Traditional and Modern Plant Breeding Methods

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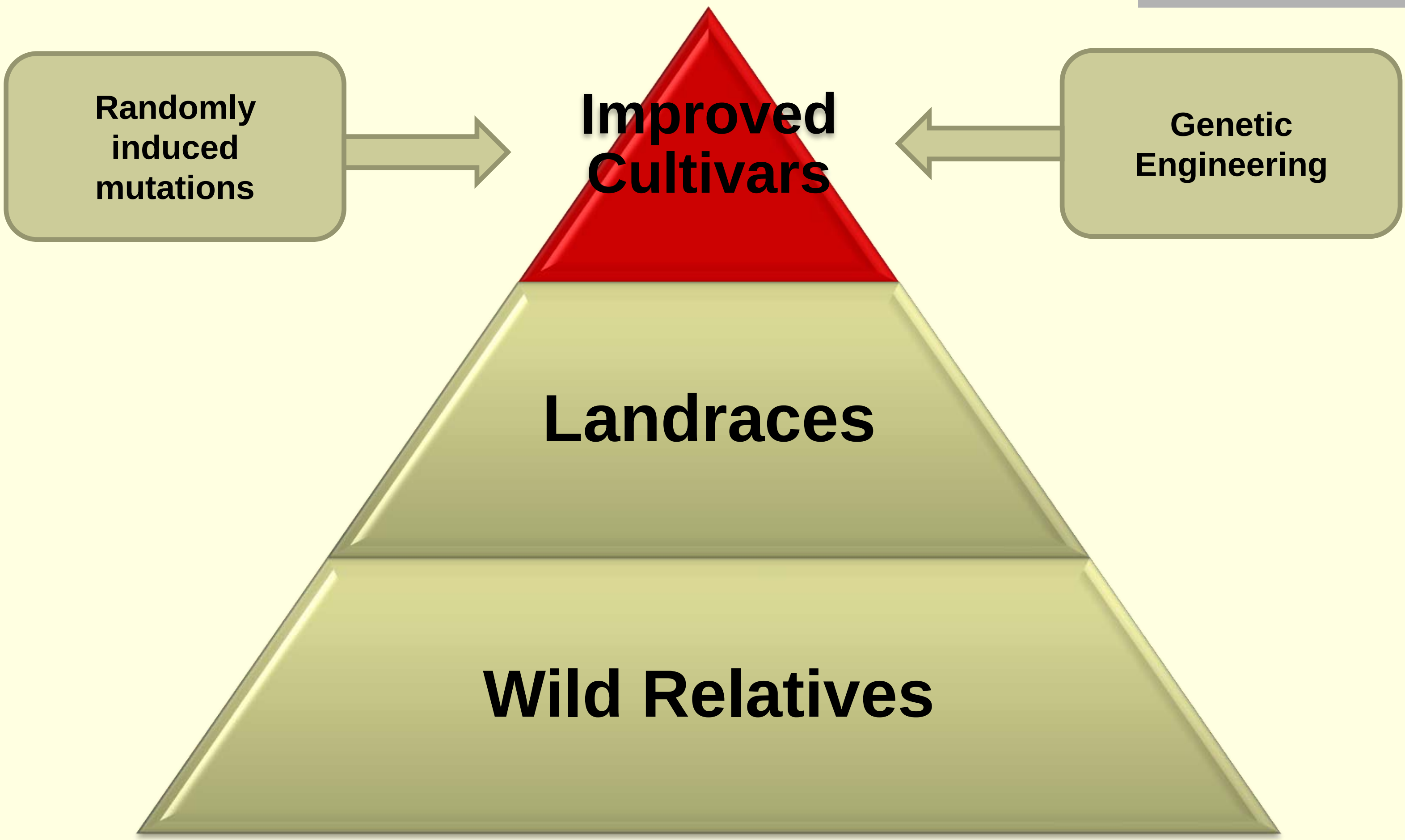
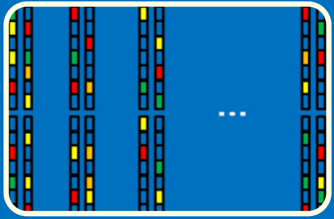
Genetic Diversity for Plant Breeding



Plant Breeding Eras

1) Plant Breeding Based on Observed Variation

2) Plant Breeding Based on Controlled Mating



3) Plant Breeding Based on Monitored Recombination

1. Phases of Plant Breeding Based on Observed Variation

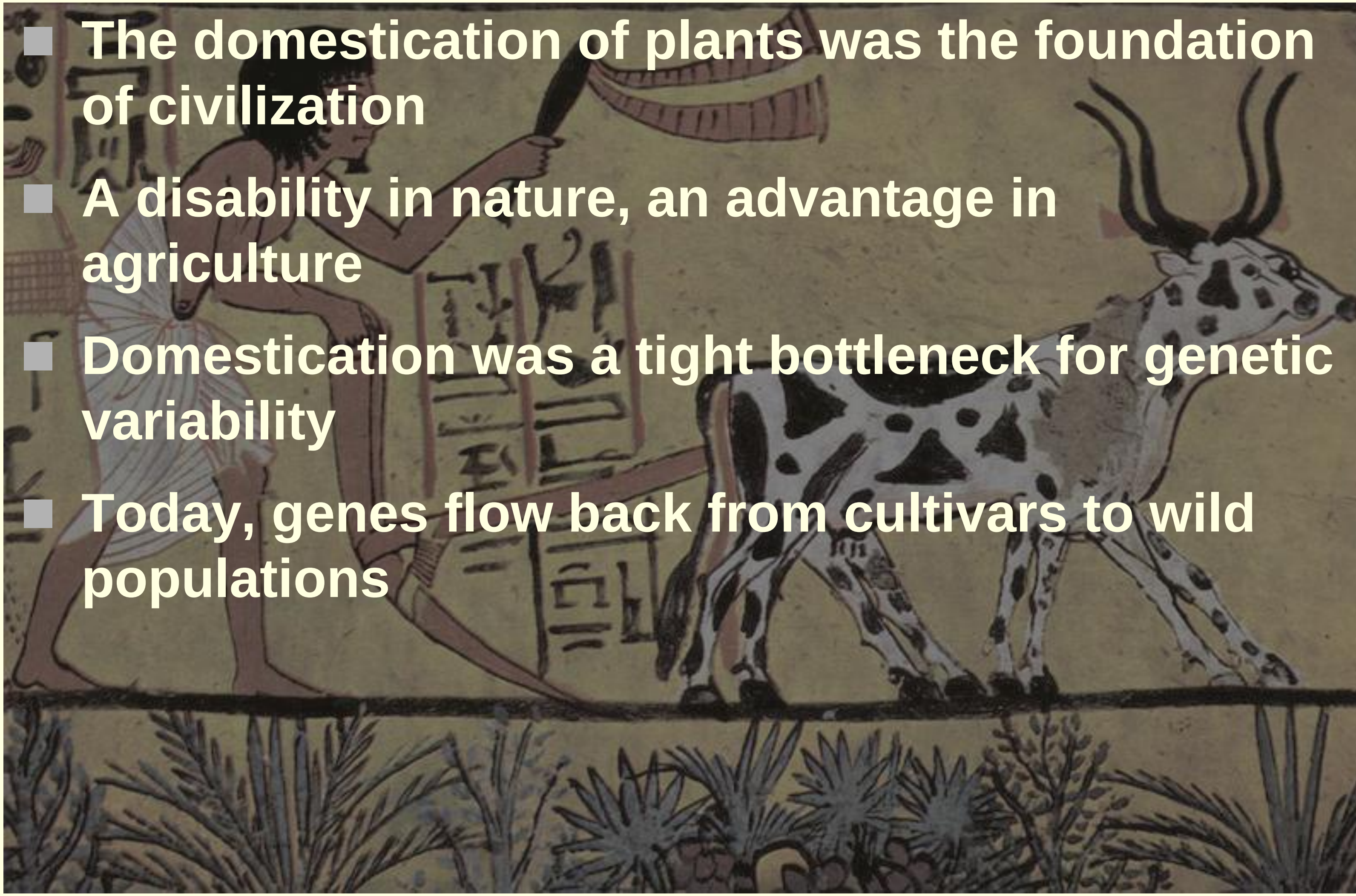
1.1 Plant domestication:
the origin of crops

1.2 Intuitive farmer selection:
the origin of landraces

1.3 Pure line selection and mass selection:
the origin of cultivars

1.1 Plant Domestication: the Origin of Crops

- The domestication of plants was the foundation of civilization
- A disability in nature, an advantage in agriculture
- Domestication was a tight bottleneck for genetic variability
- Today, genes flow back from cultivars to wild populations



1.2 Intuitive Farmer Selection: the Origin of Landraces

- Diverse, evolving populations
- Shaped by soil, climate, pests and cropping systems
- Moderate but stable yield
- Connected to local cuisine

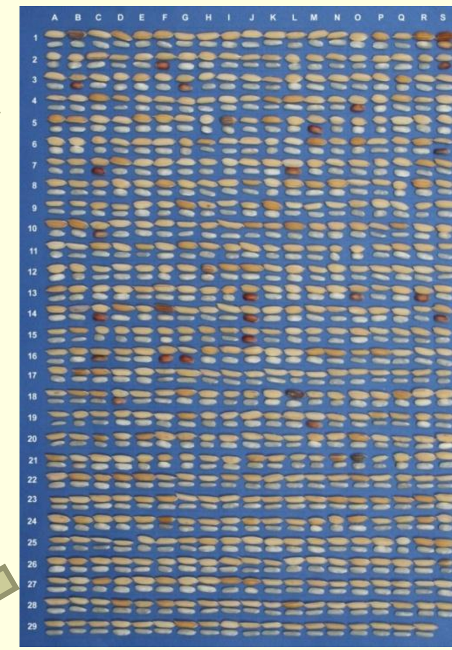
Landraces are Valuable Genetic Resources for Plant Breeding

Collecting

REPLACING

Conserving

Characterizing

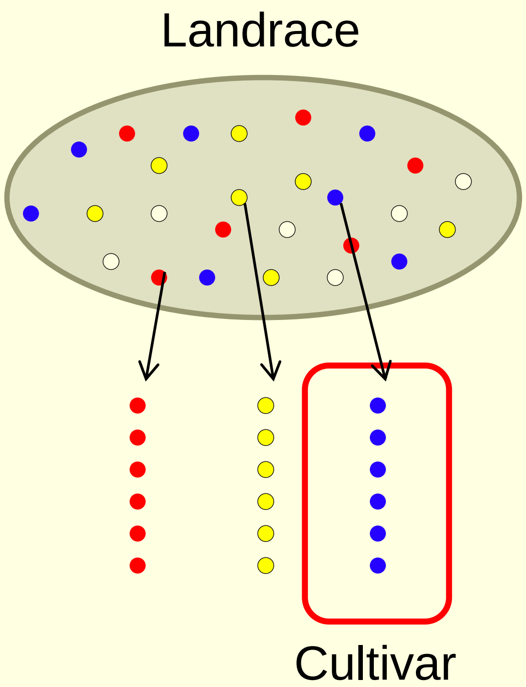


Screening

Identifying off-types and outliers

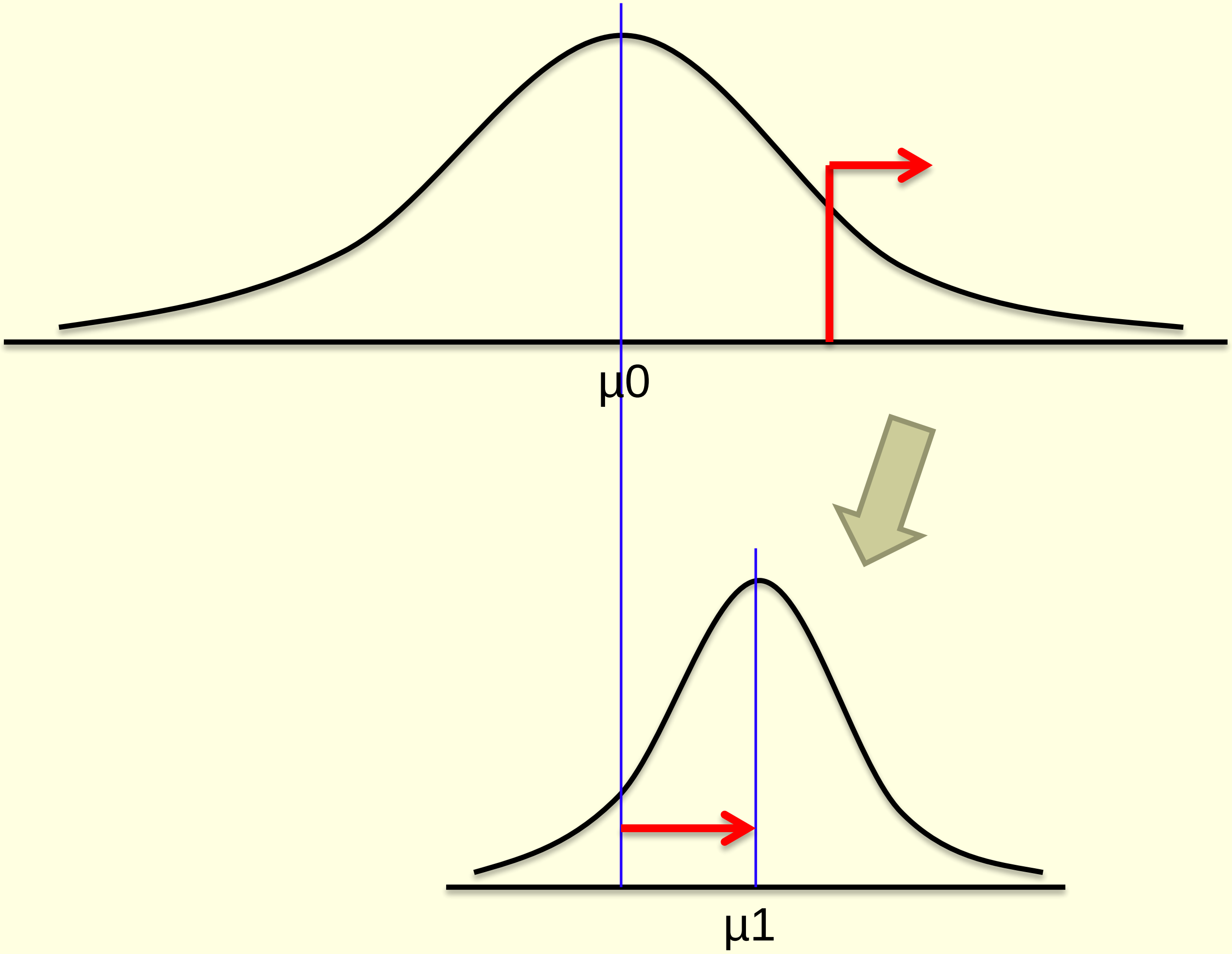
Breeding

1.3.1 Pure Line Selection (Self-pollinating species, e.g. rice or beans)



- ***Genetic variance within -> between varieties***

1.3.2 Mass Selection (Cross-pollinating species, e.g. maize)



Conclusion of Part 1

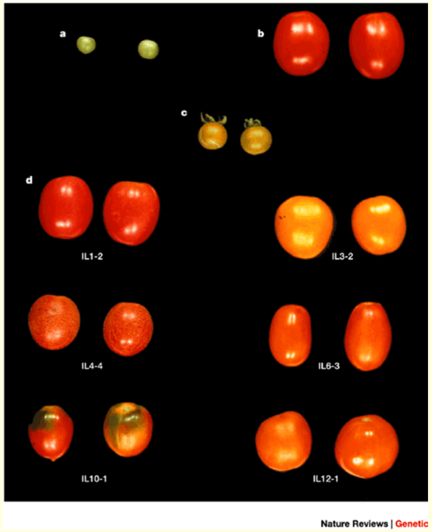
- Premise: Plant domestication and intuitive selection worked on pre-existing variation, resulting in deep changes in plant phenotypes.
- Proposition: within-landrace selection led to the **paradigm of homogeneity** in agriculture, which is in effect until today.
- Question: can we recover agriculture diversity without having a setback in productivity?

2. Plant Breeding Based on Controlled Mating

- 2.1 Pedigree Breeding
- 2.2 Ideotype Breeding
- 2.3 Population Breeding
- 2.4 Hybrid Breeding

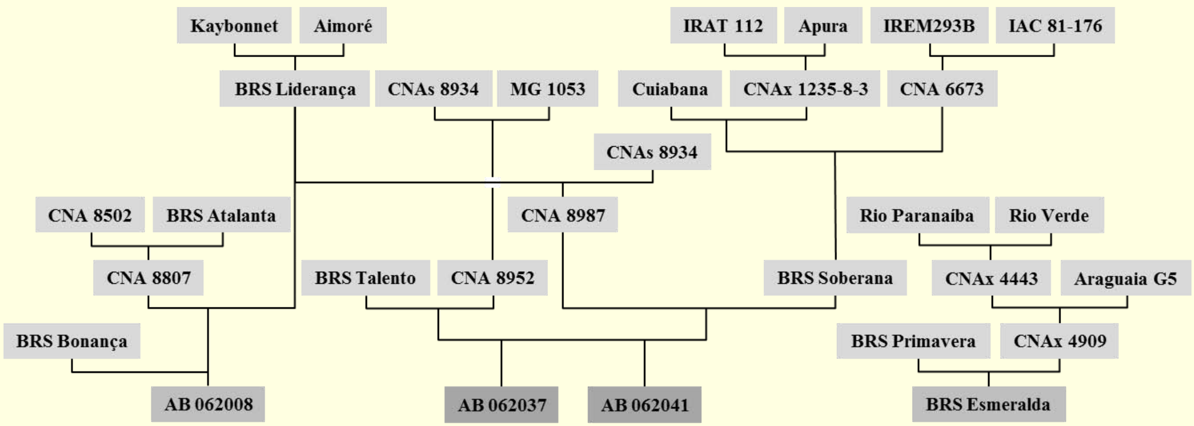
Critical Factors for the Success of a Conventional Breeding Program

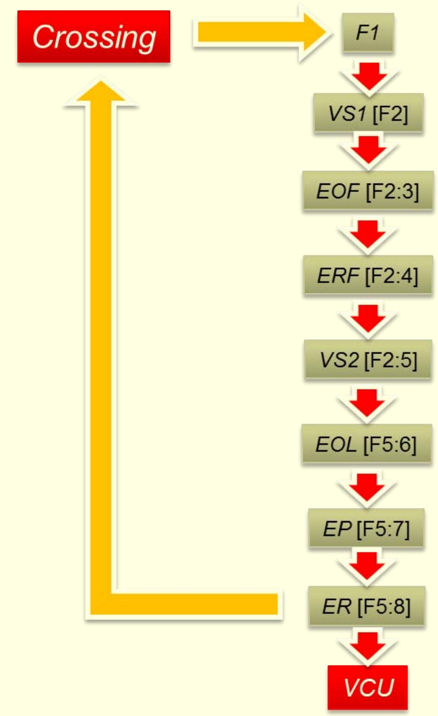
- Clear definition of target environments and priority traits
- Access to germplasm
- Reliable crossing procedures
- Fast generation advancement
- Capacity to evaluate a large number of genotypes
- Representative multiple-location trials
- Efficient production of foundation seed



2.1 Pedigree Breeding

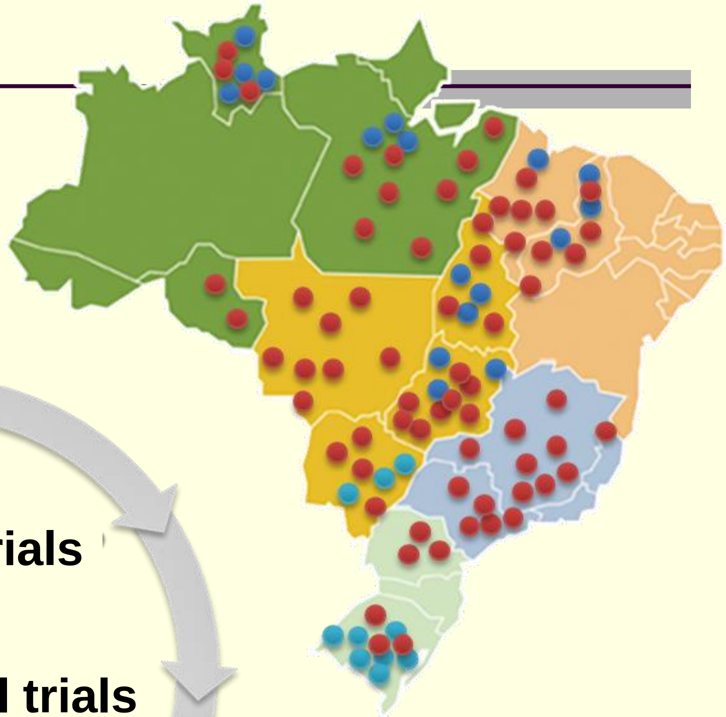
- **The most common breeding method for self-pollinated crops.**
- **Less efficient for quantitative traits**








Multiple Environment Trials



Breeding lines nurseries

Preliminary trials

Regional trials

VCU trials

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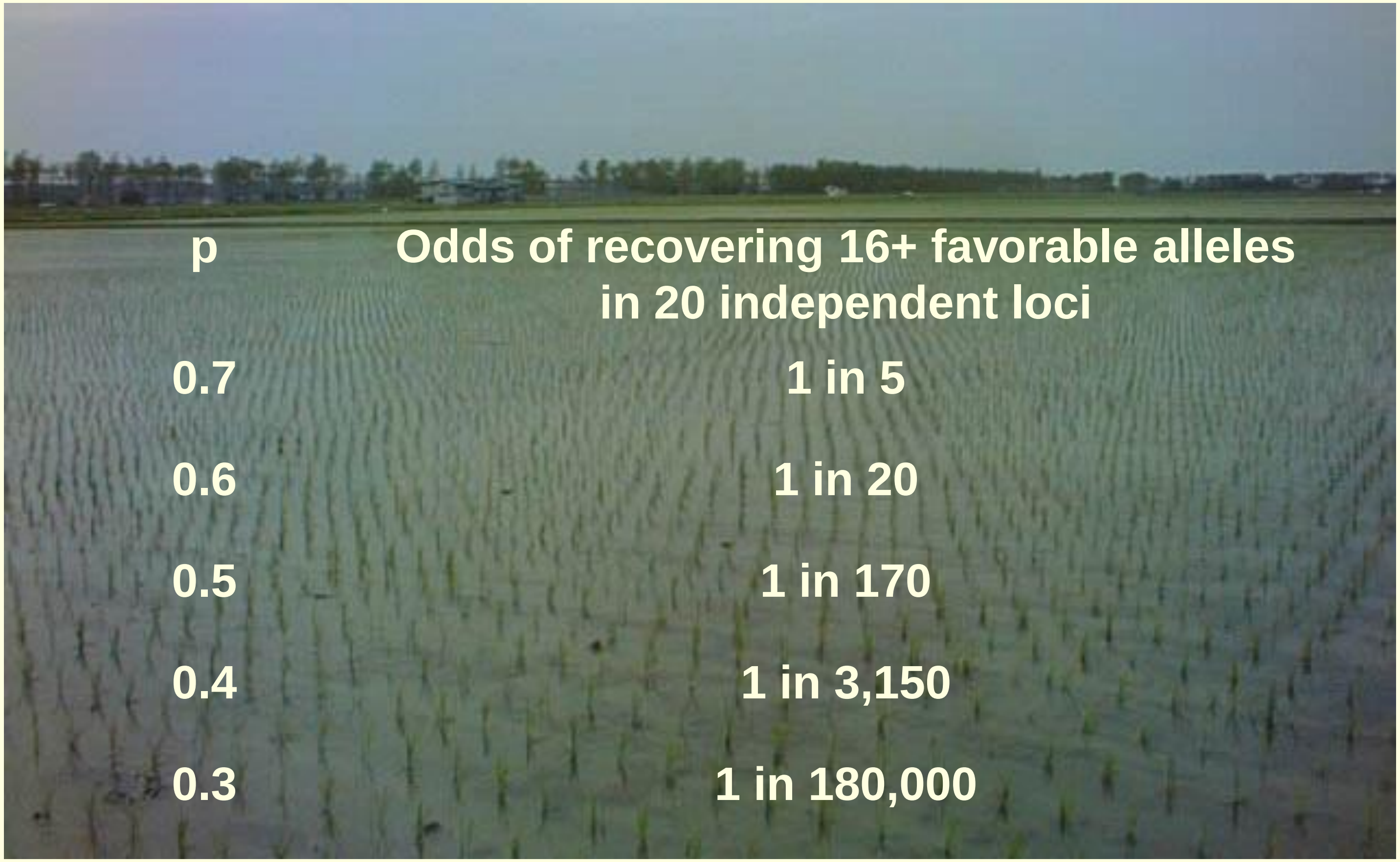
Plant Breeding is a Numbers Game



p	Odds of recovering 16+ favorable alleles in 20 independent loci
0.7	1 in 5
0.6	1 in 20
0.5	1 in 170
0.4	1 in 3,150
0.3	1 in 180,000

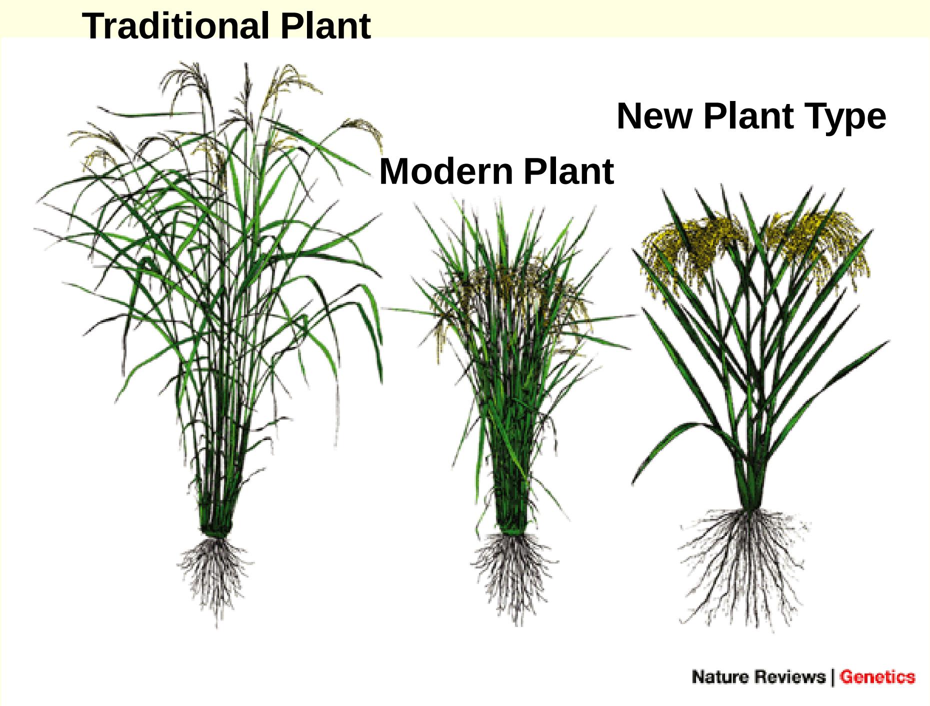
2.2 Ideotype Breeding

- A hypothesis driven approach
- Less dependent on the size of the program
- Allows remote breeding
- Examples
  - Semi-dwarf rice and wheat cultivars
  - Rice “New Plant Type” (from IRRI)
  - Super Hybrid Rice (from China)
  - “Nerica” rice varieties (from AfricaRice)

- *Risk: the breeder can become passionate about the hypothesis!*

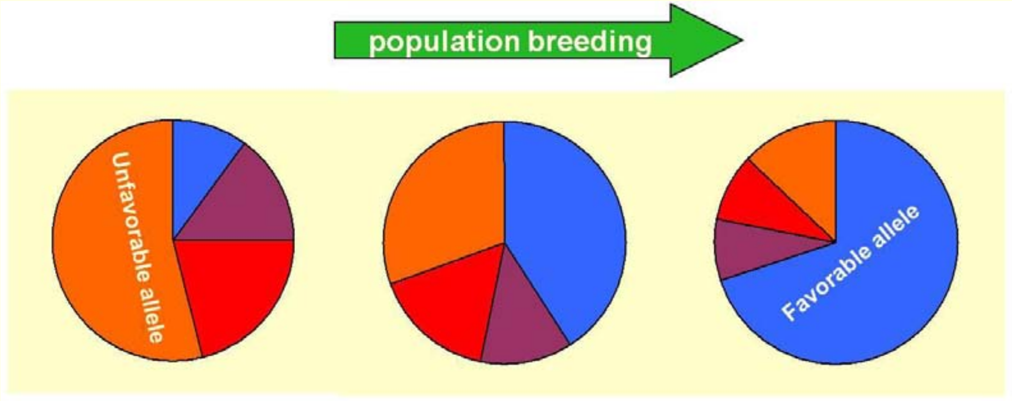
Rice “*New Plant Type*”

- Hypothesis: fewer tillers – unfertile tillers + larger panicles + stronger culms = higher yield
- Result: NPT lines failed to yield more than top performing modern type varieties.



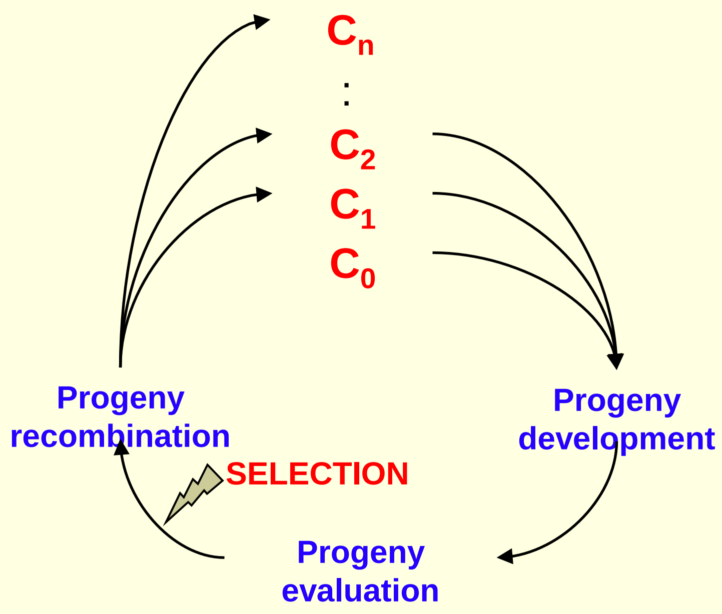
2.3 Population Breeding

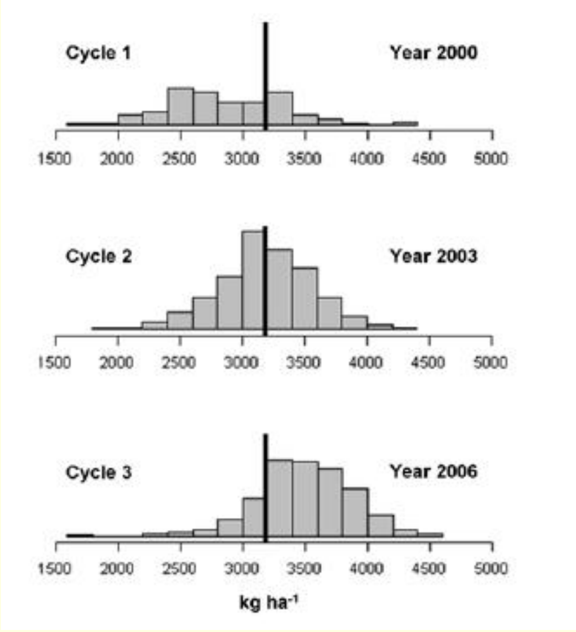
- The major framework of quantitative genetics theory
  - *Heritability*
  - *Genetic variance*
  - *Genetic correlations*
  - *Selection intensity*
  - *Selection index*
  - *Correlated responses*



Recurrent Selection: an open ended scheme

- **Increasing the genetic gain**
  - **Shorter cycle duration (efficiency)**
  - **Stronger selection pressure (size)**
  - **Better phenotyping (precision)**





Disturbing Forces in Population Breeding

- **Migration: pollen contamination, seed mixture, remaining seeds in the field**
- **Genetic Drift: sampling error due to small population size**
- **Population structure: flowering dates and plant height**
- **Unintentional selection: bird attack on early plants**

2.4 Hybrid Breeding

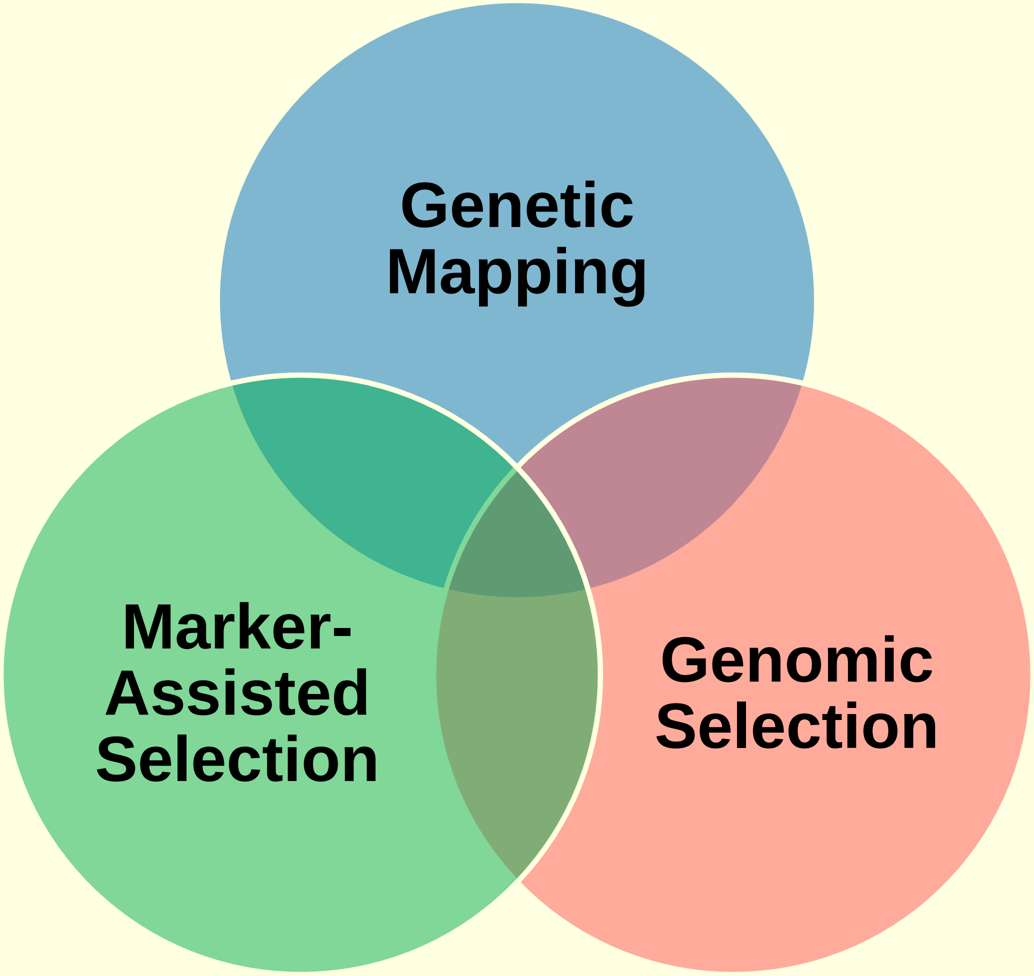
- Capturing the power of heterosis

- F1 maize hybrids: maximum heterosis and homogeneity
- Business-friendly:
  - Requires buying new seeds every year
  - Keeps GM events under proprietary control

Conclusion of Part 2

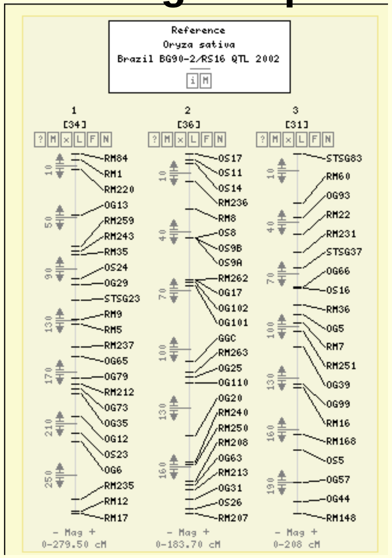
- Premise: Conventional plant breeding works within the limits of sexual compatibility of closely related species.
- Proposition: The limit of phenotypic change through recombination of alleles, followed by systematic selection, is still far from being reached.
- Question: are we putting exceedingly high expectations on plant breeding to solve global sustainability issues (end hunger, biofuels, climate change,…)?

3. Plant Breeding Based on Monitored Recombination

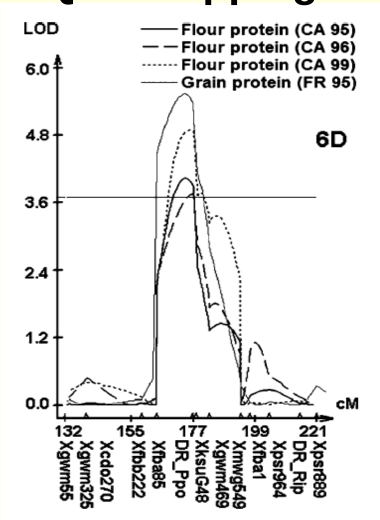


3.1 Genetic Mapping

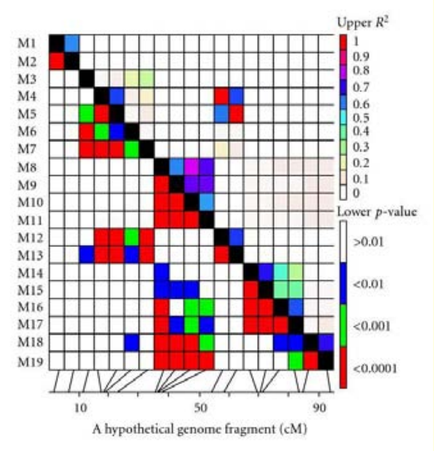
Linkage maps



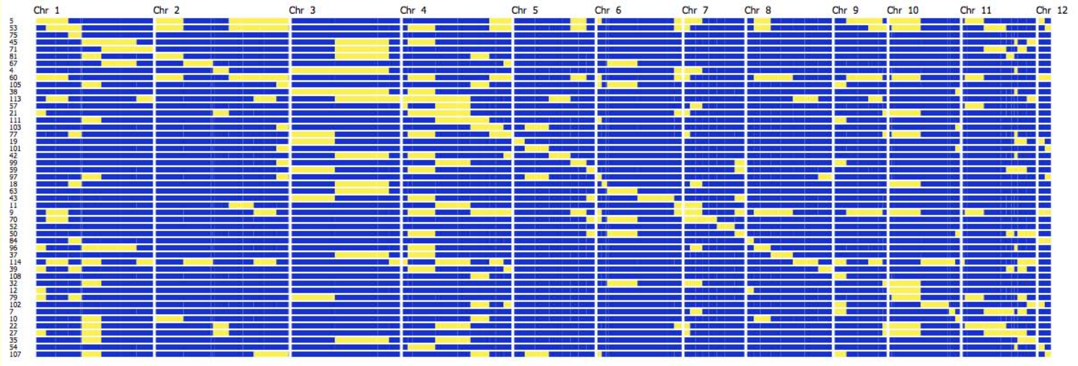
QTL mapping



Association Panels



CSSL Libraries



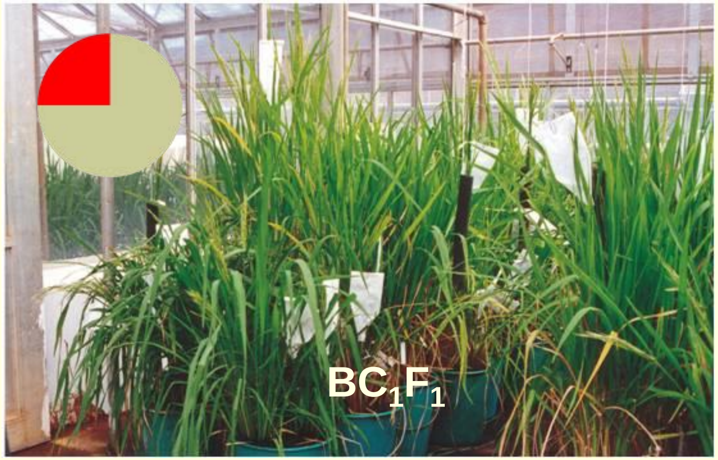
Applications of Molecular Tools in Plant Breeding

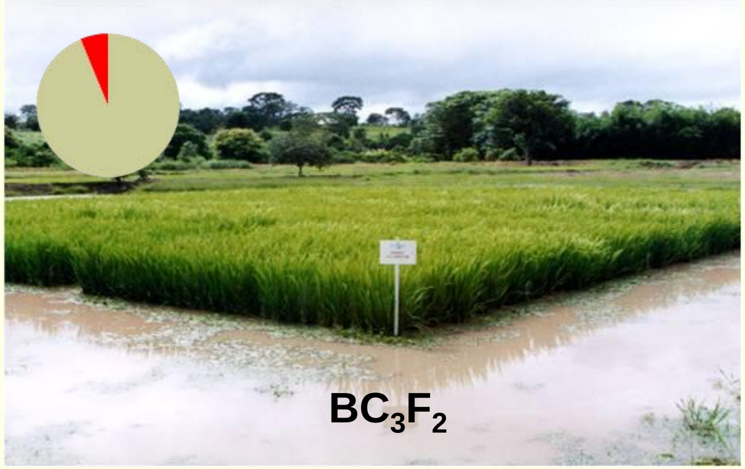
- **Assessing genetic diversity of parents**
- **Accelerating introgression of a single gene into elite lines**
- **Pyramiding disease resistance genes**
- **Selecting for genes controlling traits of difficult phenotyping**
- **Estimating breeding value based on marker profile**
- **Fingerprinting released varieties for IP protection**
- **Controlling seed quality**

3.2 Marker-Assisted Selection

	SSR	SNP
Single Locus	• Selection of major QTLs • Marker-assisted backcross • Resistance gene pyramiding	• Selection of cloned genes • Monitoring transgenes (*stewardship*)
Multiplex	• Marker-assisted backcross (background) • Genetic diversity of populations • Cultivar fingerprinting	• Characterization of parental lines (breeder's chip)

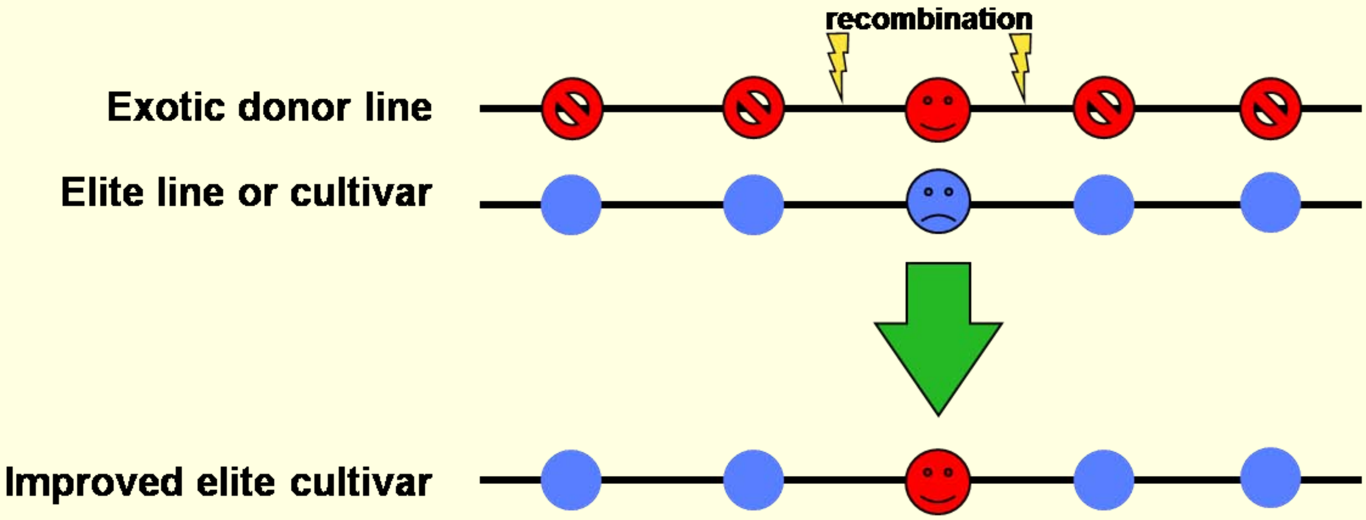
Backcross Breeding: Introgression of *O. glumaepatula* into *O. sativa*





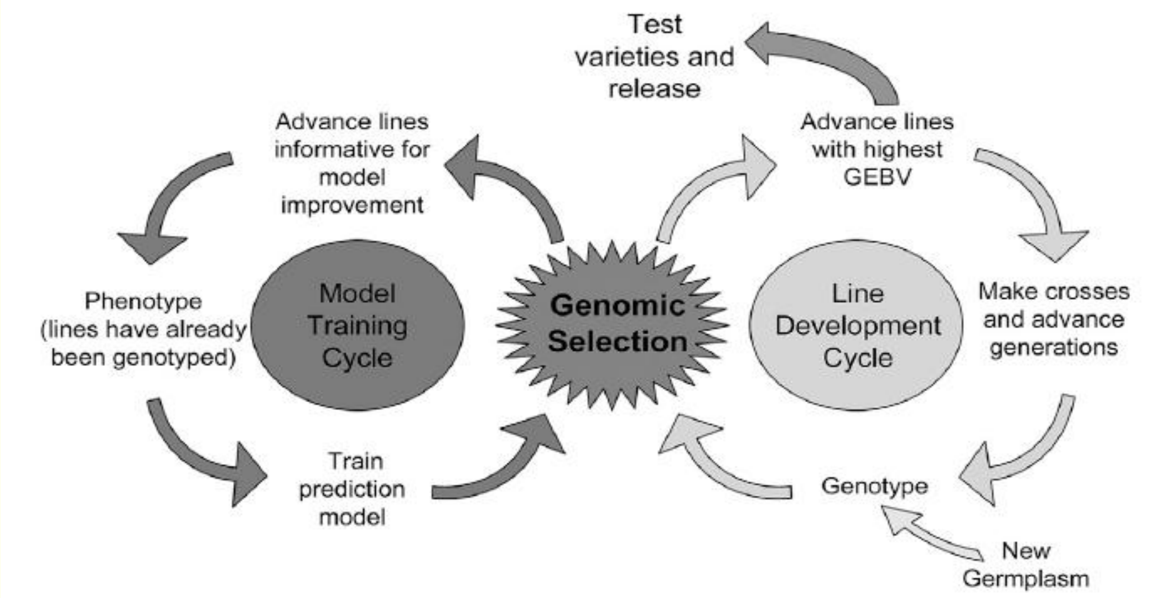
3.1 Marker-Assisted Backcross

- **The identification of short chromosome segments harboring genes facilitate the use of exotic germplasm**



3.3 Genomic Selection

- An strategy to infer breeding value from genotypic data alone, based on a subset of individuals phenotyped + genotyped.
- Reconciliate MAS with quantitative genetics.
- Requires a efficient pipeline of sample/data processing.



Heffner et al. Crop Sci., 49:1-12, 2009

Conclusion of Part 3

- Premise: New molecular tools allow better use of allele diversity, making easier handling specific genes and using exotic germplasm.
- Proposition: Molecular breeding will make a large impact on released varieties in the next decades.
- Question: Will we ever have full control of genetic recombination, thus being able to design and build entire genotypes *in silico*?


Thank you for your attention
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