



LOUISIANA STATE UNIVERSITY
College of Agriculture
School of Plant, Environmental, and Soil Sciences
AGRO 7075 Prediction-based Breeding



Selecting lines, testers and testcrosses

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Main method to obtain lines

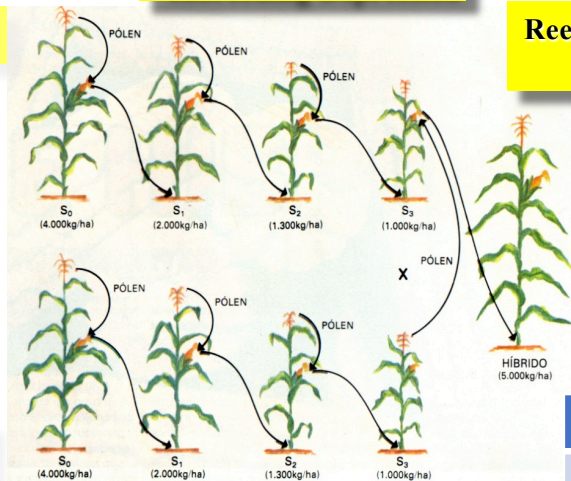
Inbreeding Depression

**Reestablish the vigor
Heterosis**

GROUP (A)

**Pedigree
within
group**

GROUP (B)

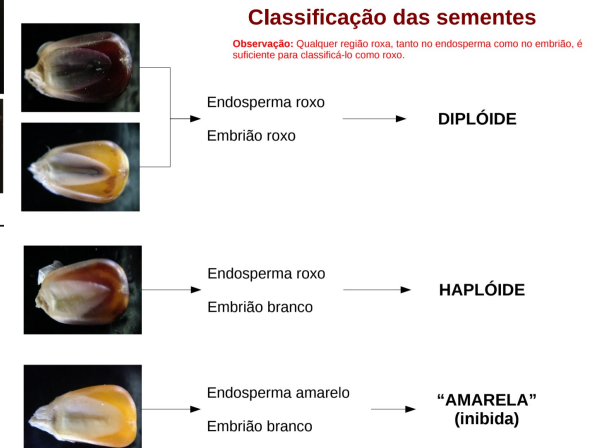
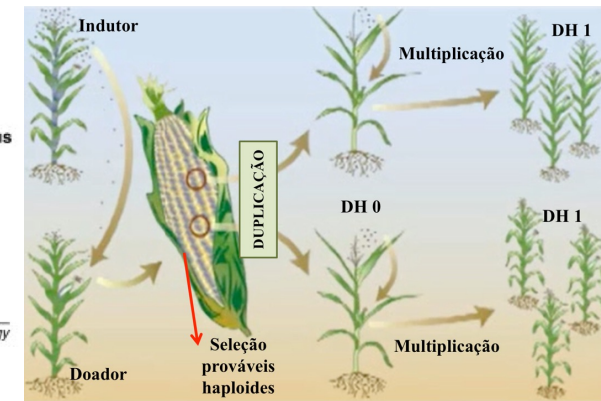
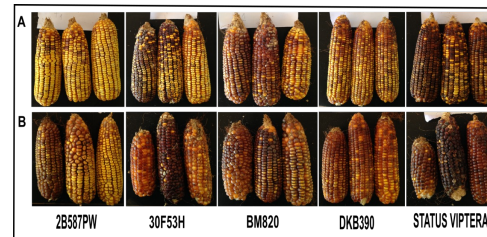
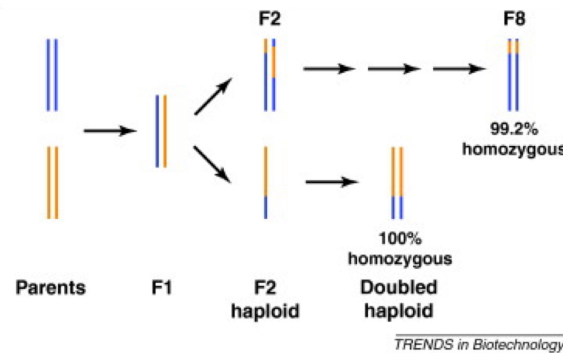


**Single-cross
(12,000 Kg / ha)**

Line	Among					Within				
	Va	Vd	D1	D2	H	Va	Vd	D1	D2	H
S1	1	0.25	1	0.12	0	0.5	0.25	1	0.38	0.25
S2	1.5	0.13	2.5	0.56	0.06	0.25	0.13	0.5	0.19	0.13
S3	1.75	0.06	3.25	0.78	0.05	0.13	0.06	0.25	0.09	0.06
S6	1.97	0.01	3.95	0.97	0.01	0.02	0.02	0.03	0.01	0.01
S _∞	2	0	4	1	0	0	0	0	0	0

Double-haploids

- **Advantages**
 - Reduce the time to obtain lines
 - The unique method to achieve $F = 1$
 - Conserve most of the parent's haplotypes
- **Drawbacks**
 - It allows just one crossing-over
 - There is no selection – too much variability
 - Lots of lines in the end
 - **Must be associated with Genomic selection**
- **Challenges**
 - Low induce rate
 - The identification is time-consuming and subjective
 - High costs to obtain the lines
 - Patents



Should we select genotypes based on lines or hybrids?

- Average degree of dominance (add)
- $add = d/a = \psi$

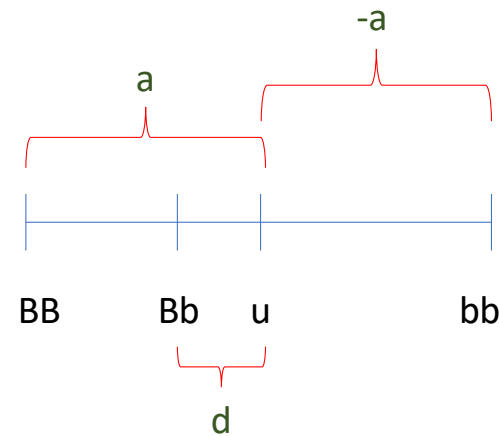
- Considering an F_2 population

- $p = q = 0.5$
- $\alpha = [a + (q - p)d]$

- $Va = 2pq\alpha^2 = 2pqa^2 = \frac{1}{2}a^2$ $a = \sqrt{2.Va}$

- $Vd = (2pqd)^2 = \frac{1}{4}d^2$ $d = \sqrt{4.Vd}$

$$add = \frac{d}{a} = \frac{\sqrt{4.Vd}}{\sqrt{2.Va}}$$



0	Absence of dominance
$0 < d/a < 1$	Partial dominance
1	Complete dominance
>1	Overdominance

Correlation between lines and hybrids

$$r_{L,H} = \frac{\sigma_{LH}}{\sigma_L \sigma_H}$$

- **Line**

- $G_{ii} = \alpha_i + \alpha_i + S_{ii}$

- **Hybrid**

- $G_{ij} = \alpha_i + \alpha_j + S_{ij}$

- **Genetic variance among lines**

- $V_{GL} = E[G_{ii} - E(G_{ii})]^2$

- $= E[u + \alpha_i + \alpha_i + S_{ii} - u]^2$

- $= E[2\alpha_i + S_{ii}]^2$

- $= E[2\alpha_i]^2 + 2E[\alpha_i S_{ii}] + E[S_{ii}]^2$

- $= 4E[\alpha_i]^2 + 2E[2\alpha_i S_{ii}] + E[S_{ii}]^2$

- $= 4E[\alpha_i]^2 + 4E[\alpha_i S_{ii}] + E[S_{ii}]^2$

- $= 2V_a + 4D_1 + D_2$

- **Genetic variance among single-crosses**

- $V_{GH} = E[G_{ij} - E(G_{ij})]^2$

- $= E[u + \alpha_i + \alpha_j + S_{ij} - u]^2$

- $= E[\alpha_i + \alpha_j + S_{ij}]^2$

- $= E[\alpha_i]^2 + E[\alpha_j]^2 + E[S_{ij}]^2 + \dots$

- $= E[\alpha_i]^2 + E[\alpha_j]^2 + E[S_{ij}]^2$

- $= \frac{1}{2}V_a + \frac{1}{2}V_a + V_d$

- $= V_a + V_d$

- **Covariance between lines and single-crosses**

- $COV_{(L,H)} = E[G_{ij} - E(G_{ij})] \cdot E[G_{ii} - E(G_{ii})]$

- $= E[\alpha_i + \alpha_j + S_{ij}] \cdot E[2\alpha_i + S_{ii}]$

- $= 2E[\alpha_i]^2 + E[\alpha_j S_{ii}] +$

- $2E[\alpha_i \alpha_j] + 2E[\alpha_j S_{ii}] + 2E[\alpha_j S_{ii}] + 2E[\alpha_i S_{ij}] + 2E[S_{ii} S_{ij}]$

- $= 2E[\alpha_i]^2 + E[\alpha_j S_{ii}]$

- $= V_a + D_1$

Correlation between lines and hybrids

$$r_{L,H} = \frac{\sigma_{LH}}{\sigma_L \sigma_H}$$

$$r_{L,H} = \frac{Va + D1}{\sqrt{(2Va + 4D1 + D2)(Va + Vd)}}$$

$$r_{L,H} = \frac{Va}{\sqrt{(2Va)(Va + Vd)}}$$

$$r_{L,H} = \frac{Va}{\sqrt{(2Va)(Va + \psi Va)}}$$

$$r_{L,H} = \frac{Va}{\sqrt{(2Va)Va(1 + \psi)}}$$

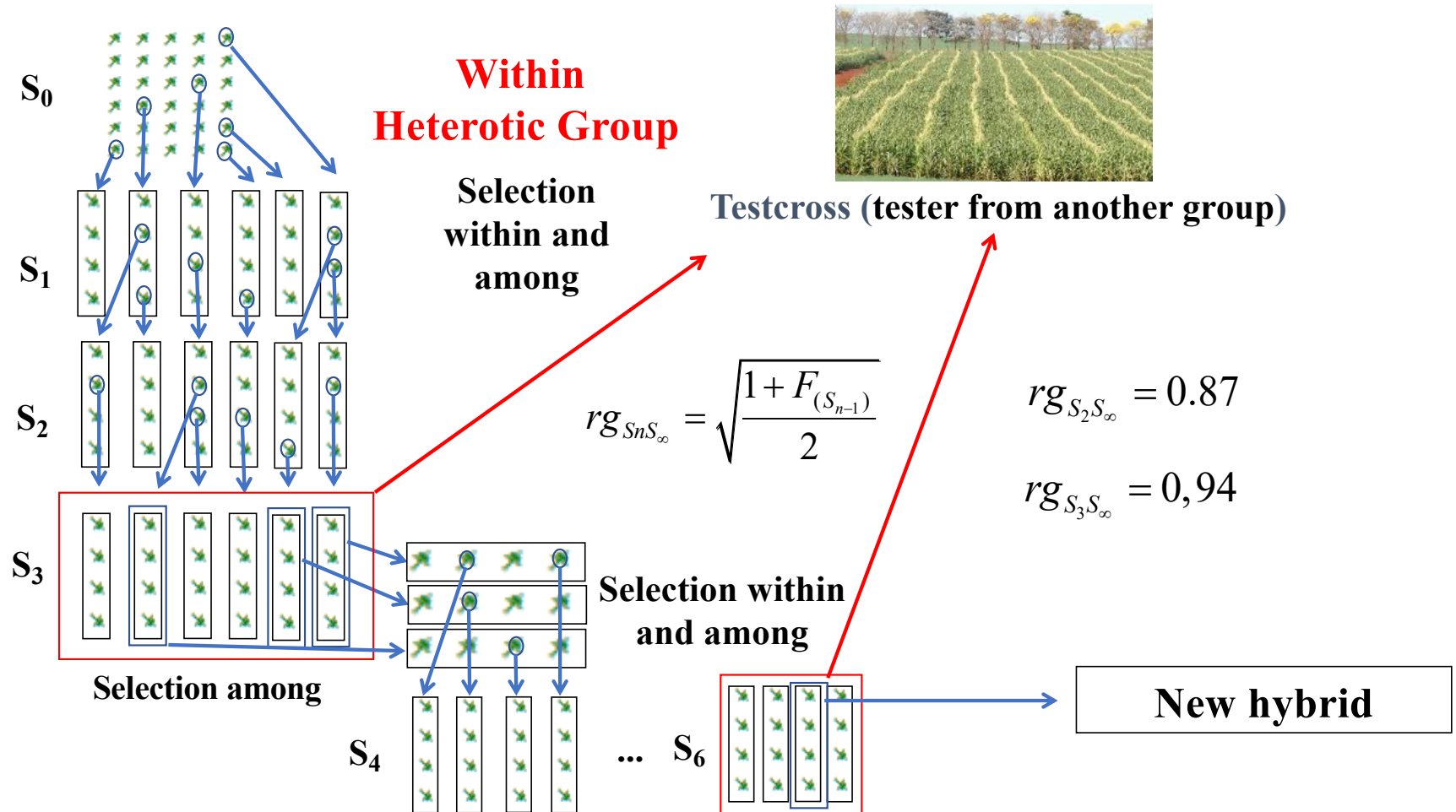
- Within population
- $F_2 = D1 = D2 = 0$
- $H = Vd$
- $\psi = Vd / Va$
- $Vd = \psi Va$

$$r_{L,H} = \frac{Va}{Va\sqrt{2(1 + \psi)}}$$

$$r_{L,H} = \frac{1}{\sqrt{2(1 + \psi)}}$$

- | | |
|--------------------------|--------------------|
| • $Vd = 0; \psi = 0$ | • $r_{L,H} = 0.71$ |
| • $Vd / Va = \psi = 1/2$ | • $r_{L,H} = 0.58$ |
| • $Vd / Va = \psi = 1$ | • $r_{L,H} = 0.50$ |

Obtaining lines – Early testcross



Early testcross

$$r_g = \frac{COV_{testcross}(g, g')}{\sqrt{V_{Tg} \cdot V_{Tg'}}$$

$$V_{Tg} = \frac{1}{2}pq[1 + Fg]\alpha_T^2$$

$$V_{Tg'} = \frac{1}{2}pq[1 + Fg']\alpha_T^2$$

$$COV_{Tg, g'} = \frac{1}{2}pq[1 + Fg]\alpha_T^2$$

$$r_g = \sqrt{\frac{1 + Fg}{1 + Fg'}} \quad r_g = \sqrt{\frac{1 + Fg}{2}}$$

- Normally, at the end we have $Fg' = 1$

TABLE 4.2. Frequencies and testcross means of genotypes (F = inbreeding coefficient).

Population		Testcross progeny			Testcross mean
Genotype	Frequency	A_1A_1	A_1A_2	A_2A_2	
A_1A_1	$p^2 + pqF$	p_T	q_T		$\mu_T + q\alpha_T$
A_1A_2	$2pq(1 - F)$	$\frac{1}{2}p_T$	$\frac{1}{2}$	$\frac{1}{2}q_T$	$\mu_T + \frac{1}{2}(q - p)\alpha_T$
A_2A_2	$q^2 + pqF$		p_T	q_T	$\mu_T - p\alpha_T$

Early generation		Late generation	
Plant	Family	S6	Inbreds
S0	S1	0.71	0.71
S1	S2	0.87	0.87
S2	S3	0.94	0.94
S3	S4	0.98	0.97

Selecting for combining ability

- Increase the frequency of favorable alleles in lines
- Ideal tester:
- *Elite line = produce the new hybrid*
- *Single cross = produce a three-way cross hybrid*

- $CA_i = (C_i - C_{..}) = g_i - \sum (p_i - p) \alpha_i^T$

- Lets consider two different lines

- $g_1 - \sum (p_1 - p) \alpha_1^T$

- $g_2 - \sum (p_2 - p) \alpha_2^T$

- $g_1 - g_2 = (p_1 - p) \alpha_1^T - (p_2 - p) \alpha_2^T$

- $g_1 - g_2 = (p_1 - p) \alpha_1^T - (p_2 - p) \alpha_2^T$

- $= (p_1 - p_2) \alpha^T$

- The difference is due to the frequency of favorable alleles

Line	f(B)	Line x tester	CA
L1	p1	C1	CA1 = C1 - C..
L2	p2	C2	CA2 = C2 - C..
L3	p3	C3	CA3 = C3 - C..
...
L100	p100	C100	CA4 = C4 - C..
Mean	p	C..	

Choosing testers

- The best tester = **correctly classify the lines**
- Normally, it comes from the another heterotic group
- Should the tester be a elite or a poor line?
- **Level of dominance and allele frequencies**
- Consequences in breeding values

$$BV_i = (t_i - \bar{t})[a + (1 - 2r)d]$$

- genetic variability, and

$$\sigma_T^2 = \frac{1}{2}pq(1 + F)[a + (1 - 2r)d]^2$$

- expected gain (**unrelated tester**)

$$\Delta_p = a + (1 - 2r)d$$

$$BV_i = (t_i - \bar{t})[a - 0.28]$$

$$\sigma_T^2 = pq[a - 0.28]^2$$

$$\Delta_p = a - 0.14$$

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A_1A_2	$2pq(1 - F)$	$\frac{1}{2}p_T$	$\frac{1}{2}$	$\frac{1}{2}q_T$	$\mu_T + \frac{1}{2}(q - p)\alpha_T$
A_2A_2	$q^2 + pqF$		p_T	q_T	$\mu_T - p\alpha_T$

$$d = 0.7$$

$$r = 0.6$$

$$F = 1$$

