TABLE 1. Expectations for genetic effects in a diallel crossbreeeding system

Breed of sire (j)	Breed of dam (i)		
	A	B	C
A	g_A^I $g_A^P+g_A^M$ 0	$1/2(g_A^I+g_B^I)$ $g_A^P+g_B^M$ $\bar{h}_{AB}^I+s_{AB}^I$	$1/2(g_A^I+g_C^I)$ $g_A^P+g_C^M$ $\bar{h}_{AC}^I+s_{AC}^I$
B	$1/2(g_B^I+g_A^I)$ $g_B^P+g_A^M$ $\bar{h}_{AB}^I+s_{BA}^I$	g_B^I $g_B^P+g_B^M$ 0	$1/2(g_B^I+g_C^I)$ $g_B^P+g_C^M$ $\bar{h}_{BC}^I+s_{BC}^I$
C	$1/2(g_C^I+g_A^I)$ $g_C^P+g_A^M$ $\bar{h}_{AC}^I+s_{CA}^I$	$1/2(G_C^I+g_B^I)$ $g_C^P+g_B^M$ $\bar{h}_{BC}^I+s_{CB}^I$	g_C^I $g_C^P+g_C^M$ 0

where:

g_i^I and g_i^M are breed average individual and maternal effects, and $\sum g_i^I=$

$\sum g_i^M=0$.

$\bar{h}_{ij}$, is the mean heterosis effect for a two-breed <u>reciprocal</u> cross

$\bar{P}_j$, is mean phenotype for one purebred $=\bar{P}+g_j^I+g_j^M$

X_{ij}, is mean phenotype for a two-breed-cross $=\bar{P}_n+1/2(g_i^I+g_j^I)+$
$g_j^M+\bar{h}_{ij}$

$\hat{g}_j^M-g_j^P=\sum_1^{n-1}(X_{ij}-X_{ij})\text{SCALESYM}100/n, =$ breed maternal less
paternal effect, because

$(n-1)(g_j^M-g_j^P)-\sum_1^n(g_i^M-g_i^P)+(g_j^M-g_j^P)=n(g_j^M-g_j^P)$.

$\hat{g}_j^I=P_j-\bar{P}_n-\hat{g}_j^M =$ breed mean individual effect

$\bar{h}_{ij}^I=\frac{1}{2}(X_{ij}+X_{ji}-P_i-P_j)=$ mean heterosis for reciprocal cross.

$s_{ij}^I=\frac{1}{2}(X_{ij}-X_{ji})-\frac{1}{2}(g_j^M-g_i^M)=$ specific reciprocal effect

$\bar{h}_i^I =$ breed mean heterosis $=\dfrac{\sum_I^{2(n-1)}X_{ij}-(n-1)P_i-\sum_I^{(n-1)}P_j}{2(n-1)}=\sum_I^{n-1}\bar{h}_{ij}^I\text{SCALESYM}125/(n-1)$

Table 2. Second phase of diallel mating design to estimate heterosis for maternal effects on progeny performance (h^M)[a].

Breed of dams	Breed of sires			
	A	B	C	D
A		B•A	C•A	D•A
B	A•B		C•B	D•B
C	A•C	B•C		D•C
D	A•D	B•D	C•D	
AB+BA			C(AB+BA)	D(AB+BA)
AC+CA		B(AC+CA)		D(AC+CA)
AD+DA		B(AD+DA)	C(AD+DA)	
BC+CB	A(BC+CB)			D(BC+CB)
BD+DB	A(BD+DB)		C(BD+DB)	
CD+DC	A(CD+DC)	B(CD+DC)		

$$h^M_{AB}+1/8r^I_{AB} = (C•AB+C•BA - C•A - C•B+D(AB)+D(BA) - D•A-D•B)/4$$

[a]Sampling error for estimates of $h^M_{ij}+1/8\,r^I_{ij}$ will be minimum, for any total scale of experiment, when equal numbers of contemporary progeny are produced for each mating combination, i.e. DA, DB, D(A•B) and D(B•A), and when each sire of a breed produces the same proportion of progeny in each cross.

Table 3. Expected fraction of defined genetic components in deviations of alternative crossbreeding categories from weighted mean of parental breeds relative to F_t heterosis, $h = d + 1/2gg$.

generation[a]	Heterosis			Recombination[b]							
	h^I	h^M	h^P	r_{gg}^I	r_{dd}^I	r_{gg}^M	r_{dd}^M	r_{gg}^P	r_{dd}^P	g^M	g^P
$\overline{F_1}$	1	0	0	0	0	0	0	0	0	0	0
$\overline{F_2}$	1/2	1	1	1/4	1/2	0	0	0	0	0	0
$\overline{F_3}$	1/2	1/2	1/2	1/4	1/2	1/4	1/2	1/4	1/2	0	0
A(A•B)	1/2	1	0	1/8	1/2	0	0	0	0	0	0
$\overline{B_1}$ B(A•B)	1/2 SCALESYM32}	0	1								
AB×A											
AB×B	$1-\sum_1^n q_i^2$	—	>	$\frac{1}{2}-(1-\sum_1^n q_i^2)$	$1-\sum_1^n q_i^2$	$\frac{1}{2}(1-\sum_1^n q_i^2)$	$1-\sum_1^n q_i^2$	$\frac{1}{2}(1-\sum_1^n q_i^2)$	$1-\sum_1^n q_i^2$		
<u>Composite</u>											
n=2	1/2	1/2	1/2	1/4	1/2	1/4	1/2	1/4	1/2	0	0
n=3	2/3	2/3	2/3	1/3	2/3	1/3	2/3	1/3	2/3	0	0
n=4	3/4	3/4	3/4	3/8	3/4	3/8	3/4	3/8	3/4	0	0
Rotation	$(\frac{2^n-2}{2^n-1})$	$\longrightarrow$	0	$\frac{1}{6}(\frac{2^n-2}{2^n-1})$	$\frac{2}{3}(\frac{2^n-2}{2^n-1})$	$\frac{1}{6}(\frac{2^n-2}{2^n-1})$	$\frac{2}{3}(\frac{2^n-2}{2^n-1})$	0	0		
n=2	2/3	$\longrightarrow$ 0		1/9	4/9	1/9	4/9	0	0	0	0
n=3	6/7	$\longrightarrow$ 0		1/7	4/7	1/7	4/7	0	0	0	0
n=4	14/15	$\longrightarrow$ 0		7/45	28/45	7/45	28/45	0	0	0	0
<u>C♂ Rotation♀</u>											
n=2	1	2/3	0	1/9	4/9	1/9	4/9	0	0	0	0
n=3	1	6/7	0	1/7	4/7	1/7	4/7	0	0	0	0
n=4	1	14/15	0	1/45	28/45	7/45	28/45	0	0	0	0
3-breed Cross											
C♂ × A • B♀	1	1	0	1/8	1/4	0	0	0	$\frac{A+B}{4}-\frac{C}{2}$	$\frac{C}{2}-\frac{(A+B)}{4}$	
A • B♂ × C♀	1	0	1	1/8	1/4	0	0	0	$\frac{C}{2}-\frac{(A+B)}{4}$	$\frac{1}{4}(A+B)-\frac{C}{2}$	
<u>4 Breed Cross</u>											
CD♂ × AB♀	1	1	1	1/4	1/2	0	0	0	$\frac{1}{4}(A+B-C-D)$	$\frac{1}{4}(C+D-A-B)$	

[a]Mean of reciprocal crosses, equilibrium for <u>n</u> sire breed rotation, or for q_i, fractions of <u>n</u> breeds in a composite at F_3 or later generation.
[b]From Dickerson (1973) and Hill (1982).

Table 4. Expected fraction of defined genetic components in linear contrasts between means for alternative mating[a]

Code	Linear Contrast	g^I	h^I	r^I	g^M	h^M	r^M
1 BA–AA		(B–A)/2	BA	0	0	0	0
2 BA–CA		(B–C)/2	BA–CA	0	0	0	0
3 A(BA)–AA		(B–A)/4	BA/2	BA/8	(B–A)/2	BA	0
4 (BA)²–AA		(B–A)/2	BA/2	BA/4	(B–A)/2	BA	0
5 B(BA)–AA		3(B–A)/4	BA/2	BA/8	(B–A)/2	BA	0
5–3		(B–A)/2	0	0	0	0	0
4–(3+5)/2		0	0	BA/8	0	0	0
6 A(BA)–A(CA)		(B–C)/4	(BA–CA)/2	(BA–CA)/8	(B–C)/2	BA–CA	0
7 (BA)²–(CA)²		(B–C)/2	(BA–CA)/2	(BA–CA)/4	(B–C)/2	BA–CA	0
8 B(BA)–C(CA)		3(B–C)/4	(BA–CA)/2	(BA–CA)/8	(B–C)/2	BA–CA	0
8–6		(B–C)/2	0	0	0	0	0
7–(8+6)/2		0	0	(BA–CA)/8	0	0	0
9 D(BA)–AA		$\dfrac{D}{2}+\dfrac{B}{4}-\dfrac{3}{4}A$	(DB+DA)/2	BA/8	(B–A)/2	BA	0
10 D(A·BA)–AA		$\dfrac{D}{2}+\dfrac{B}{8}-\dfrac{5}{8}A$	$\dfrac{DB}{4}+\dfrac{3}{4}DA$	3BA/32	(B–A)/4	BA/2	BA/8
11 D(BA)²–AA		$\dfrac{D}{2}+\dfrac{B}{4}-\dfrac{3}{4}A$	(DB+DA)/2	4BA/32	(B–A)/2	BA/2	BA/4
12 D(B·BA)–AA		$\dfrac{D}{2}+\dfrac{3B}{8}-\dfrac{7}{8}A$	$\dfrac{D}{2}DB+\dfrac{DA}{4}$	3BA/32	3(B–A)/4	BA/2	BA/8
12–10		(B–A)/4	(DB–DA)/2	0	(B–A)/2	0	0
9–11		0	0	0	0	BA/2	–BA/4
13 D(BA–D(CA)		(B–C)/4	(DB–DC)/2	(BA–CA)/8	(B–C)/2	BA–CA	0
14 D(A·BA)–D(A·CA)		(B–C)/8	(DB–DC)/4	3(BA–CA)/32	(B–C)/4	(BA–CA)/2	(BA–CA)/8
15 D(BA)² ̄D(CA)²		(B–C)/4	(DB–DC)/2	(BA–CA)/8	(B–C)/2	(BA–CA)/2	(BA–CA)/4
16 D(B·BA)–D(C·CA)		3(B–C)/8	3(DB–DC)/4	3(BA–CA)/32	(B–C)/4	(BA–CA)/2	(BA–CA)/8
13–15		0	0	0	0	(BA–CA)/2	–(BA–CA)/4
15–(14+16)/2 11–(10+12)/2		0	0	(BA–CA)/32	0	0	(BA–CA)/8

[a]"Individual (I) and maternal (M) additive (g^I and g^M), heterosis h^I and h^M and non-allelic gene interaction (r^I and r^M) effects on performance traits.

Table 5. Level of significance (P) for a 5% mean difference (+ or -) between two strains in traits with differing Coefficient Variation (CV) and heritability (h^2).

No progeny per strain n_G	sire n_{GS}	No. sires /strain N_s	$\overline{SE}^a$ $(\overline{G_1} - \overline{G_2})$	$t = \dfrac{\overline{G_1} - \overline{G_2}}{SE}$	Minimum t for[c] P_{05}	P_{01}
a. CV = 20%; h^2 = 10%						
280	28	10	1.95	2.57	2.10	2.88
	20	14	1.87	2.67	2.06	2.78
	14	20	1.81	2.76	2.02	2.71
	10	28	1.77	2.82	2.01	2.67
	5	56	1.72	2.90	1.98	2.62
220	20	11	2.11	2.37	2.09	2.85
	10	22	2.00	2.50	2.02	2.71
	5	44	1.94	2.57	1.99	2.63
b. CV = 10%; h^2 = 10%						
140	20	7	1.45	3.44	2.18	3.06
	10	14	1.32	3.78	2.06	2.78
	5	28	1.25	3.99	2.01	2.67
100	20	5	1.72	2.91	2.31	3.36
	10	10	1.56	3.20	2.10	2.88
	5	20	1.48	3.37	2.02	2.71
80	20	4	1.92	2.60	2.45	3.71
	10	8	1.75	2.85	2.14	2.98
	5	16	1.66	3.02	2.04	2.75
60	20	3	2.22	2.25	2.78	4.60
	10	6	2.02	2.47	2.23	3.17
	5	12	1.92	2.60	2.07	2.82
40	20	2	2.72	1.84	4.30	9.92
	10	4	2.48	2.02	2.45	3.71
	5	8	2.34	2.13	2.14	2.98

[a] $\%SE(\overline{G_1} - \overline{G_2}) = \sqrt{2(390/N_G + 10/N_S)}$ with $df = 2(N_s - 1)$. Total phenotypic variance are expressed as the squared coefficient of variation (%), assuming one (1) progeny per dam.

[b] $\% SE(G_1 - G_2) = \sqrt{2(97.5/n_G + 2.5/N_s)}$

[c] See Table A.3 in Steele and Torrie (1960) or any other source of probability values for t-ratio, plus or minus mean difference (i.e. 2-tailed distributions).

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