Inbreeding, heterosis, heterotic pools, and hybrids

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Inbreeding

F_1		Aa $\otimes$		100
F_2	25% AA	50%Aa	25%aa	50
		12,5% AA 12,5% aa $\otimes$		
F_3	37,5 % AA	25%Aa	37,5%aa	25
		6,25% AA 6,25% aa $\otimes$		
F_4	43,75 % AA	12,5%Aa	43,75%aa	12,5
		$\otimes$ ...		
F_∞	50 % AA	0,0%Aa	50%aa	0,0

- Mating between related individuals

- The most extreme is self-pollination

- Increases homozygosity in the offspring (accumulative process)

- Lost in vigor, increase the Vg, changes in genotypic frequencies, and anomalies

- F = *Malécot coefficient* – IBD
  $$F_I = \left(\frac{1}{2}\right)^n$$

- *n number of shared parents*
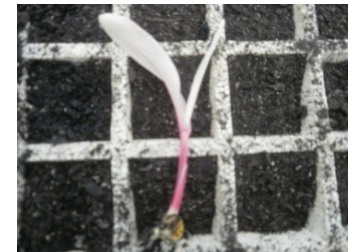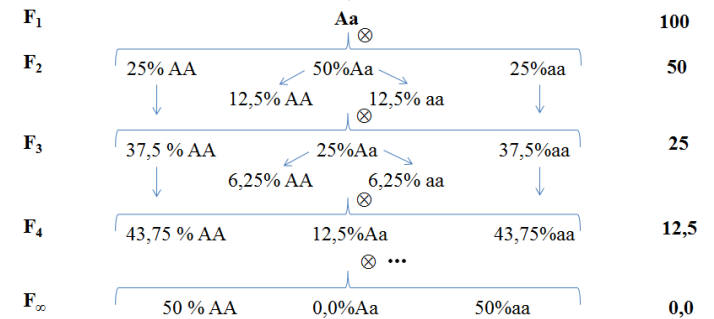
Inbreeding Depression = lost in d + genetic load

- *Inbreeding depression:* a decrease in the average phenotypic value of the population due to inbreeding

- *Genetic load:* reduction of the average adaptability of the population due to the existence of genotypes with less adaptability than the most adapted genotype

- It is not linear and depends on the trait

- First, define a reference population (F = 0)

- $u_{X0/F} = (p - q)a + 2pqd - 2pqdF$

- $u_{X0/F} = (p - q)a + 2pqd$ (F = 0; S_0)

- $u_{X1/F} = (p - q)a$ (F = 1; S_∞)

- $ID = u_{X1/F} - u_{X0/F} = (p - q)a - ((p - q)a + 2pqd) = $ -2pqd

$$ID_{\%} = \frac{X_F - X_0}{X_0} = \frac{-2pqF}{(p - q)a + 2pqd}$$

$$ID_{\%} = \frac{S_1 - S_0}{S_0} = \frac{-pq}{(p - q)a + 2pqd}$$

- Components: deviations of dominance and deleterious genes

Heterosis

- The F_1 differential performance regarding the parents mean (mid-parent heterosis)

$$H = F_1 - \left(\frac{P_1 + P_2}{2}\right) \qquad H = \sum_{i=1}^{i}(p_i - r_i)^2 d$$

- High-parent heterosis - F_1 regarding the best parent

$$Hb = F_1 - P_s$$

- Depends on the trait (can be + or -)

$$Hb = \sum_{i}(r_i - p_i)\alpha_{i1}$$

- Dominance deviations theory (it must be in trans)

- *weakness:* Superior line was never found and no there is no asymmetric distribution

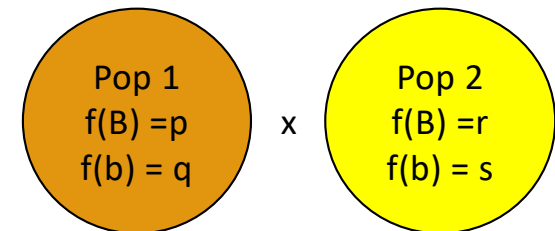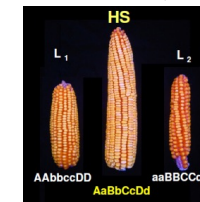- Components: d, divergence, and complementarity

Table 6.1. Estimates of the world-wide contribution of heterosis to both yield and land savings. The percent hybrid advantage is the yield increase of the hybrid over the best single variety. After Duvick (1999).

Crop	% planted as hybrids	% Hybrid yield advantage	Annual added yield Percent	Annual added yield tons	Annual Land savings
Maize	65	15	10	55×10^6	13×10^6 ha
Sorghum	48	40	19	13×10^6	9×10^6 ha
Sunflower	60	50	30	7×10^6	6×10^6 ha
Rice	12	30	4	15×10^6	6×10^6 ha

Heterosis *vs.* Inbreeding depression

- Either are non-additive

- They are not faces of the same coin:
- H: dominance, divergence, and complementarity
- ID: dominance and deleterious genes

- The first can happen without the presence of the second

- It is an within population phenomena

- Their estimates depends on the parents and the mating design used

Heterotic groups

- Group of plants that when crossed between the hybrids do not show heterosis, but when crossed with plants from another group there is significant heterosis

- They are important to
- Build hybrids and Open-Pollination Varieties
- Identify testers
- Organize the germplasm and reduce the number of crosses
- *Example*

- Methods to define them
- Full Diallel
- Molecular markers
- Tester

dent – tuxeño   *flint* – cateto

Diallel method

- Group of plants that when crossed within the group the hybrids do not show heterosis, but when crossed with plants from another group there is significant heterosis

- Crossing pairwise lines to see the performance of their hybrids

Hybrids (t ha)	L1	L2	L3	L4
L1	1.4	2,2	7,5	8,1
L2		1,3	6,9	9,5
L3			1,7	3.4
L4				1,2

- **Group A** = L1 and L2
- **Group B** = L3 and L4

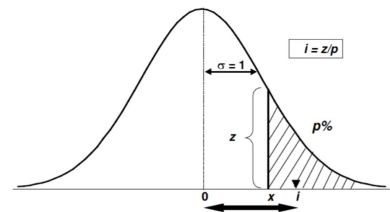# Hybrids

- Cross between two divergent but complementary lines

- Normally, they belong to different heterotic groups

- Why hybrids?
- *Combine traits that are in different parents*
- *Take advantage of heterosis*
- *Uniformity*
- *Just the best genotype (single-cross)*
- *Market seed control*


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$i = z/p$

Open Pollinated Varieties (OPV)

- **Group A = L1 and L2; Group B = L3 and L4**

- **L1 (A1A1); L2 (A2A2); L3 (A3A3); L4 (A4A4)**

- Freq. A1 (p) + A2 (q) + A3 (r) + A4 (s) = 1,0

- **Thus, let's consider** $p = q = r = s = 0,25$

- **HWE - Multinomial distribution**

- p^2 **(A1A1)+** q^2 **(A2A2) +** r^2 **(A3A3) +...+** **2pq(A1A2)+...+2rs(A3A4) =1,0**

- Homozygotes = p^2 (A1A1) + q^2 (A2A2) +...+ s^2 (A4A4) = $4*0,25^2$ = **0,25**

- HS within GH = 2pq (A1A2) + 2rs (A3A4) = $2*2*0,25*0,25$ = **0,25**

- HS between GH = 2pr (A1A3) + 2ps (A1A4) + 2qr (A2A3) + 2qs (A2A4)

-                 = $4*2*0,25*0,25$ = **0,50 (HS with significant hetesosis)**

Types of Hybrids

- SC- Single-cross – A x B
- TWC - Three-way cross - (A x A') x B
- DC - Double-Cross - (A x A') x (B x B')
- Predictions by Jenkins
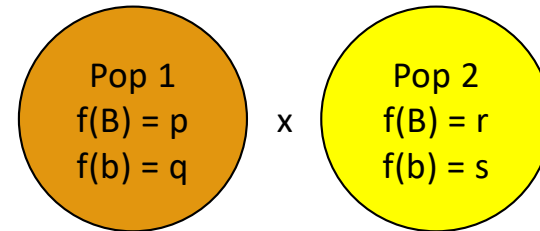
$$TWC_{(12)3} = \frac{(SC_{13} + SC_{23})}{2} \qquad DC_{(12)(34)} = \frac{(SC_{13} + SC_{23} + SC_{14} + SC_{24})}{4}$$

- Heterozygous, "homogeneous", and high-technology
- Number of hybrids (based on the groups)
- $N_{SC} = NL_1 \times NL_2$
- $N_{TWC} = NL_1(NL_1-1)/2 \times NL_2 + NL_2(NL_2-1)/2 \times NL_1$
- $N_{DC} = NL_1(NL_1-1)/2 \times NL_2(NL_2-1)/2$

Pop 1
f(B) = p
f(b) = q

x

Pop 2
f(B) = r
f(b) = s