

Inbreeding, heterosis, and hybrids between populations

Prof. Roberto Fritsche-Neto

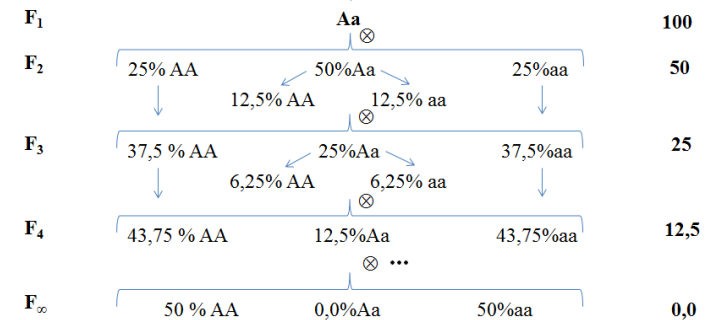
roberto.neto@usp.br

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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 V_g , changes in genotypic frequencies, and anomalies
- $F = \text{Malécot coefficient} - \text{IBD}$
- n number of shared parents

$$F_1 = \left(\frac{1}{2}\right)^n$$



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 ($F = 0$)

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

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

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

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

- $u_{X1/F} = (p - q)a$ ($F = 1$; S_{∞})

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

- *Components*: deviations of dominance and deleterious genes

Heterosis

- The F_1 differential performance regarding the parents mean

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

- Heterobeltiosis** - F_1 regarding the best parent

$$Hb = F_1 - P_s$$

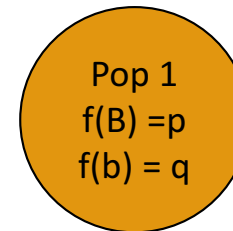
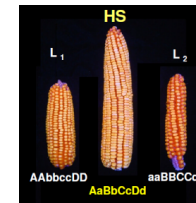
- Depends on the trait (**can be + or -**)

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

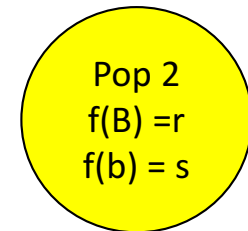
- Dominance deviations theory (**it must be in trans**)

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

- Components**: d, divergence, and complementarity



x



Heterosis vs. Inbreeding depression

- Either are non-additive
- They are 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



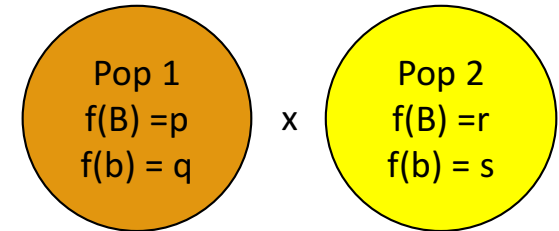
dent – tuxpeño

flint – cateto

Hybrids between populations

- $u_{F1} = u + (pr - qs)a + (ps + qr)d$
- $E(G_{ij}) = u$
- $E(\alpha_i) = \sum_i p_i \alpha_i = 0$
- $E(\alpha_j) = \sum_j p_j \alpha_j = 0$
- $E(\mathcal{S}_{ij}) = \sum_{ij} p_i p_j \mathcal{S}_{ij} = 0$
- $E(\alpha_i, \alpha_j) = E(\alpha_i) E(\alpha_j) = 0$
- $E(\alpha_i, \mathcal{S}_{ij}) = E(\alpha_i) E(\mathcal{S}_{ij}) = 0$
- $E(\alpha_j, \mathcal{S}_{ij}) = E(\alpha_j) E(\mathcal{S}_{ij}) = 0$

$$G_{ij} = u + \alpha_i + \alpha_j + \delta_{ij}$$



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

- **Variance in inter population hybrids**
- $V(G_{ij}) = E[G_{ij} - E(G_{ij})]^2 = E[u + \alpha_i + \alpha_j + \mathcal{S}_{ij} - u]^2 = E[\alpha_i + \alpha_j + \mathcal{S}_{ij}]^2$
- $= E(\alpha_i)^2 + E(\alpha_j)^2 + E(\mathcal{S}_{ij})^2 + dp$
- $= \sum p_i (\alpha_i)^2 + \sum p_j (\alpha_j)^2 + \sum p_i p_j (\mathcal{S}_{ij})^2$
- $= \frac{1}{2} Va_{(1:2)} + \frac{1}{2} Va_{(2:1)} + Vd_{(1:2)}$

Variance among hybrids between populations

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

- **Within population variances – they have both alleles**

- $Va_{(1)} = 2\sum p_i(\alpha_i)^2 = 2pq\alpha_1^2$

- $Va_{(2)} = 2\sum p_i(\alpha_i)^2 = 2rs\alpha_2^2$

- $Vd_{(1)} = \sum p_i p_j (S_{ij})^2 = (2pqd)^2$

- $Vd_{(2)} = \sum p_i p_j (S_{ij})^2 = (2rsd)^2$

- $\alpha_1 = a + (p - q)d$

- $\alpha_2 = a + (r - s)d$

$$G_{ij} = u + \alpha_i + \alpha_j + \delta_{ij}$$

- **Inter populations variances**

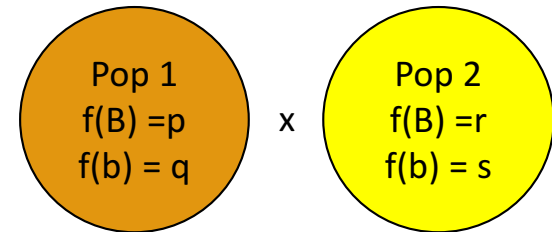
- $Va_{(1:2)} = 2pq\alpha_2^2$

- $= 2pq[a + (r - s)d]^2$

- $Va_{(2:1)} = 2rs\alpha_1^2$

- $= 2rs[a + (p - q)d]^2$

- $Vd_{(1:2)} = 4pqrsd^2$



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

Genetic covariance between two hybrids

$$G_{ij} = u + \alpha_i + \alpha_j + \delta_{ij}$$

- $f_{xy1} = \frac{1}{2} [P(x_i^1 \equiv y_i^1)]$
- $f_{xy2} = \frac{1}{2} [P(x_j^2 \equiv y_j^2)]$
- $f_{xy12} = P(x_i^1 \equiv y_i^1) = P(x_j^2 \equiv y_j^2) = P(x_i^1 \equiv y_i^1; x_j^2 \equiv y_j^2)$
- $x_{ij(12)} = u_{(12)} + \alpha_{i(12)x} + \alpha_{j(21)x} + \mathcal{S}_{ij(12)x}$
- $y_{ij(12)} = u_{(12)} + \alpha_{i(12)y} + \alpha_{j(21)y} + \mathcal{S}_{ij(12)y}$
- $\text{COV}(x_{ij}, y_{ij}) = E[x_{ij} - E(x_{ij})] \cdot E[y_{ij} - E(y_{ij})]$
- $= E(\alpha_{i12x}, \alpha_{i12y}) + E(\alpha_{j21x}, \alpha_{j21y}) + E(\mathcal{S}_{ij(12)x}, \mathcal{S}_{ij(12)y}) + dp$
- $E(\alpha_{i12x}, \alpha_{i12y}) = \sum_i p_i \alpha_{i12} [P(x_i^1 \equiv y_i^1)] \alpha_{i12} = \sum_i p_i \alpha_{i12}^2 P(x_i^1 \equiv y_i^1) = f_{xy1} \text{Va}_{12}$
- $E(\alpha_{j21x}, \alpha_{j21y}) = \sum_j p_j \alpha_{j21} [P(x_j^2 \equiv y_j^2)] \alpha_{j21} = \sum_j p_j \alpha_{j21}^2 P(x_j^2 \equiv y_j^2) = f_{xy2} \text{Va}_{21}$
- $E(\mathcal{S}_{ij(12)x}, \mathcal{S}_{ij(12)y}) = \sum_{ij} p_i p_j \mathcal{S}_{ij12} P(x_i^1 \equiv y_i^1; x_j^2 \equiv y_j^2) \mathcal{S}_{ij(12)} = u_{xy12} \text{Vd}_{12}$
- $\text{COV}_g(x_{ij(12)}, y_{ij(12)}) = f_{xy1} \text{Va}_{12} + f_{xy2} \text{Va}_{21} + u_{xy12} \text{Vd}_{12}$
- **These values can be estimated by the kinship matrix**