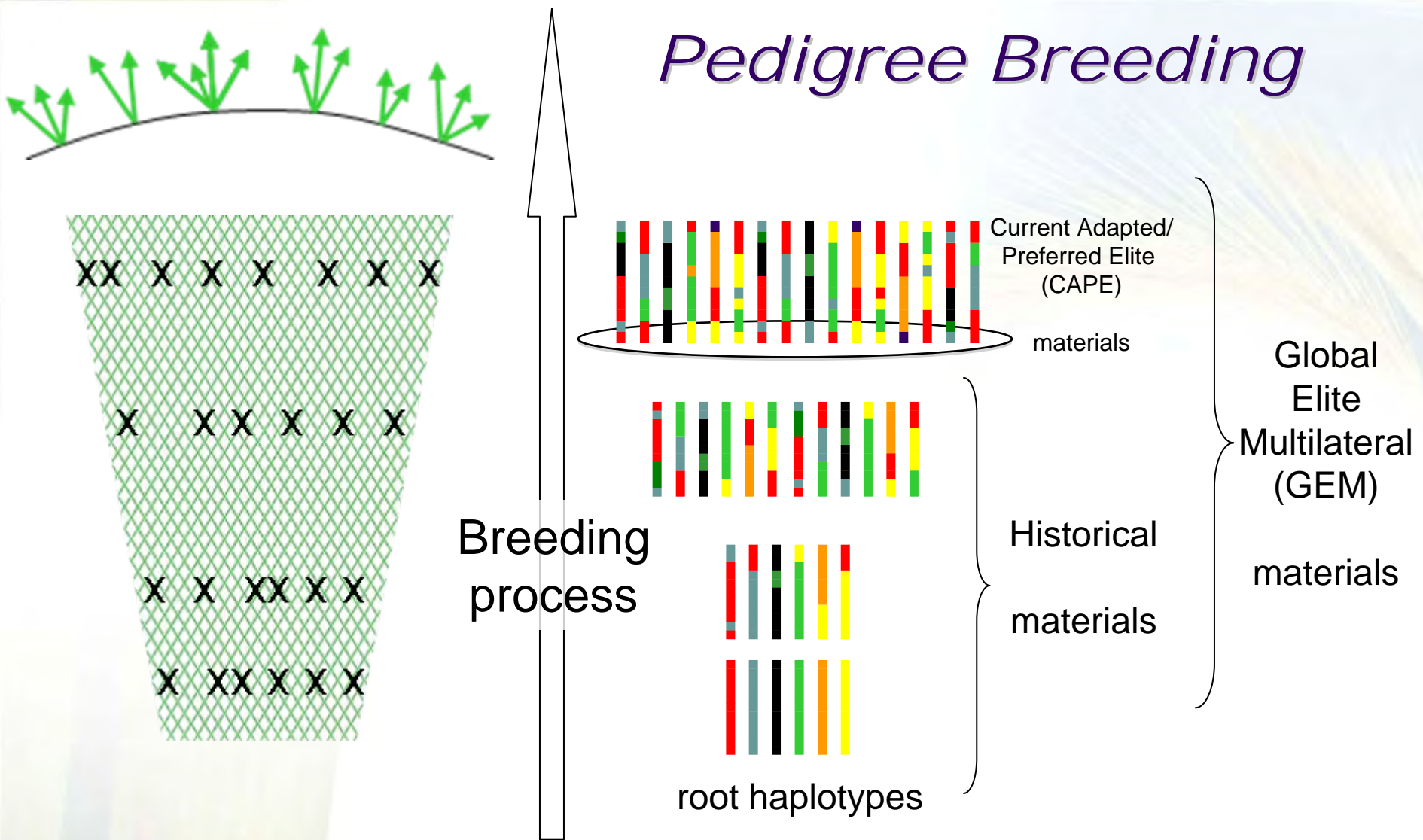
Crop improvement: mobilising genetic diversity to produce materials better adapted to human needs in diverse agricultural systems

Pedigree Breeding



The use of molecular markers enables bridging elite breeding materials to founder materials through haplotype reconstruction across historical materials

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Use of Genetic Resources

Challenges:

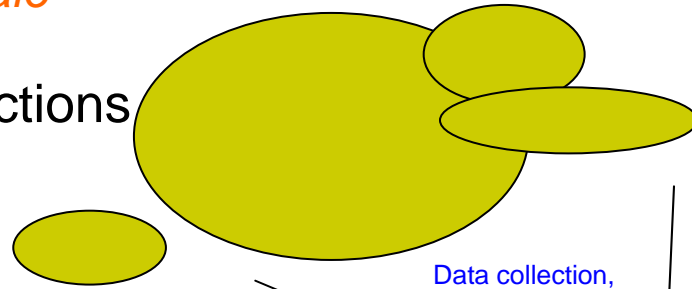
- The number and the diversity of the Genebank accessions
- The phenotypic characterisation of non-elite and unfixed material
- The sterility issue and general low level of seed production
- The uncertainty of predicting genetic breeding value in elite material

Importance of creating new genetic resources to support breeding activities

Global rationale

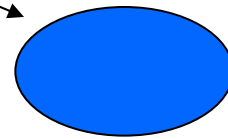
Accessing the diversity: The reference sets (A GCP initiative)

Various collections



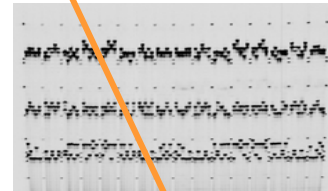
Data collection,
Analysis

Step 1: from passport information,
sampling global resources
to produce a core sample



Representative composite sample
(10%, up to 3000)

Step 2: from molecular data
sampling the core sample
to produce a reference sample
for integrated characterisation
and evaluation efforts

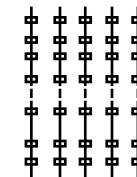
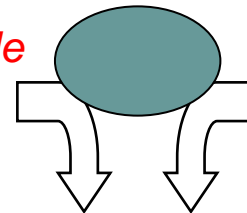


Marker development
Genotyping,
Sampling

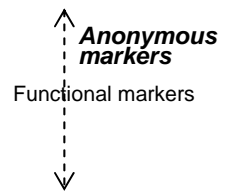
Reference sample



Phenotyping



Genotyping



Step 3. Association studies



genes/alleles tagged for marker-assisted breeding

Three steps to elaborate reference collections in order to
mine genes, alleles and markers

Identification of Favorable Genes in “Bad” Genetic Background: a Real Challenge

Genetic Resource use is challenged because of the difficulty to characterize and phenotype them in target environments

- ◆ Not fixed material
- ◆ Inbreeding issues
- ◆ Adaptation affects plant phenotype
- ◆ Phenotyping per se is of little value

Often a need to:

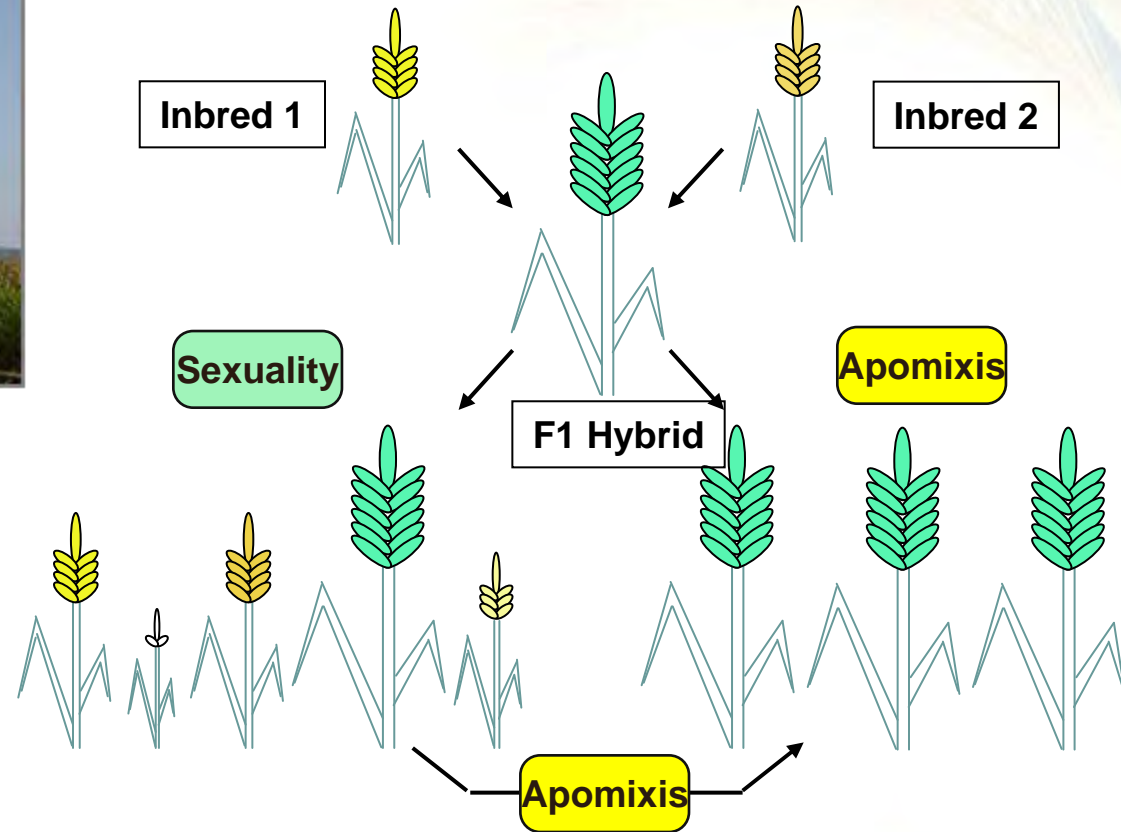
Go to the gene in the material of origin
Cross with more elite material



New genes: The Apomictic Crops From Tripsacum to Maize



- **Transfer from apomictic wild relatives**
- **Breeding approach did not work**
- **From a simple to a complex genetic regulation**
- **Going to the gene(s)**
- **Private-public partnership**



New Alleles in Wild Relatives for Peanut

José Valls, Embrapa; David Bertioli, Universidade Catolica de Brasilia; Serge Braconnier, CERAAS; Jonathan Crouch, CIMMYT; Pietro Piffanelli, CIRAD; Guillermo Seijo, IBONE; Jens Stougaard, University of Aarhus; Vincent Vadez, ICRISAT

Problem:

Peanut's limited parentage in cultivated varieties resulted in a genetic bottleneck for breeding

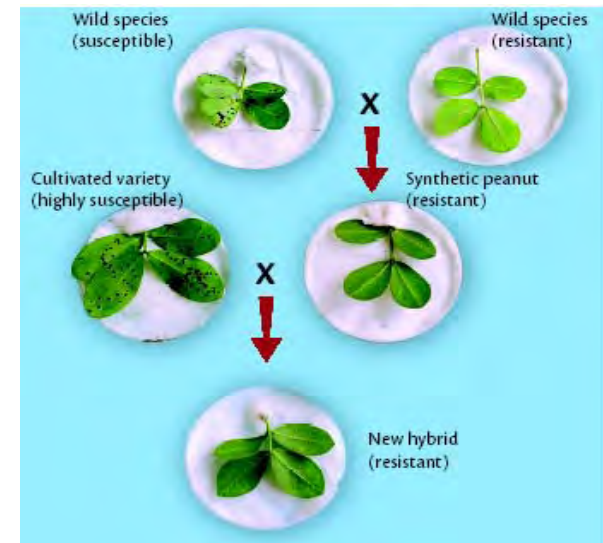
Objectives:

- Overpass a technical limitation
- Bring new alleles to the peanut crop
- Identify and introgress new traits into cultivated peanut

Products:

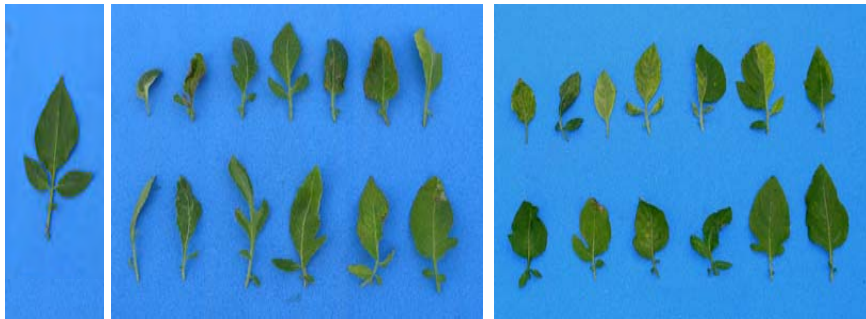
- New genetic basis for pre-breeding
- Improved germplasm for marginal environments

A GCP project led by Embrapa



Novel Genomic Resources: Creating Diversity Through Mutations

Solanum verrucosum (TRHRG23)
mutant stock -phenotypic variation



Ghislain et al. CIP



Bean mutant leaf phenotypes
observed in the screenhouse
evaluation of TILLING mutant
(Blair et al. CIAT)

Novel Genetic Resources: The Access

- Most of this material is in the hands of the scientists
- Commitments from Institutions to centralize the management of novel genetic resources in Genebanks or through international testing
- The Genetic Resource Supply Service initiative:
Shall ensure maintenance, quality control and distribution, of well-characterised (genotypic and phenotypic data) and diverse “new” genomic resources that include:
 1. reference sets
 2. collections of mutants
 3. introgression lines
 4. mapping populations
 5. near isogenic line
 6. Prebreeding material



There is a need to add value to these genetic resources by running more phenotyping studies under different environment.