Theor Appl Genet (1988) 76:136–142

Heterosis x nutrition interaction in *Drosophila melanogaster*

P. S. Ruban *[1,2], **E. P. Cunningham** [1,2] **and P. M. Sharp** [1]

[1] Department of Genetics, Trinity College, Dublin 2, Ireland
[2] The Agricultural Institute, 19 Sandymount Avenue, Dublin 4, Ireland

Received July 10, 1987; Accepted March 10, 1988
Communicated by L. D. Van Vleck

Summary. The relationship between heterozygosity and the expression of heterosis at two different nutrition levels was investigated using *Drosophila melanogaster*. Average daily egg production and egg hatchability were measured in two parental strains and in F_1, F_2 and reciprocal backcross generations. Heterosis was more pronounced in the poor nutritional conditions. Two electrophoretic markers used to estimate the level of heterozygosity in F_2 and backcrosses revealed an excess of heterozygous genotypes. Quantitative genetic effects (an additive line effect and individual and maternal heterosis) were estimated for both traits in the two environments. Although this model gave a reasonable fit in most cases, some epistatic interaction would have to be invoked in order to explain fully the results.

Key words: *Drosophila melanogaster* – Genotype × Environment interaction – Heterosis – Epistasis – Electrophoresis

Introduction

Despite the existence of various explanations for interactions between genotype and environment, the problem of variable expression of heterosis in different environments remains unresolved (Barlow 1981; Cunningham 1985; Hohenboken 1985). Experiments often involve undefined genetic materials and ill-defined, compound environmental variables. Also, there are practical difficulties in sustaining experiments, particularly in large animals, on the scale and with the control and precision necessary to produce reliable data. Finally, a good theoretical model, to provide some framework of expectations against which the experimental results can be tested, is often lacking.

The main objective of this study was to investigate heterosis × environment interaction, using the dominance model (the "Greek-Temple" model) proposed by Cunningham (1987). This model describes the performance of individuals in terms of additive genetic (A) and dominance or maximum heterosis (H) effects in different environmental conditions. The model can also be used to analyse crossbreeding studies involving two breeds. The experimental animal used was *Drosophila melanogaster*. Two traits, egg production and egg hatchability, were measured in populations on two levels of nutrition. Two inbred strains and their F_1, F_2 and reciprocal backcross generations were investigated.

Reliable interpretation of heterosis depends upon knowing the relative heterozygosity of the individuals involved. While mean expected heterozygosity values can be derived easily in crossbred populations, some variability in these values will arise in F_2 and backcross individuals, due to linkage and chance. Weir et al. (1980) have pointed out that, even in pedigreed populations, variation among individuals in the proportion of their genes that are identical by descent arises due to linkage causing blocks of genes to be identical or nonidentical. Since fitness traits generally suffer inbreeding depression (Falconer 1981), then it is possible that natural selection against more homozygous individuals at a pre-adult stage could increase the average heterozygosity of the individuals scored. Indeed, this seemed to have occurred in a previous experiment with *D. melanogaster* (Sharp 1984). The second objective was, therefore, to compare observed and expected heterozygosity in F_2 and backcross generations using electrophoretic techniques.

* To whom reprint requests should be addressed. Present address: Department of Animal Science, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA

Table 1. Structure of the experiment[a]

Genotype		Subgroup[b]	Egg production		Egg hatchability	
			GOOD	POOR	GOOD	POOR
Parents	1 P_1	W.W	88	110	51	63
	2 P_2	C.C	95	109	53	47
F_1	3 F_1	C.W	122	164	42	62
		W.C	148	118	37	47
Backcrosses	4 B_1	WC.W	62	61	32	34
		W.WC	60	58	55	58
	5 B_2	WC.C	46	48	46	48
		C.WC	57	64	33	35
F_2	6 F_2	WC.WC	131	128	28	58
		CW.CW	114	101	29	49
		CW.WC	58	69	26	–
		WC.CW	88	134	21	–
F_3	7 F_3	(WC.WC) (WC.WC)	–	–	131	128
		(CW.CW) (CW.CW)	–	–	114	101
		(CW.WC) (CW.WC)	–	–	58	69
		(WC.CW) (WC.CW)	–	–	88	134
Inter se backcrosses	8	(WC.W) (WC.W)	–	–	62	61
		(CW.W) (CW.W)	–	–	60	58
	9	(CW.C) (CW.C)	–	–	46	48
		(WC.C) (WC.C)	–	–	57	64
Grand total			1,069	1,164	1,069	1,164

[a] Values are numbers of observations for each group in each environment
[b] Female parent in cross is listed first in all cases

Materials and methods

Breeding structure

Two inbred strains of *D. melanogaster*, here denoted "C" and "W", were chosen because (1) they did not give rise to hybrid dysgenesis when crossed, according to the procedure described by Kidwell (1979), (2) they exhibited heterosis in test crosses, and (3) they are homozygous for different alleles at each of three loci examined. Genotypes at the three marker loci – Alcohol dehydrogenase (Adh, II-50.1), αGlycerophosphate dehydrogenase (αGpdh, II-20.5) and Aldehyde oxidase (Aldox, III-50.6) were determined using a cellulose acetate electrophoresis system (Bird and Semeonoff 1982). The C strain is homozygous for Adh^F, $\alpha Gpdh^S$ and $Aldox^F$, while the W strain is homozygous for Adh^S, $\alpha Gpdh^F$ and $Aldox^S$. During the course of this work the alleles at the Adh and αGpdh loci were in complete disequilibrium, probably indicating the presence of an inversion, as observed in a Spanish population of *D. melanogaster* by Briscoe et al. (1975). Thus, there were in effect only two independent genetic markers, one on each of the major autosomes. The two strains were each cultured for 9–10 generations in two environments before commencement of the experiment. The two environments, representing 'GOOD' (optimal) and 'POOR' (stress) nutritional levels, were based on standard and potato flour media, respectively. The experiment was carried out at 24 °C.

Both parental strains, as well as F_1, F_2 and reciprocal backcross generations, were produced in both environments. The F_1 and backcross genotypic classes were produced by using equal proportions of reciprocal crosses. Since eggs produced by females of generation 't' belong to the next generation (t+1), egg hatchability was scored in three additional genotypes: an F_3 generation and two types of inter se backcrosses. Numbers of observations for each genotype, trait and environmental group are in Table 1.

Egg production (EP) and egg hatchability (EH)

A random sample of approximately 100 virgin males and females was collected from each group. Single pairs of 3-day-old flies were mated for two days. On the sixth, seventh and eighth days, females were transferred to fresh medium. Daily egg production per female was scored during this 3 day period (days 6–8). Twenty five eggs were collected each day from each single pair mating for each strain or cross and transferred to 2% agar medium lightly seeded with live yeast. Egg hatchabilities were scored after 30 h. A total of 2,233 observations were made for the two traits in the two environments. After the 3 day egg-laying period, each female was homogenized for the determination of genotypes at electrophoretic marker loci.

Statistical methods

All individual flies and eggs were coded for proportion of their inheritance from strain W (the additive genetic effect, A) and for expected proportions of individual heterosis (H^I) and maternal heterosis (H^M) contributing to their phenotypic value for each trait. The expected values for these A, H^I and H^M coefficients for the nine genotypic groups are given in Table 2. EP and EH were analysed separately for each environment, by fitting the following models:

$$Y_{ij} = u + G_i + e_{ij} \quad (1)$$

$$Y = u + b_1 A + b_2 H^I + b_3 H^M + e \quad (2)$$

Table 2. Coefficients of additive genetic effects (A), individual heterosis (H^I) and maternal heterosis (H^M) for the genotypic groups in Table 1

Genotype	A	H^I	H^M
1 $P_1 = W$	1	0	0
2 $P_2 = C$	0	0	0
3 $F_1 = W \times C$	1/2	1	0
4 $B_1 = (WC \times W + W \times WC)/2$	3/4	1/2	1/2[a]
5 $B_2 = (WC \times C + C \times WC)/2$	1/4	1/2	1/2[a]
6 $F_2 = WC \times WC$	1/2	1/2	1
7 $F_3 = (WC.WC) \times (WC.WC)$	1/2	1/2	1/2
8 $B_3 = (WC.W) \times (WC.W)$	3/4	3/8	1/2
9 $B_4 = (WC.C) \times (WC.C)$	1/4	3/8	1/2

[a] Coefficient of H^M is the average value of zero and 1, on the assumption of equal numbers of reciprocal crosses

Table 3. Mean egg production and egg hatchability in parental strains

Environment	Egg production		Egg hatchability (%)	
	GOOD	POOR	GOOD	POOR
W strain	32.5±1.0	24.7±2.6	71.1±2.3	53.0±3.9
C strain	49.9±1.2	32.3±3.9	58.6±2.3	48.6±6.9

Table 4. Heterosis[a] for egg production and egg hatchability (model 1)

Genotype	Egg production		Egg hatchability	
	GOOD	POOR	GOOD	POOR
F_1	93	155	11	32
F_2	65	42	4	2
B_1	55	94	8	9
B_2	79	130	12	15
F_3	–	–	−7	−4
B_3	–	–	−1	12
B_4	–	–	6	24

[a] Heterosis expressed as percentage of parental mean

where Y_{ij} (or Y) is the observation of the j^{th} individual in the i^{th} genotypic group; u is the overall mean; G_i is the effect of the i^{th} genotypic group ($i = 1$ to 6 for EP, and 1 to 9 for EH); b_1, b_2 and b_3 are regression coefficients of the observed phenotype on the genetic components A, H^I and H^M; and e_{ij} (or e) is the residual.

Observed heterosis was calculated from least squares means of the genotypes (G_i) represented in model 1. In these estimates, maternal heterosis is ignored. These heterosis estimates (in units of measurement of the traits as recorded) were then used to construct estimates of percentage heterosis for the two traits in the two environments for each of the seven crossbred generations. Thus, for example, the estimates from the F_1 are simply the differences between the F_1 and parental means, as a percentage of the parental mean. For the B_1, B_2, F_2 and F_3 genotypes, the estimate is twice the mean value for that genotype, minus the weighted parental mean, as a percentage of the weighted parental mean. For B_3 and B_4 genotypes, computed heterosis must be multiplied by 8/3, since individuals in those genotypic classes were expected to have only 3/8 of the maximum potential heterozygosity found in the F_1 genotypic group.

Preliminary analysis indicated that there were no significant differences between subgroups (listed in Table 1) within the genotypic groups. Estimates of A, H^I and H^M from fitting the 'dominance model' (model 2) were used to compute the expected performance of the inbreds, and their F_1, F_2, F_3 and backcross generations for both traits in each environment. The significance of interactions between the genetic components and environment was also calculated, based on model 2.

Results

The overall unweighted means for egg production and egg hatchability of the two parental inbred lines 'C' and 'W' in each environment are shown in Table 3. As expected, progeny reared in the good environment performed better than those reared in the poor environment. EP for strain C was greater than that of strain W in both environments, EH was greater for strain W in both environments. The differences between two parental strains were significant only in the good environment. Total larval production (EP × EH/100) for the C strain was 29.2 and 15.7, and for the W strain 23.1 and 13.1, in the good and poor environments, respectively.

For strain C, the difference in EH between the two environments was not significant. Strain × environment interaction was not significant for either trait in the parental strains. However, for each trait, the strain with higher performance in the good environment had a proportionately greater reduction in score in the poor environment.

Observed heterosis

The simplest estimates of heterosis can be obtained from differences between each of the crossbred genotypic means and the appropriate parental mean. Least squares estimates of the genotypic group means were obtained using model 1. The estimates of heterosis percentage for the two traits in the two environments for each of the seven genotypic groups are presented in Table 4.

EP exhibited much higher levels of heterosis than EH. For example, heterosis in EP for the F_1 populations was 93% and 155% in the good and poor environments, respectively, compared to 11% and 32% for EH. Within the F_1 and backcross generations, both traits exhibited greater heterosis in the poor environment. The F_2 and backcross generations are expected to have equivalent levels of heterozygosity. However, there was a substantial difference for EH between the backcrosses and the F_2 in both environments, and for EP between the same two types of crosses in the poor environment. In each case, the F_2 showed unexpectedly low levels of heterosis in the poor environment, when compared to the F_1 generation.

Table 5. Least squares estimates of genetic effects (model 2)

Genetic effect	Egg production		Egg hatchability	
	GOOD	POOR	GOOD	POOR
A	-13.3 ± 2.8**	-5.0 ± 2.9	$3.4 \pm 3,8$	-1.7 ± 4.0
H^I	37.2 ± 2.1***	39.3 ± 2.1***	6.9 ± 3.9	12.1 ± 3.8**
H^M	7.0 ± 1.5***	-9.0 ± 1.6***	-3.0 ± 3.2	-8.3 ± 3.3*

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

Table 6. Parental means and individual and maternal heterosis[a] (model 2)

	Egg production		Egg hatchability	
	GOOD	POOR	GOOD	POOR
Parental mean (u+A/2)	42.4	29.0	62.3	52.4
H^I	87.6	135.4	11.1	23.1
H^M	16.6	−30.9	−4.8	−15.8

[a] Expressed as percentage of parental means

Table 7. Significance of interactions between the genetic components and environment (model 2)[a]

Trait	Genetic components				
	A	H^I		H^M	
		absolute[b]	(%)	absolute[b]	(%)
EP	2.09*	0.69	18.23**	6.49**	68.36**
EH	1.18	1.14	7.89**	1.16	2.68*

[a] Figures in the table are 't' values, with 2232 degrees of freedom
[b] Expressed in those units in which the trait was measured
* $p < 0.05$
** $p < 0.001$

For EH, considerable heterosis was observed in the inter se backcross generations in both environments, with the exception of the B_3 generation in the good environment. The F_3 generation, on the other hand, did not exhibit heterosis in either environment.

Heterosis × environment interaction

Estimates of both additive and heterotic effects on EP and EH were obtained by fitting model 2. The estimates, in units of measurement in which the traits were recorded, are shown in Table 5. In only one of the four cases (EP in the good environment) was the difference between the additive effects of the two strains significant. For individual heterosis, highly significant effects of similar magnitude were found for EP in both environments. For EH, the heterosis effect was significant only in the poor environment. The estimate was nearly twice as large as that obtained in the good environment. In all cases, individual heterosis effects were positive.

Significant maternal heterosis effects were also found for EP in both environments. However, the effect was positive in the good environment and negative in the poor environment. For EH, negative maternal heterosis effects were observed in both environments, with that in the poor environment again being twice as large as that in the good. In the poor environment, maternal heterosis for EH was marginally significant, while it was non-significant in the good environment. Individual and maternal heterosis effects are shown as percentages of the parental mean in Table 6. Because parental means were smaller in the poor environment for both traits, the percentage individual heterosis was substantially larger in the poor environment than in the good environment. For maternal heterosis, the percentage values are much lower, and they are rather difficult to interpret since they vary in sign.

Results of significance tests of the interaction between genetic components and the environment based on model 2 are presented in Table 7. As was the case with the parental means, the additive effect did not interact significantly with environment for EH. The interaction was marginally significant for EP. Values for individual heterosis (in actual units of measurement) did not interact with environment for either trait, but the interaction of percentage individual heterosis with environment was highly significant in both cases. For maternal heterosis, the interaction with environment was highly significant for EP in absolute and percentage terms. For EH, the interaction was not significant in absolute terms, but marginally significant as a percentage.

Frequencies of electrophoretic genotypes

The frequencies of the three electrophoretic genotypes for F_2 and backcross generations in the two environments are presented in Table 8. Deviations from expected segregation ratios were tested by Chi-square. In the case of Adh, the frequency of genotypes in the F_2 generation in the good environment did not deviate significantly from

Table 8. Frequencies of marker genotypes in F_2 and backcross generations[a]

Genotype environment		Adh				Aldox				Average H^b
		FF	FS	SS	H^b	FF	FS	SS	H^b	
F_2	GOOD	98	201	92	0.51	97	217	77*	0.56	0.54
	POOR	26	390	16**	0.90	129	248	55**	0.57	0.74
B_1	GOOD	45	74**	–	0.62	–	75	44**	0.63	0.63
	POOR	30	92**	–	0.75	–	61	61	0.50	0.63
B_2	GOOD	–	66	40*	0.62	52	54	–	0.51	0.57
	POOR	–	82	27**	0.75	59	50	–	0.54	0.65

[a] Deviations from expected ratios tested by χ^2: * $p<0.05$; ** $p<0.001$
[b] Heterozygosity

the expected 1:2:1 ratio. However, the ratio for Aldox was significantly different from expectation. There was a highly significant excess of Adh heterozygotes in both backcrosses in both environments. However, for Aldox, only the B_1 backcross differed from the expected 1:1 ratio, and only in the good environment.

Discussion

In the present experiment both egg production and (though to a lesser extent) egg hatchability, exhibited heterosis on two different nutritional regimes. There was a heterosis × environment interaction, in that traits generally exhibited a greater degree of heterosis in the poor environment. Interactions between environment and both individual and maternal heterotic effects were significant for both traits. The degree of heterosis for EP in the poor environment (155%) was similar to values of 154% and 130% previously reported for *D. melanogaster* by Gowen (1952) and Robertson and Reeve (1955), respectively. However, those values were observed under standard ('GOOD') nutritional conditions. The lower level of percentage heterosis in the good environment in the present experiment probably reflects differences between the populations used.

Heterosis × nutrition interaction

The main purpose of the present experiment was to detect and measure any genotype × environment interaction. The differences between the two pure strains used were of the order of 40% for EP and 15% for EH. For both traits, the difference between strains was larger in absolute terms in the good environment than in the poor. However, there was no evidence of significant interaction of these differences with environment.

For EP, there was a clear and significant interaction between percentage individual heterosis and environmental level. For both traits, percentage heterosis was significantly higher in the poor environment. Sang (1964) found similar heterosis for egg production in *Drosophila* on normal and modified diets. Our results are somewhat similar to those of Rich and Bell (1980) who reported higher heterosis for larval weight in flour beetles under poor nutritional conditions than under normal nutritional levels. Similarly, Festing (1976) found higher heterosis for fertility in mice on an impoverished diet than on a normal diet. Klosterman et al. (1968) found no interaction of heterosis with nutritional level in beef cattle, though when heterosis was expressed in percentage terms there was a difference. In plants, Pederson (1968) and McWilliam and Griffing (1965) found no interaction of level of heterosis with environment in *Arabidopsis* or maize, respectively. In his 1981 review, Barlow concluded that while heterosis × environment interaction was more often found than not, the cases where interaction was absent were more often those involving nutritional differences in the environment. Our results appear to support the generalization made in that review that heterosis by environment interaction can be expected, with higher levels of heterosis found in the more stressful environment.

Significant maternal heterosis effects were detected in three of the four cases in the present experiment. In particular, there was a substantial negative H^M effect for EP and EH under the poor nutritional regime. For EP, the maternal heterosis effect was positive in the good environment and negative in the poor. For EH, maternal heterosis was small and non-significant in the good environment, and almost as large as the individual heterosis effect in the poor environment, though in the opposite direction. Interpretation of the H^M effect in an oviparous animal like *Drosophila* is rather difficult, although cytoplasmically inherited effects on both viability and fertility have been observed (McDaniel and Grimwood 1971; Reily and Thomas 1980). For EH, it is possible to interpret the negative maternal heterosis as a consequence of the higher number of eggs produced by more heterozygous females. For EP, there was significant positive heterosis in the good environment, and equally significant negative heterosis in the poor environment. The

negative effect in the poor environment could be due to environmental reinforcement of a negative effect at the egg stage. That is, selection for total reproduction may be more effective in the poor environment, and could cause a decrease in number of eggs produced, in order to increase hatchability and total number of offspring produced. While this interpretation is admittedly tenuous, somewhat similar situations have been reported in mice (Falconer 1955, 1960) and pigs (Van der Steen and Groot 1984).

The model which was used in the analysis of these data included only additive, individual heterosis and maternal heterosis effects. The heterosis effect was estimated on the basis of the dominance model, i.e., on the assumption that heterosis effects were due solely to the aggregate effects of dominance at single loci. While significant heterosis was estimated using this model, significant deviations from linear dependence on heterozygosity were also observed. This could be due to several causes: incorrect levels of heterozygosity could be assumed; maternal effects could be confounded with the estimates; or epistatic effects could be influencing performance in some genotypic groups but not in others. The first of these possibilities was explored by measuring heterozygosity at two marker loci.

Heterozygosity at marker loci

In F_2 and backcross generations, individuals are expected to be identical by descent for regions of the chromosomes comprising, on average, 50% of the genome. Linkage could give rise to considerable between-individual variability in this value, particularly in *D. melanogaster* where there are only three major chromosomes, and there is no recombination in males. Homozygosity of either of the major autosomes leads to a great decrease in viability in this species (e.g., Sved 1971, 1975), presumably due to the presence of deleterious recessive alleles. Natural selection in the F_2 and backcross generations could result in the individuals tested being on average more heterozygous than expected. This effect was indeed observed for marker loci on chromosomes II and III. That the excess of heterozygosity observed was due to selection is suggested by two considerations. First, the excess of heterozygotes was generally more marked for Adh than for Aldox. Due to the presence of an inversion linked to Adh, that marker locus was probably indicative of homo- or heterozygosity of a larger chromosomal region than was the case for Aldox. Second, the excess heterozygosity was more pronounced in the poor environment, where selection would be expected to be stronger.

Hybrid breakdown

Hybrid breakdown can be defined as a reduction in fitness and/or metric traits in post-F_1 segregating generations, such as the F_2 or backcrosses. In theory, hybrid breakdown can be expected if recombination causes a disruption of favourable epistatic gene combinations which had become established in the parental populations during adaptation to specific environments (Falconer 1981). The degree of heterosis in the F_2 and subsequent generations was generally lower than would be predicted from the F_1. Surprisingly, the one generation which did not show excess heterozygosity (the F_2 for EP in the good environment) had the highest mean performance. Hybrid breakdown in the F_2 in general could be the explanation for the poorer performance in that generation. The exhibition of abundant heterosis in the F_1 could still occur as long as the interacting alleles were not recessive. Vetukhiv (1956), working with *D. pseudoobscura*, reported that the F_1 hybrids were mostly superior to both parental lines. The F_2 hybrids, on the other hand, did not show heterosis, and in some cases their fecundity was even lower than that of the parental lines. This might have been due to polymorphic inversions in that species. Similar unexpectedly low levels of heterosis in the F_2 have been observed for traits in several other species, for example, longevity, reproductive rate, fleece production, birth weight and weaning weight in sheep (Boylan 1982; Oltenacu and Boylan 1982), and lactation yield, lactation length and first calving interval in cattle (Syrstad 1985). In our result, the loss of heterosis was greatest for the F_2 in the poor environment, and the F_3 in both environments. It was also found that heterosis was retained to some extent for EH in the inter se backcrosses but not in the F_3. This could be due to a greater extent of loss of favourable epistatic gene combinations in the F_3 generation, compared to the inter se backcrosses. A similar observation has been made in the F_3 generation of Angus × Hereford cattle for survival rate, pregnancy rate and degree of intramuscular fat deposition (Koch et al. 1985). However, those authors did find heterosis for post-weaning gain, carcass weight and rib-eye area in the same generation. Sheridan (1981) has reviewed hybrid breakdown or epistatic effect (also called "parental epistasis") in cattle, pigs and poultry and concluded that generally the level of heterosis in crossbred generations other than the F_1 was less than would be predicted by the dominance model.

The results of hybrid breakdown affect the expression of heterosis. The breakdown of heterosis in the F_2 and subsequent generations suggests that the gene pool of each population was a coherent adaptive system evolved under the control of natural selection. Even considering the two nutritional regimes separately, the relationship between heterozygosity and performance was generally nonlinear. This lack of fit would be accentuated if the heterozygosity estimated from marker loci were taken into account. A dominance model including maternal heterosis effects gave a reasonable fit in some cases. How-

ever, the comparatively poor performance of generations subsequent to the F_1 is perhaps best explained in terms of loss of positive epistasis in those generations. Thus, the level of heterosis in various secondary crossbred populations should not be deduced from the performance of purebred and F_1 populations (Sheridan 1980).

Acknowledgements. We are grateful to P. McGloughlin, G. J More O'Ferrall and W. D. Hohenboken for much assistance, including their critical reading of this manuscript and many fruitful suggestions. We also thank J. Connolly for his statistical and computational assistance. PSR was supported by grants from the Irish Department of Foreign Affairs, and the Agricultural Institute.

References

Barlow R (1981) Experimental evidence for interaction between heterosis and environment in animals. Anim Breed Abstr 49:715–737

Bird SR, Semeonoff R (1982) Electrophoretic analysis of many enzyme loci from a single fly homogenate. Dros Inf Ser 58:153

Boylan WJ (1982) Crossbreeding for fecundity. In: Coop IE (ed) Sheep and goat production. Elsevier, Amsterdam

Briscoe DA, Robertson A, Malpica J-M (1975) Dominance at Adh locus in response of adult *Drosophila melanogaster* to environmental alcohol. Nature 255:148–149

Cunningham EP (1985) Theoretical aspects of crossbreeding. FAO/UNEP Expert Consult Methodol Anim Genet Resources Data Banks (AGR/DB) Rome, June 1985

Cunningham EP (1987) Crossbreeding – the Greek-temple model. Z Tierz Züchtungsbiol 104:2–11

Falconer DS (1955) Pattern of response in selection experiments with mice. Cold Spring Harbor Symp Quant Biol 20:178–196

Falconer DS (1960) The genetics of litter size in mice. J Cell Comp Physiol 56:153–167

Falconer DS (1981) Introduction to quantitative genetics, 2nd ed. Longman, London

Festing MFW (1976) Effect of marginal malnutrition on the breeding performance of inbred and F_1 hybrid mice – a diallel study. In: The laboratory animal in the study of reproduction. G. Fischer, Stuttgart (6th Symp Inter Comm Lab Animals, Thessaloniki, July 1975, pp 99–113)

Gowen JW (1952) Hybrid vigor in *Drosophila*. In: Gowen JW (ed) Heterosis. Iowa State College Press, Ames/IA, pp 474–493

Hohenboken WD (1985) Phenotypic, genetic and environmental correlation and genotype × environment interaction. In: Chapman AB (ed) General and quantitative genetics. Elsevier, Amsterdam

Kidwell MG (1979) Hybrid dysgenesis in *Drosophila melanogaster*: the relationship between the *P-M* and *I-R* interaction systems. Genet Res 33:205–217

Klosterman EW, Cahill VR, Parker CF (1968) A comparison of the Hereford and Charolais breeds and their crosses under two systems of management. Res Bull, Ohio Agr Res Dev Centre no 1011

Koch RM, Dickerson GE, Cundiff LV, Gregory KE (1985) Heterosis retained in advanced generations of crosses among Angus and Hereford cattle. J Anim Sci 60:1117–1132

McDaniel RG, Grimwood BC (1971) Hybrid vigour in *Drosophila*: Respiration and mitochondrial energy conservation. Comp Biochem Physiol 38:309–315

McWilliam JR, Griffing B (1965) Temperature-dependent heterosis in maize. Aust J Biol Sci 18:569–583

Oltenacu EAB, Boylan WJ (1982) Productivity of purebred and crossbred Finnsheep II. Lamb weight and production indices of ewes. J Anim Sci 52:998–1006

Pederson DG (1968) Environmental stress, heterozygote advantage and genotype-environment interaction in *Arabidopsis*. Heredity 23:127–138

Reily JG, Thomas CA (1980) Length polymorphisms, restriction site variation and maternal inheritance of mitochondrial DNA of *Drosophila melanogaster*. Plasmid 3:109–115

Rich SS, Bell AE (1980) Genotype-environment interaction effects in long-term selected populations of *Tribolium*. J Heredity 71:319–322

Robertson FW, Reeve ECR (1955) Studies in quantitative inheritance VIII. Further analysis of heterosis in crosses between inbred lines of *Drosophila melanogaster*. Z Indukt Abstamm Vererbungsl 86:439–458

Sang JH (1964) Nutritional requirements of inbred lines and crosses of *Drosophila melanogaster*. Genet Res 5:50–67

Sharp PM (1984) The effect of inbreeding on competitive male-mating ability in *Drosophila melanogaster*. Genetics 106: 601–612

Sheridan AK (1980) A new explanation for egg production heterosis in crosses between White Leghorns and Australorps. Brit Poultry Sci 21:85–88

Sheridan AK (1981) Crossbreeding and heterosis. Anim Breed Abstr 49:131–144

Sved JA (1971) An estimate of heterosis in *Drosophila melanogaster*. Genet Res 18:97–105

Sved JA (1975) Fitness of third chromosome homozygotes in *Drosophila melanogaster*. Genet Res 25:197–200

Syrstad O (1985) Heterosis in *Bos taurus* × *Bos indicus* crosses. Livest Prod Sci 12:299–307

Van der Steen HAM, Groot PND (1984) Genotype-energy intake interaction for growth and backfat thickness in gilts. 35th EAAP Meet, The Hague, August 6–9, 1984

Vetukhiv M (1956) Fecundity of hybrids between geographical populations of *Drosophila pseudoobscura*. Evolution 10: 139–146

Weir BS, Avery PJ, Hill WJ (1980) Effect of mating structure on variation in inbreeding. Theor Popul Biol 18:396–429