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

I. EXTENT OF THE VARIATION FOR ALCOHOL DEHYDROGENASE ACTIVITY

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SUMMARY

The variation of alcohol dehydrogenase specific activity in a sample of inbred lines derived from a population of *Drosophila melanogaster* has been investigated. The results demonstrated the existence of extensive genetical variation for activity which, in part, was not detected electrophoretically. The narrow heritability of individuals in the population was estimated as 20·6 per cent.

1. INTRODUCTION

THE evidence that has accumulated from the many electrophoretic surveys of proteins leaves no doubt that considerable genetic polymorphism exists within natural populations of many species (Harris, 1966, 1969; Hubby and

Lewontin, 1966; Lewontin and Hubby, 1966; Selander and Yang, 1969; Ayala and Powell, 1972). However, it has been suggested that perhaps only one-third of mutations produce molecular changes which can be detected electrophoretically (Harris, 1969, 1971).

In a number of cases, quantitative differences in the activity of the electrophoretically distinct products of the common alleles have been demonstrated (Harris, 1966, 1971; Gibson and Miklovich, 1971). Variation in specific activity may also result from some of the mutations of the structural gene which do not alter the molecular charge of the protein and hence are undetected electrophoretically. In addition, differences in activity may be determined by variation at loci quite separate from the structural gene. This has recently been demonstrated for the alcohol dehydrogenase locus in *Drosophila melanogaster* by Ward and Hebert (1972).

The purpose of this study is to determine the extent of the genetical variation for specific activity of alcohol dehydrogenase in a population of *Drosophila melanogaster*.

2. Materials and methods

The population used in this study, Texas, originated from a sample of inseminated females caught at Austin, Texas in 1965. The population was subsequently maintained in a population cage; further details are given by Barnes and Kearsey (1970). A set of 19 inbred lines was derived by sib-mating for 42 generations the progeny of single pair matings from this population.

In order to estimate the the allele frequency at the *Adh* locus a sample of eggs was collected from the cage and raised at low density; from the resulting progeny 250 females were selected at random and assayed by starch gel electrophoresis. The gel and electrode buffers are as described by Poulik (1957). An 11 per cent. starch (Connaught Medical Research Laboratories) gel was used. After electrophoresis the gel was stained for alcohol dehydrogenase by the method described by Ayala *et al.* (1972).

Measurements of alcohol dehydrogenase specific activity were made on single virgin female flies raised at 25° C. and aged for 5 days after eclosion. Homogenates were prepared in 0·6 ml. of 0·05 M Tris-phosphate buffer *p*H 8·5. The homogenates were centrifuged at $3000 \times g$ for 30 minutes at 4° C. The activity of the supernatant was determined by observing the time taken for a change of 0·05 OD units at 340 mμ in 1 ml. quartz cuvettes at 25° C. in a SP 1800 Pye Unicam recording spectrophotometer. The reaction mixture contained 2·3 mM β—NAD^+ and 0·08 M propan-2-ol. Total protein was measured in each extract using the modified Folin technique described by Miller (1959).

3. Results

The results of the electrophoretic assay, given below, show that two *Adh* alleles are segregating in the population. The allele frequencies are 0·89 for Adh^S and 0·11 for Adh^F.

	Genotype		
	Adh^S/Adh^S	Adh^S/Adh^F	Adh^F/Adh^F
Number of females	199	47	4

Of the 19 inbred lines derived from the Texas population, 17 were homozygous for the slow allele and two were homozygous for the fast allele. These frequencies indicate that there has been very little selection at this locus during the inbreeding programme.

TABLE 1

Analysis of variance of the Adh^S specific activities

Item	d.f.	M.S.	V.R.	P
Lines	16	21·8456	5·14	$\ll 0{\cdot}1\%$
Assays	3	6·9221	1·63	20%
L × A	48	4·1330	< 1	n.s.
Duplicates	68	4·3287	—	—
Pooled error	116	4·2477	—	—

TABLE 2

Components of Variation

Component	Percentage of variation
σ^2_L	33·706
σ^2_A	1·205
$\sigma^2_{L\times A}$	0
σ^2	65·088

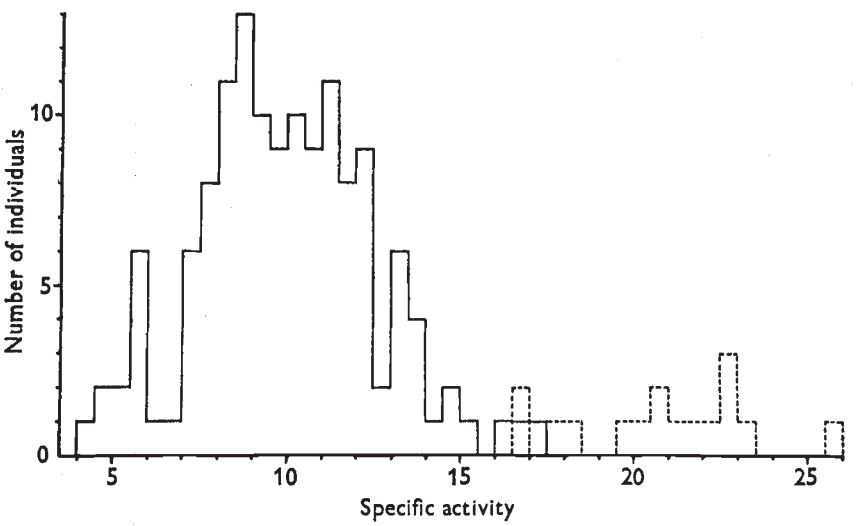

FIG. 1.—Frequency distribution of alcohol dehydrogenase specific activity of individual from lines homozygous Adh^S (continuous line) and homozygous Adh^F (broken line).

The specific activity of *Adh* was measured on two individuals from each inbred line on four separate occasions. On each ocasion the whole experiment was set up as a single randomised block. The results of the analysis of the lines homozygous for Adh^S are given in table 1.

The analysis shows no interaction between lines and assays, and no difference between assays. The difference between lines is highly significant. The components of variation, assuming both lines and assays are random variables, are given in table 2.

As a random sample of inbred lines derived from the population was used in this study we may estimate the narrow heritability of individuals in the Texas population as 20·6 per cent.

The range of variation for individual scores over the full set of lines is shown in fig. 1. It is interesting to note that the most active individuals of the slow morph approach the specific activity of the fast morph.

4. Discussion

This study has revealed extensive variation in specific activity for *Adh*. This variation was related in part to the two electrophoretically distinguishable alleles segregating in the population. Lines homozygous for Adh^F are more active than lines homozygous for Adh^S, as previously reported (Gibson, 1970; Gibson and Miklovich, 1971). But of more interest is the heritable variation found between the lines homozygous for Adh^S. The nature of thi variation is being investigated further.

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