GENETICAL VARIATION FOR ENZYME ACTIVITY IN A POPULATION OF *DROSOPHILA MELANOGASTER*

III. DOMINANCE RELATIONSHIPS FOR ALCOHOL DEHYDROGENASE ACTIVITY

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SUMMARY

Four inbred lines, two homozygous *Adh^{S/S}* and two homozygous *Adh^{F/F}*, were extracted from a laboratory cage population of *Drosophila melanogaster* and crossed in all combinations. Directional dominance for low ADH activity was present and confined to *Adh^{F/S}* heterozygotes. The remaining genetical differences between the four lines for ADH activity were due to additive genetical variation. The frequency of the *Adh^S* allele in the population was 0.89. The observed directional dominance for low ADH activity in *Adh^{F/S}* heterozygotes corresponded to the general direction of selection for ADH activity within the population.

1. INTRODUCTION

GENETICAL variation has been demonstrated for ADH activity in a sample of inbred *Adh^{S/S}* lines which had been extracted from a laboratory cage population of *Drosophila melanogaster* (Birley and Barnes, 1973). The inheritance of activity in two homozygous *Adh^{S/S}* lines with differing activities was subsequently investigated and found to be under additive genetical control with the X chromosome having a significant effect (Barnes and Birley, 1975). In this study we have investigated some aspects of the inheritance of ADH activity in crosses between *Adh^{F/F}* and *Adh^{S/S}* lines.

2. MATERIALS AND METHODS

Nineteen independently derived inbred lines were extracted from the laboratory cage population "Texas". From amongst the 17 lines which were homozygous *Adh^{S/S}*, two lines *P₁₅*, the line with the highest ADH activity, and *P₂₅*, the line with the lowest ADH activity, were selected for this study together with the two lines homozygous *Adh^{F/F}*, *P₆* and *P₁₉*. These four inbred lines were crossed in all combinations, i.e. a diallel set of crosses. The families were raised in a single randomised block at 25°C.

Alcohol dehydrogenase activity was measured using the method described by Birley and Barnes (1973). Four female flies were assayed individually from each of the 16 families on three separate occasions (blocks). In all a total of 192 flies were assayed.

3. RESULTS

The metric specific activity $\left(\frac{1}{\bar{T}} \times \frac{1}{\bar{P}} \times 100 \right)$ which has been used in

previous papers (Birley and Barnes, 1973; Barnes and Birley, 1975) is preferable to activity $\left(\frac{1}{T} \times 100\right)$ only if the total soluble protein (P) consistently reflects the amount of ADH protein. This assumption may not be justified as there is evidence of genetic variation for soluble protein in

TABLE 1
Alcohol dehydrogenase activity of parents and F_1 's

	Line			
	25	15	19	6
25	5.42	11.78	18.20	14.09
15	9.84	17.48	20.08	15.00
19	17.30	22.88	36.24	32.08
6	12.61	18.79	30.55	24.50

TABLE 2
Analysis of variance of diallel table

Item	d.f.	M.S.	P
<i>a</i>	3	108.64	<0.1%
<i>F/F v. S/S</i>	1	258.99	<0.1%
15 v. 25	1	31.13	<0.1%
6 v. 19	1	35.78	<0.1%
<i>b</i>	6	3.40	1.0-1%
b_1	1	5.33	5.1%
b_2	3	0.99	n.s.
b_3	2	6.07	1.0-1%
<i>c</i>	3	1.44	n.s.
<i>d</i>	3	0.30	n.s.
Blocks (<i>B</i>)	2	1.12	n.s.
$B \times a$	6	0.56	
$B \times b_1$	2	0.06	
$B \times b_2$	6	1.51	
$B \times b_3$	4	0.55	
$B \times c$	6	0.88	
$B \times d$	6	1.19	
Pooled interactions	30	0.90	

crosses between lines 15 and 25 (Barnes and Birley, 1975), of which ADH protein would constitute only a *small* part. If this is the case, then the reliability of specific activity becomes much reduced. For this reason the analysis presented below is concerned with activity.

The results, summed over blocks, are shown in table 1 and the analysis of variance of diallel tables (Hayman, 1954) is given in table 2. The main items in the analysis have all been tested against a pooled error mean square with 30 degrees of freedom as the individual error variances were homogeneous, $\chi^2_{(5)} = 5.20$. This shows that there are no genotype-environment

interactions. The analysis shows that there is significant additive variation between the lines (*a* item) together with significant non-additive variation (*b* item). A partition of the *a* sum of squares shows genetical differences in activity between the two electrophoretic morphs, and between lines of the same morph, *i.e.* 15 *v.* 25 and 6 *v.* 19. On the assumption that there are no non-allelic interactions—we will test this later—the non-additive variation is attributed to dominance. The significant b_1 item shows that on average the F_1 mean differs from the mean of the parents and we can see from an inspection of the data (table 1) that dominance is for low activity.

Furthermore, the significant b_3 item shows that the dominance effects are specific to certain crosses. This is apparent from the percentage potency values given in table 3.

Large values are associated with $Adh^{F/S}$ heterozygotes and dominance is most pronounced in crosses involving line 15. Although we are unable to test individually the significance of the values in table 3, we have already shown (Barnes and Birley, 1975) that in crosses between lines 15 and 25

TABLE 3
Percentage potency values

	Line			
	25	15	19	6
25	—	-10.6	-20.0	-16.9
15	—	—	-57.4	-116.5
19	—	—	—	3.1
6	—	—	—	—

there is no evidence for dominance. The $Adh^{F/S}$ heterozygotes are consistent in showing dominance for low activity. The analysis also shows that there are no significant reciprocal differences (*c* and *d*) or differences between occasions (blocks).

The variance-covariance analysis of Jinks (1954, 1956) allows us to test whether the non-additive genetic variation results from dominance or from non-allelic interactions. The test depends on calculating the variance of each array (Vr) and the covariance of the array on the non-recurrent parent (Wr). We can see from table 4 that the non-additive genetic variation, demonstrated by the differences between the ($Wr + Vr$) values, can be attributed solely to dominance variation as the ($Wr - Vr$) values do not differ significantly over arrays.

TABLE 4
Analysis of variance of ($Wr + Vr$) and of ($Wr - Vr$)

Item	d.f.	($Wr + Vr$)		($Wr - Vr$)	
		M.S.	P	M.S.	P
Arrays	3	124.97	6%	0.44	n.s.
Blocks	2	40.45	n.s.	1.44	n.s.
Arrays $\times$ Blocks	6	28.18		1.07	

Further information on the nature of the dominance between the lines may be obtained from the relationship between Wr and Vr shown in fig. 1. The Wr and Vr values have each been corrected for the respective environmental component and then averaged over the three blocks. The slope of the regression line does not differ from one, and the intercept is positive showing incomplete dominance. Lines 15 and 25 contain most dominant alleles as these points lie nearest to the origin while 6 and 19 contain most recessive alleles. We should recall that the activities of 15 and 25 and of

FIG. 1.—Relationship between the covariance of arrays (Wr) and the variance of arrays (Vr).

6 and 19 differ significantly. The direction of dominance can be obtained by examining the relationship between $(Wr + Vr)$ and the mean of the common parent. The dominant parents have low activity while the recessive parents have high activity. We conclude that there is directional dominance for low activity—although the association is not complete since line 25 which has the lowest activity is not the most dominant.

4. DISCUSSION

In this experiment dominance for low activity was apparent in crosses between the $Adh^{S/S}$ and $Adh^{F/F}$ lines. The frequency of the Adh^S allele

in the population was 0.89 and the *Adh^{S/S}* lines are less active than the *Adh^{F/F}* lines (Birley and Barnes, 1973). Previous work on lines extracted from a number of other populations also showed the *Adh^{F/F}* homozygotes to be more active than the *Adh^{S/S}* homozygotes (Gibson, 1970; Gibson and Miklovich, 1971; Day *et al.*, 1974*a* and *b*). Day *et al.*, (1974*b*) further showed that in lines derived from the Kaduna population the molecular activity of ADH F is approximately twice that of ADH S and a similar number of ADH molecules was produced by the two genotypes.

The ADH molecule has been reported to be a dimer and the *Adh^{F/S}* heterozygote possesses unique hybrid enzymes (Ursprung and Leone, 1965). The enzyme also exists in different conformations and interconversion of the conformers can be accomplished, for example, by changes in the *in vitro* concentration of NAD (Jacobson *et al.*, 1972). Furthermore, Day and Needham (1974) have shown that two conformers (ADH-5 and ADH-3) extracted from *Drosophila melanogaster* homozygous for the *Adh^S* allele differ in their specific activities. This situation lends itself to one whereby allosteric properties of the enzyme could result in dominance for enzyme activity; such possibilities are further discussed by Fincham (1972).

Gibson and Miklovich (1971) reported ADH specific activity measurements for lines which had been independently extracted from a population of *Drosophila melanogaster* maintained in Professor J. A. Beardmore's department at the University College of Swansea, Wales, U.K. This population originated from a sample of inseminated females collected in Groningen (the Netherlands) and subsequently maintained as a laboratory cage population for 3 years. The measurements were made at 25°C upon four lines, two of which were *Adh^{F/F}* and two *Adh^{S/S}* together with the *Adh^{F/S}* heterozygotes. The percentage potency values are shown below.

		<i>Adh^{S/S}</i> Parent line	
		B ₁	B ₂
<i>Adh^{F/F}</i> line	B ₁	25.0*	0
	B ₂	0	26.3*

* Heterozygote enzyme activity significantly different from the mid-parental value (Gibson and Miklovich, 1971).

The direction of dominance is for high ADH activity and in the population from which these lines were extracted the frequency of the *Adh^F* allele was 0.84 (Birley, unpublished). Dominance is again incomplete and restricted to specific crosses.

Although the data are limited we can see that in the two populations that have been studied dominance for ADH activity is for the common allele. Ward and Hebert (1972) have shown that other loci can modify ADH activity and similarly Barnes and Birley (1975) have established a significant effect of the X chromosome. The differing dominance relationship between *Adh^S* and *Adh^F* in the two populations may be interpreted, therefore, as resulting from a modification process of the type proposed by Fisher (1930). Alternatively, there may be differences between the *Adh*

alleles from the two populations which are undetectable electrophoretically and which give rise to different dominance relationships.

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