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

Hybrids between populations or lines

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Hybrids between populations

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

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

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

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
- $V(G_{ij}) = E[G_{ij} - E(G_{ij})]^2 = E[u + \boldsymbol{\alpha}_i + \boldsymbol{\alpha}_j + \delta_{ij} - u]^2 = E[\boldsymbol{\alpha}_i + \boldsymbol{\alpha}_j + \delta_{ij}]^2$
- $= E(\boldsymbol{\alpha}_i)^2 + E(\boldsymbol{\alpha}_j)^2 + E(\delta_{ij})^2 + dp$
- $= \sum p_i(\boldsymbol{\alpha}_i)^2 + \sum p_i(\boldsymbol{\alpha}_j)^2 + \sum p_i p_j(\boldsymbol{\delta}_{ij})^2$
- $= \frac{1}{2} Va_{(1:2)} + \frac{1}{2} Va_{(2:1)} + Vd_{(1:2)}$

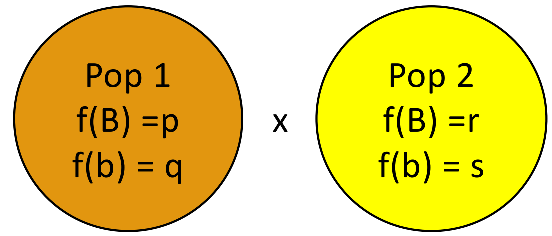
Variance among hybrids between populations

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

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

- 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

Hybrids between lines

- TC - Three-way cross - (A x A') x B

Parents	Gametes	Possible TWC	GV
SC_{12} AaBb (AABB x aabb)	AB Ab aB ab	AABb	$u + \boldsymbol{\alpha}_A + d_{Bb}$
		AAbb	$u + \boldsymbol{\alpha}_A - \boldsymbol{\alpha}_b$
L3 AAbb	Ab	AaBb	$u + d_{Aa} + d_{Bb}$
		Aabb	$u + d_{Aa} - \boldsymbol{\alpha}_b$
Mean		$u + ½ (\boldsymbol{\alpha}_A - \boldsymbol{\alpha}_b + d_{Aa} + d_{Bb})$	

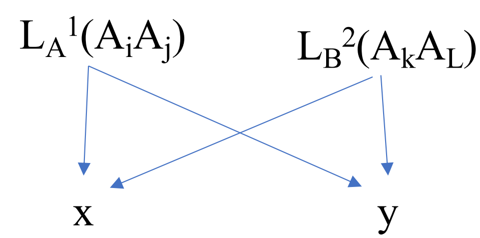
SC non-parents	Genotype	GV
SC_{13}	AABb	$u + \boldsymbol{\alpha}_A + d_{Bb}$
SC_{23}	Aabb	$u + d_{Aa} - \boldsymbol{\alpha}_b$
Mean		$u + ½ (\boldsymbol{\alpha}_A - \boldsymbol{\alpha}_b + d_{Aa} + d_{Bb})$

Covariance and response to selection in hybrids

- $COV_g(X_{ij(12)}, y_{ij(12)}) = f_{xy1}Va_{12} + f_{xy2}Va_{21} + u_{xy12}Vd_{12}$
- $f_{xy1} = ½\,[P(x_i^{1} \equiv y_i^{1})]$
- $f_{xy2} = ½\,[P(x_j^{2} \equiv y_j^{2})]$
- $u_{xy12} = P(x_i^{1} \equiv y_i^{1}) = P(x_j^{2} \equiv y_j^{2}) = P(x_i^{1} \equiv y_i^{1};\, x_j^{2} \equiv y_j^{2})$
- As they different populations, the latter can be reduced to
- $u_{xy12} = 2f_{xy1}Va_{12}\,.\,2f_{xy2}Va_{21}$
- The covariance within is equal to variance between
- Single-cross
- $f_{xy1} = ½\,[P(x \equiv y \equiv A_i) + P(x \equiv y \equiv A_j) + 2.P(x \equiv y \equiv A_j \equiv A_j)]$
- ½ ½ ½ ½ ½ ½ F
- $f_{xy1} = ½\,[¼ + ¼ + 2.¼.F] = ¼(1+F)$
- $f_{xy2} = ½\,[P(x \equiv y \equiv A_k) + P(x \equiv y \equiv A_L) + 2.P(x \equiv y \equiv A_K \equiv A_L)] = ¼(1+F)$
- $u_{xy12} = 2f_{xy1}Va_{12}\,.\,2f_{xy2}Va_{21} = 2.¼(1+F)\,.\,2.\,¼(1+F) = ¼(1+F)^2$
- $COV_{gSC12} = ¼(1+F)[Va_{12} + Va_{21}] + ¼(1+F)^2Vd_{12}$

$$RS = \frac{i}{\sigma_P} COV_G(x, y)$$

$$RS = \frac{i}{\sigma_P} \sigma_H^2$$



Covariance and response to selection in hybrids

- $COV_{gSC12} = ¼(1+F)[Va_{12} + Va_{21}] + ¼(1+F)^2 Vd_{12}$

- Thus, for SC between S_1 lines (F = 0 = parents F)
- $COV_{gSC12} = ¼(1+0)[Va_{12} + Va_{21}] + ¼(1+0)^2 Vd_{12}$
- $COV_{gSC12} = ¼[Va_{12} + Va_{21}] + ¼Vd_{12}$

- and for SC between inbred lines (F=1)
- $COV_{gSC12} = ¼(1+1)[Va_{12} + Va_{21}] + ¼(1+1)^2 Vd_{12}$
- $COV_{gSC12} = ½[Va_{12} + Va_{21}] + Vd_{12}$

- The latter takes advantage of the whole dominance and additive genetic variability

- Therefore, there is no VG within hybrids. Just among them

- The covariance within is equal to the variance between

Covariance and response to selection in hybrids

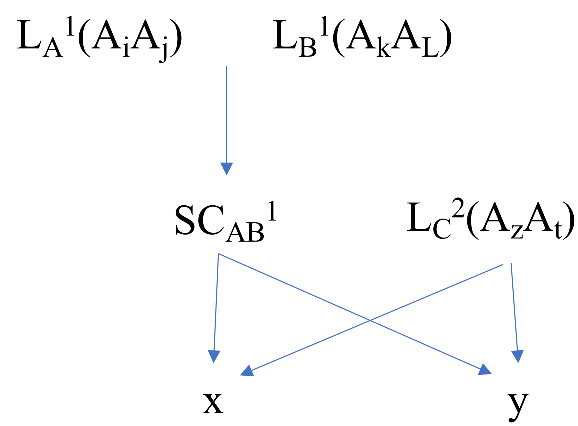
- Three-way cross
- $f_{xy1} = ½\,[P(x \equiv y \equiv A_i) + P(x \equiv y \equiv A_j) + 2.P(x \equiv y \equiv A_j \equiv A_j) +$
- ¼ ¼ ¼ ¼ ¼ ¼ F
- $+ P(x \equiv y \equiv A_k) + P(x \equiv y \equiv A_L) + 2.P(x \equiv y \equiv A_K \equiv A_L)]$
- $f_{xy1} = ½\,[1/16 + 1/16 + 2.\,1/16.F + 1/16 + 1/16 + 2.\,1/16.F] = 1/8(1+F)$

- $f_{xy2} = ½\,[P(x \equiv y \equiv A_z) + P(x \equiv y \equiv A_t) + 2.P(x \equiv y \equiv A_z \equiv A_t)]$
- $f_{xy2} = ½\,[¼ + ¼ + 2.¼.F] = ¼(1+F)$

- $u_{xy12} = 2f_{xy1}Va_{12} \,.\, 2f_{xy2}Va_{21} = 2.1/8.(1+F) \,.\, 2.¼(1+F) = 1/8(1+F)^2$

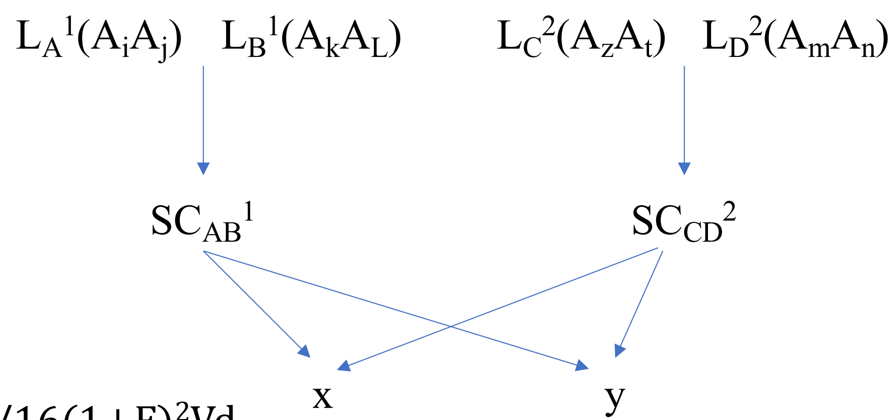
- $COV_{gTWC(12)3} = 1/8(1+F)Va_{12} + 1/4(1+F)Va_{21} + 1/8(1+F)^2Vd_{12}$

- TWC between S_1 lines (F = 0 = parents F)
- $COV_{gTWC(12)3} = 1/8Va_{12} + 1/4Va_{21} + 1/8Vd_{12}$
- TWC between inbred lines (F=1)
- $COV_{gTWC(12)3} = 1/4Va_{12} + 1/2Va_{21} + 1/2\,Vd_{12}$



Covariance and response to selection in hybrids

- Double-cross



- $f_{xy1} = 1/8(1+F)$
- $f_{xy2} = 1/8(1+F)$
- $u_{xy12} = 1/16(1+F)^2$
- $COV_{gDC(12)(34)} = 1/8(1+F)Va_{12} + 1/8(1+F)Va_{21} + 1/16(1+F)^2Vd_{12}$
- DC between S_1 lines (F = 0 = parents F)
- $COV_{gDC(12)(34)} = 1/8Va_{12} + 1/8Va_{21} + 1/16Vd_{12}$
- DC between inbred lines (F=1)
- $COV_{gDC(12)(34)} = 1/4Va_{12} + 1/4Va_{21} + 1/4\,Vd_{12}$

Comparison between cultivars

Hybrid	Vg (among)			Vg (within)		
	Va_{12}	Va_{21}	Vd_{12}	Va_{12}	Va_{21}	Vd_{12}
SC	1/2	1/2	1	0	0	0
TWC	1/4	1/2	1/2	1/4	0	1/2
DC	1/4	1/4	1/4	1/4	1/4	3/4

Cost, yield, heterosis, homogeneity, and technology $\longrightarrow$

Varieties DC TWC SC

$\longleftarrow$ Variability and yield stability