UNIVERSIDADE DE SÃO PAULO
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LGN5825 Genética e Melhoramento de Espécies Alógamas

Inbreeding, heterosis, and hybrids between populations

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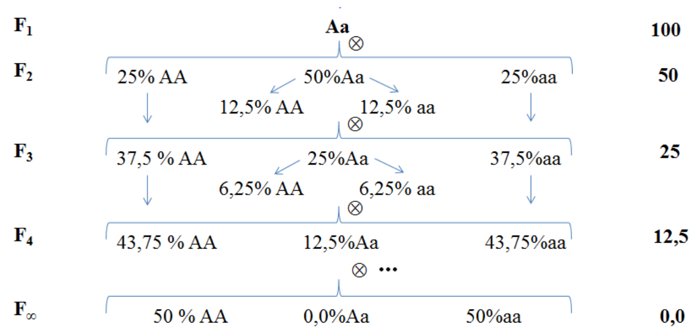
Inbreeding



- 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)
- $u_{X0/F} = (p - q)a + 2pqd - 2pqdF$
- $u_{X0/F} = (p - q)a + 2pqd$ ($F = 0; S_0$)
- $u_{X1/F} = (p - q)a$ ($F = 1; S_\infty$)
- $ID = u_{X1/F} - u_{X0/F} = (p - q)a - ((p - q)a + 2pqd) = -2pqd$

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

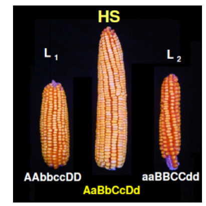
$$ID_{\%} = \frac{S_1 - S_0}{S_0} = \frac{-pq}{(p-q)a + 2pqd}$$

- Components: deviations of dominance and deleterious genes

Heterosis

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

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

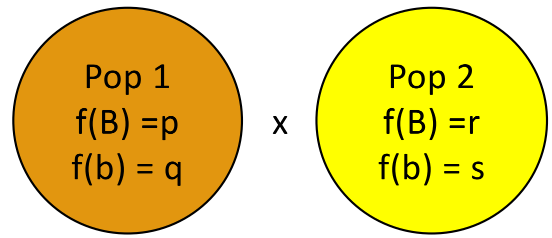


- High-parent heterosis - F_1 regarding the best parent

$$Hb = F_1 - P_s$$

- 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* – tuxpeño** ***flint* – cateto**

Hybrids between populations

- $u_{F1} = u + (pr - qs)a + (ps + qr)d$

- $E(G_{ij}) = u$
- $E(\boldsymbol{\alpha}_i) = \sum_i p_i \boldsymbol{\alpha}_i = 0$
- $E(\boldsymbol{\alpha}_j) = \sum_j p_j \boldsymbol{\alpha}_j = 0$
- $E(\mathcal{S}_{ij}) = \sum_{ij} p_i p_j \mathcal{S}_{ij} = 0$
- $E(\boldsymbol{\alpha}_i, \boldsymbol{\alpha}_j) = E(\boldsymbol{\alpha}_i)\, E(\boldsymbol{\alpha}_j) = 0$
- $E(\boldsymbol{\alpha}_i, \mathcal{S}_{ij}) = E(\boldsymbol{\alpha}_i)\, E(\mathcal{S}_{ij}) = 0$
- $E(\boldsymbol{\alpha}_j, \mathcal{S}_{ij}) = E(\boldsymbol{\alpha}_i)\, E(\mathcal{S}_{ij}) = 0$

$$G_{ij} = u + \propto_i + \propto_j + \delta_{ij}$$

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

x

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

Genotype	*f*	*VG*
BB	pr	a
Bb	ps	d
bB	qr	d
bb	qs	-a

- Variance in inter population hybrids
- $V(G_{ij}) = E[G_{ij} - E(G_{ij})]^2 = E[u + \boldsymbol{\alpha}_i + \boldsymbol{\alpha}_j + \mathcal{S}_{ij} - u]^2 = E[\boldsymbol{\alpha}_i + \boldsymbol{\alpha}_j + \mathcal{S}_{ij}]^2$
- $= E(\boldsymbol{\alpha}_i)^2 + E(\boldsymbol{\alpha}_j)^2 + E(\mathcal{S}_{ij})^2 + dp$
- $= \sum p_i(\boldsymbol{\alpha}_i)^2 + \sum p_i(\boldsymbol{\alpha}_j)^2 + \sum p_i p_j(\boldsymbol{\mathcal{S}}_{ij})^2$
- $= ½\, Va_{(1:2)} + ½\, Va_{(2:1)} + Vd_{(1:2)}$

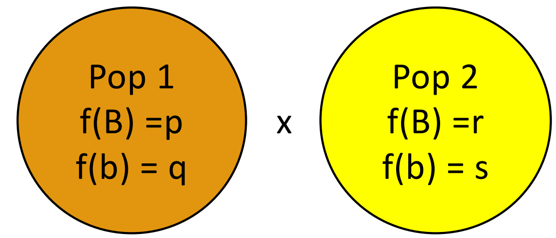
Variance among hybrids between populations

- $u_{F1} = u + (pr - qs)a + (ps + qr)d$

- Within population variances – they have both alleles
- $Va_{(1)} = 2\sum p_i(\boldsymbol{\alpha}_i)^2 = 2pq\boldsymbol{\alpha}_1^2$
- $Va_{(2)} = 2\sum p_i(\boldsymbol{\alpha}_i)^2 = 2rs\boldsymbol{\alpha}_2^2$
- $Vd_{(1)} = \sum p_i p_j(\mathcal{S}_{ij})^2 = (2pqd)^2$
- $Vd_{(2)} = \sum p_i p_j(\mathcal{S}_{ij})^2 = (2rsd)^2$
- $\boldsymbol{\alpha}_1 = a + (p - q)d$
- $\boldsymbol{\alpha}_2 = a + (r - s)d$

- Inter populations variances
- $Va_{(1:2)} = 2pq\boldsymbol{\alpha}_2^2$
- $= 2pq[a + (r - s)d]^2$
- $Va_{(2:1)} = 2rs\boldsymbol{\alpha}_1^2$
- $= 2rs[a + (p - q)d]^2$
- $Vd_{(1:2)} = 4pqrsd^2$

$$G_{ij} = u + \propto_i + \propto_j + \delta_{ij}$$



Genotype	*f*	*VG*
BB	pr	a
bB	ps	d
Bb	qr	d
bb	qs	-a

Genetic covariance between two hybrids

$$G_{ij} = u + \propto_i + \propto_j + \delta_{ij}$$

- $f_{xy1} = ½ [P(x_i^1 \equiv y_i^1)]$
- $f_{xy2} = ½ [P(x_j^2 \equiv y_j^2)]$
- $f_{xy12} = P(x_i^1 \equiv y_i^1) = P(x_j^2 \equiv y_j^2) = P(x_i^1 \equiv y_i^1; x_j^2 \equiv y_j^2)$

- $x_{ij(12)} = u_{(12)} + \boldsymbol{\alpha}_{i(12)x} + \boldsymbol{\alpha}_{j(21)x} + \mathcal{S}_{ij(12)x}$
- $y_{ij(12)} = u_{(12)} + \boldsymbol{\alpha}_{i(12)y} + \boldsymbol{\alpha}_{j(21)y} + \mathcal{S}_{ij(12)y}$

- $COV(x_{ij}, y_{ij}) = E[x_{ij} - E(x_{ij})] . E[y_{ij} - E(y_{ij})]$
- $= E(\boldsymbol{\alpha}_{i12x},\boldsymbol{\alpha}_{i12y}) + E(\boldsymbol{\alpha}_{j21x},\boldsymbol{\alpha}_{j21y}) + E(\mathcal{S}_{ij(12)x},\mathcal{S}_{ij(12)y}) + dp$

- $E(\boldsymbol{\alpha}_{i12x},\boldsymbol{\alpha}_{i12y}) = \sum_i p_i \boldsymbol{\alpha}_{i12}[P(x_i^1 \equiv y_i^1)]\boldsymbol{\alpha}_{i12} = \sum_i p_i \boldsymbol{\alpha}_{i12}^2 P(x_i^1 \equiv y_i^1) = f_{xy1} Va_{12}$
- $E(\boldsymbol{\alpha}_{j21x},\boldsymbol{\alpha}_{j21y}) = \sum_j p_j \boldsymbol{\alpha}_{j21} [P(x_j^2 \equiv y_j^2)]\boldsymbol{\alpha}_{j21} = \sum_j p_j \boldsymbol{\alpha}_{j21}^2 P(x_j^2 \equiv y_j^2) = f_{xy2} Va_{21}$
- $E(\mathcal{S}_{ij(12)x},\mathcal{S}_{ij(12)y}) = \sum_{ij} p_i p_j \mathcal{S}_{ij12} P(x_i^1 \equiv y_i^1; x_j^2 \equiv y_j^2)\mathcal{S}_{ij(12)} = u_{xy12} Vd_{12}$

- $COV_g(x_{ij(12)}, y_{ij(12)}) = f_{xy1} Va_{12} + f_{xy2} Va_{21} + u_{xy12} Vd_{12}$
- These values can be estimated by the kinship matrix