

## A GENETIC ANALYSIS OF THE ADAPTIVE VALUES OF POPULATIONS\*

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Every species of organisms exists because it perpetuates itself in a given ecological niche more effectively than do its competitors. It has been pointed out by Gause<sup>1</sup> that no two species can permanently occupy the same niche because one of them will always prove to be more efficient than the other and the less efficient one will eventually be crowded out. Hence, where two closely related species co-exist, each specializes in a slightly different habitat.

Within the same species, wherever individuals from populations of different origin come together, the problem of competition is complicated by interbreeding and the mingling of genetic material. But when interbreeding is prevented by experimental control, it can be generally shown that two populations need not be exactly equal in the efficiency with which they perpetuate themselves. Such efficiency of perpetuation may be termed adaptive value and its determination is of primary importance in the study of populations. Numerous methods, usually measures of selected physiological traits obviously relevant to the maintenance of the population, have been used for estimating adaptive values. Some estimates for five experimental populations of *Drosophila melanogaster* have previously been reported by Wallace and King,<sup>2</sup> and Wallace.<sup>3</sup> The present paper deals with some attempts at identifying the determinants of these adaptive values.

The technique used for obtaining estimates of the adaptive values for these more detailed analyses was the genetic test described in the above references. Through the use of a stock of flies carrying a genetically marked second chromosome (*Cy L*) samples of second chromosomes were isolated from the populations. The effect of these sampled chromosomes on the viability of individuals carrying them in the homozygous condition or in heterozygous combinations with other chromosomes from the same population was determined. These viabilities were determined in relation to the *Cy L*/+ flies hatching in the same cultures and in both cases ranged from complete lethal (0% wild type) to "normal" (approximately the 33.3% wild flies of the theoretically expected 2*Cy L*/:1 +/+ ratio). This technique then, resulted in the assignment of characteristic viabilities to certain chromosomes on the basis of the homozygous tests and the determination of viabilities of combinations of these chromosomes. In order to get a comprehensive cross-section of the populations, limited data on a great many combinations were collected rather than enormous data on a

few; these studies include over 6000 heterozygous combinations, and for over 2700 of these the corresponding homozygous tests are available.

The adaptive values of the populations were estimated from the average frequencies of wild flies in all heterozygous tests for each population. These average frequencies proved to be characteristic for each population (table 1) and from them the adaptive values were calculated. These adaptive values remained constant over a long period of time in spite of profound genetic changes revealed by the homozygous tests.

In estimating the adaptive values by this technique all the tests were included in the calculations. Each test culture gave an estimate of the viability of individuals possessing a given genotype (second chromosome only) and the use of all tests guaranteed the inclusion of the widest possible array of genotypes to be found within the populations. Certain of these tests resulted in lethal or semilethal combinations; either no wild flies or less than half of those expected appeared. These latter tests indicated that occasionally certain genotypes were missing from the populations because of their lethal nature.

TABLE 1

THE AVERAGE FREQUENCY OF WILD FLIES IN *All* AND IN *Normal* HETEROZYGOUS TESTS OF THE EXPERIMENTAL POPULATIONS.  $s-a$  AND  $s-n$  EQUAL THE DIFFERENCES FROM THE VIABILITY OF NORMAL HETEROZYGOTES OF POPULATION 1 TO ALL AND NORMAL HETEROZYGOTES, RESPECTIVELY, OF THE OTHER POPULATIONS.  $\% = (s-n)/(s-a)$

POP.	ALL	NO.	NORMAL	NO.	$s-a$	$s-n$	%
1	35.06	1454	35.16	1450	..	..	..
3	34.14	1181	34.19	1179	1.02	0.97	95
5	31.85	1007	32.23	994	3.31	2.93	89
6	32.48	1326	32.66	1318	2.68	2.50	93
7	33.40	1350	33.44	1348	1.76	1.72	98

It is widely—if often tacitly—assumed that a population consists of a majority of identically “normal” individuals and a varying—from population to population—proportion of “subnormal” individuals whose presence determines the adaptive value of the population. Here we have extensive data on the viabilities of large numbers of different genotypes from several populations. It appears that these data can throw light on the influence of lethal and semilethal genotypes on the adaptive value of the whole population. Table 1 gives the average frequency of wild flies in all and in the “normal” (non-lethal, non-semilethal) heterozygous tests of the five populations. The highest average frequency in the table is that of normal individuals of population 1; this frequency can be regarded, then, as a standard of viability. To determine the role of drastically weakened individuals of population 3, for instance, in determining the adaptive value of that population, one compares the amount by which the average of all cultures of this population falls short of the standard and the amount by which the

average of the normal cultures is deficient. Actually, 95% of the total deficit in the average frequency of all cultures can be ascribed directly to those genotypes with normal viability; the inclusion of the lethals and semilethals adds only another 5% to the deficit already present. Lethals and semilethals have their greatest effect in population 5, a population of 100–1000 adult individuals that received 2000r per generation for some 40 generations. In population 7 those genotypes with very poor viabilities lowered the adaptive value only an additional 2%. In each population the data indicate that the outstanding determinant of the adaptive value of that population is the large bulk of normal individuals; the obviously non-normal ones have a very minor role in establishing the adaptive value.

The properties of a population of interbreeding diploid organisms at any given time can be best estimated by summing the attributes of the indi-

TABLE 2

VIABILITIES OF FLIES HETEROZYGOUS FOR SECOND CHROMOSOMES WITH DRASTIC OR NON-DRASTIC EFFECTS WHEN HOMOZYGOUS AS EXPLAINED IN TEXT. BOTH THE MEAN AND 95% FIDUCIAL LIMITS OF VIABILITIES ARE GIVEN. RANK OF EACH MEAN IS SHOWN. NUMBERS IN PARENTHESES ARE NUMBER OF COMBINATIONS STUDIED

POP.	2-DRASTIC	1-DRASTIC	NO-DRASTIC
1	35.32 (33.74–36.90) 15 (38)	34.74 (34.18–35.30) 13 (223)	34.75 (34.31–35.19) 14 (352)
3	33.66 (32.44–34.88) 8 (28)	34.43 (33.91–34.95) 10 (216)	34.53 (34.09–34.97) 11 (292)
5	31.62 (31.08–32.16) 1 (239)	32.38 (31.86–32.90) 3 (235)	32.03 (31.03–33.03) 2 (54)
6	32.54 (32.00–33.08) 4 (231)	33.15 (32.63–33.67) 7 (243)	34.54 (33.40–35.68) 12 (54)
7	32.69 (31.11–34.27) 5 (29)	32.98 (32.38–33.58) 6 (163)	33.77 (33.37–34.17) 9 (339)
Rank total	33	39	48

viduals alive at that moment but the enduring characteristics of the group from one generation to another are determined by the genetic pool which the individuals represent only as transitory combinations. The pool—except as changed by selection or genetic drift—remains the same; the individuals change. A corresponding situation is found in a bridge game where the deck of cards is constant but the hands change from one deal to the next. We can know the value of a bridge hand from a knowledge of the cards it contains only within limits. Much depends upon the position of other cards in other hands and the skill of the player in bidding and selecting his plays. Can we predict from the behavior of a chromosome in homozygous condition what its contribution will be to the adaptive value of the population where in all likelihood it will be in heterozygous condition? By studying each second chromosome, whose behavior in homozygous condition is

known, in combination with two other randomly chosen second chromosomes, it was possible to get some measure of the contributions made by different types of chromosomes to the adaptive values of the different populations.

For purposes of analysis, the second chromosomes were divided into two classes on the basis of viabilities of individuals carrying them in the homozygous condition: "drastic" chromosomes that permitted fewer than half of the homozygous individuals to survive in the test cultures, and "normal" chromosomes that permitted more than half the expected number to survive. The heterozygous combinations were made before the nature of the chromosomes was known; consequently, the frequency of the various types of combinations approached that found in the populations. For convenience, one can designate the various combinations as "2-drastic," "1-drastic" and "no-drastic" or "normal."

Table 2 gives the average frequencies of wild type flies found in heterozygous test cultures of the three types of combinations. The limits of the 95% confidence interval ( $\pm 2$  sigmas) and the number of combinations studied in each case are also given. Only the combinations that gave heterozygotes of normal viability are included in this table; lethal and semilethal heterozygous combinations always arose from 2-drastic combinations. From an inspection of the table it is clear that we are operating very close to the limit of statistical resolution; the confidence intervals (even though the standard error in some cases is less than 0.3%) are large relative to the differences found between populations or between different categories within populations. Nevertheless, considerable information can be gleaned from the figures.

The mean viabilities of the three types of combinations are not identical. There is a tendency for no-drastic combinations to yield higher frequencies of wild type flies than the 1-drastic and for the latter to exceed the 2-drastic ones. This fact is brought out in the table by assigning a rank of from 1 to 15 to the mean frequencies from low to high and by summing these ranks in the columns; the orderly increase from 33 through 39 to 48 reflects the trend. This trend fails most obviously in population 1 and, to a lesser degree, in population 5. The exception seen in population 1 is interesting for it is in this population that the greatest proportion of lethals have been exposed to the action of selection for the longest period of time; in the other populations a higher percentage of lethals at any time are of more recent origin.

The different populations also show their characteristic mean values. If the ranks are summed by rows, population 1 has the highest total, 3 is next, and 5 is lowest. These values reflect the differences upon which the relative adaptive values were estimated except that here we are considering only the normal heterozygotes.

Various comparisons of the means of the same and different types of combinations made within and between populations bring to light some interesting and suggestive facts. (a) Only in population 6 is there a significant difference between the means of the 2-drastic and the no-drastic combinations. (b) 2-drastic combinations of population 5 give fewer wild flies than the same combinations of populations 1, 3 and 6. Similarly, 2-drastics of 6 give fewer wild flies than 2-drastics of 1 or 3. (c) 1-drastic combinations of population 5 yield fewer wild flies than similar combinations of population 1, 3 or 6 and, also, this combination in either 6 or 7 yields fewer wild flies than in 1 or 3. (d) The normal combinations of populations 5 and 7 gave fewer wild flies than those of 1 and 3. (e) The no-drastic combinations of population 5 yield fewer wild flies than 2-drastic or 1-drastic combinations of either 1 or 3 and the no-drastic combinations of population 7 produce fewer wild flies than the 2-drastics of population 1 or the 1-drastic combinations of either 1 or 3.

In spite of the fact that additional data to decrease the errors present in table 2 are desirable, it seems reasonable to conclude that chromosomes within the experimental populations which, when homozygous, reduced viability drastically tended to reduce viability in the heterozygous condition. That selection could operate to counteract this tendency was strongly suggested by the data on population 1. To determine the extent by which drastics lower the viability of heterozygotes, the 2-drastic and 1-drastic combinations of populations 3, 5, 6 and 7 were compared to the normal combinations of these populations. The following are the percentage changes in viability attributable to the 2-drastics: (3)  $-2.5\%$ , (5)  $-1.3\%$ , (6)  $-5.8\%$  and (7)  $-3.2\%$ ; and to the 1-drastics: (3)  $-0.3\%$ , (5)  $+0.35\%$ , (6)  $-1.39\%$  and (7)  $-0.79\%$ . Interestingly, the average change in viability attributable to the 2-drastic and 1-drastic combinations are, respectively,  $-3.2\%$  and  $-1.4\%$ —decreases in nearly a two to one ratio.

These data give us some measure of the effect of lethal and semilethal chromosomes on the adaptive values of the populations. For "standard viability" we can use the  $35.16\%$  given in table 1. The simplest comparison is that between the decrease in viability (relative to the standard) exhibited by the no-drastic combinations of populations 3, 5, 6 and 7 and the decrease exhibited by the average "normal" combination without regard to the particular chromosomes involved. The latter can be obtained as weighted averages of the mean viabilities shown in table 2; these averages are: (3)  $34.45\%$ , (5)  $32.00\%$ , (6)  $33.03\%$  and (7)  $33.47\%$ . Using population 3 as an example once more, we calculate the difference between  $35.16\%$  and  $34.53\%$  (the average viability of no-drastic combinations in this population) and divide this difference by  $(35.16\% - 34.45\%)$ . The result— $89\%$ —tells us that  $89\%$  of the decrease in viability from the arbitrary standard ( $35.16\%$ ) to the average representative of normal individuals of

population 3 is directly ascribable to the no-drastic heterozygous combinations of that population. Similarly, 99% of the decrease in population 5, 29% of the decrease in population 6 and 82% of the decrease in population 7 can be localized in the no-drastic combinations. The complete elimination of lethal and semilethal chromosomes from these populations, then, would not result in an increase in the average viability to a common level indicated by the standard of 35.16%; the actual increases one would observe after such an elimination would vary from 1 to 71% of the expected increase. (The results of both population 5 and population 6, the two extremes in the above calculations, should be regarded with caution because of the relatively small number of no-drastic combinations available for analysis in those populations. In populations 3 and 7 where larger numbers of combinations were available, the increase observed after elimination of lethal and semilethal chromosomes would seem to be about 15% of that expected on the basis of our "standard.") We conclude then that although nearly all the responsibility for determining the adaptive value of a population lies with the normal individuals of that population, a substantial amount—but far from all—of the effect of these normal individuals is determined by the lethal and semilethal chromosomes carried by them. The individuals from different populations that carry "normal" chromosomes are not identical and the differences between these individuals play extremely large parts in determining the relative adaptive values of the populations. Nor is this latter relation merely a reflection of the effect of these chromosomes when homozygous, for tests of viabilities of homozygotes have consistently indicated a higher average frequency of wild flies in the homozygous test cultures of populations 3 and 7 than in 1; populations 5 and 6 have given lower frequencies than the other three.

It has already been indicated that individuals heterozygous for lethals and semilethals can, in some populations, have average viabilities lower than individuals from the same populations that carry normal chromosomes. The existence of one population that did not follow the expected pattern indicated that not all lethals and semilethals are equally effective in lowering viability in the heterozygous condition. It may now be asked whether each chromosome tends to have a characteristic effect on the viability of heterozygous individuals regardless of the other chromosome of the combination. It may be mentioned here that flies heterozygous for different second chromosomes do differ in viability; this has been shown in a series of over 100 intercrosses of independently induced second chromosome lethals, in random heterozygotes formed in the routine tests of the experimental populations, and in a special series of more than 100 heterozygous tests involving only normal chromosomes of high viability when homozygous. The latter series involved counts of nearly 1000 flies per test and, for each population, the probability of getting the observed variability by chance was less than

0.001. Cordeiro<sup>4</sup> has shown a similar heterogeneity among individuals of *D. willistoni* heterozygous for different second chromosomes of that species.

Many instances of divergent viabilities between pairs of heterozygous

TABLE 3

PAIRS OF HETEROZYGOUS COMBINATIONS, INVOLVING COMMON CHROMOSOMES, THAT HAVE WIDELY DIVERGENT VIABILITIES. THE NUMERATORS AND DENOMINATIONS GIVE THE VIABILITIES OF THE CHROMOSOMES WHEN HOMOZYGOUS; THE CHROMOSOME COMMON TO BOTH MEMBERS OF EACH PAIR IS ITALICIZED

		VIABILITY OF CHROMOSOMES WHEN HOMOZYGOUS, %	VIABILITY OF HETEROZYGOUS COMBINATIONS, %
Pop. 1	1	33.5/ <i>27.8</i>	39.1
		<i>27.8</i> /0	24.1
	2	33.9/ <i>35.4</i>	43.0
		<i>35.4</i> / <i>26.9</i>	27.3
	3	<i>35.4</i> / <i>26.9</i>	27.3
<i>26.9</i> /0		42.6	
4	<i>20.2</i> /0	18.3	
	0/ <i>27.3</i>	38.9	
5	13.1/ <i>1.9</i>	21.7	
	<i>1.9</i> / <i>30.6</i>	38.8	
Pop. 3	1	<i>26.9</i> / <i>32.8</i>	41.2
		<i>32.8</i> / <i>30.8</i>	26.8
Pop. 5	1	0/ <i>31.4</i>	18.2
		<i>31.4</i> /0	31.0
	2	0/0	42.7
0/0		24.4	
3	0/6.0	16.9	
	<i>6.0</i> / <i>29.2</i>	34.5	
Pop. 6	1	0/0	33.5
		0/7.4	16.6
	2	0/7.4	16.6
		<i>7.4</i> /0	32.2
	3	<i>35.1</i> / <i>33.0</i>	42.4
<i>33.0</i> /1.9		27.3	
4	0/ <i>35.4</i>	41.0	
	<i>35.4</i> /0	18.6	
	35.4/0	18.6	
5	0/0	38.1	
	0/0	38.1	
Pop. 7	1	0/ <i>33.0</i>	27.5
		<i>33.0</i> / <i>32.9</i>	43.9
	2	<i>34.6</i> /0	46.1
0/0		26.3	

combinations carrying a common second chromosome have been observed in the routine tests. Without considering those pairs in which one combination is lethal or semilethal, there are 2736 tests in the data that can be

compared. With such a large number of observations, numerous pairs of combinations containing a common chromosome should differ in viabilities as a result of chance; over 100 instances with probabilities of 5% or less would be expected through chance error even if the viabilities of all combinations were really identical. In table 3 are listed all observed cases in which the viabilities differed so much that the probability of observing them by chance were they really subsamples of the same statistical population was less than 0.001. One would expect 2 or 3 such instances through chance alone among the 2700 combinations; the total of 16 cases actually observed differs significantly from this expected number. The viability of an individual carrying two second chromosomes, then, depends upon the combination of these two chromosomes; the same chromosome can produce widely divergent viabilities in different combinations. The data of table 3 are presented in fractional form; the two numbers of the fraction indicate the viabilities of the two second chromosomes when each is homozygous. The viability of the heterozygous combination follows the fraction. The chromosome common to the two combinations is italicized. In eight cases (1, 2, 4 and 5 of population 1; 3 of population 5; 3 of population 6; and 1 and 2 of population 7) those combinations with the lowest viabilities involve chromosomes that give the lowest viabilities when homozygous; the reverse is true in four other cases (3 of population 1; 1 of population 3; and 1 and 5 of population 6); and in the remaining four cases the two combinations are composed of chromosomes of similar homozygous viabilities. Cases 4 and 5 of population 6 present an interesting relationship; a chromosome with normal viability when homozygous gave good viability in combination with one lethal but poor with another. However, the second lethal gave good viability when in combination with still another lethal chromosome. A similar situation is seen in cases 1 and 2 of the same population; a semilethal in combination with a lethal gave a heterozygote of poor viability but the lethal in combination with another lethal and the semilethal with still another lethal each produced heterozygotes of good viability. A third example exists in cases 2 and 3 of population 1. It is unfortunate that such widely divergent viabilities were required to give a statistical probability of proper magnitude, still the examples show that a chromosome can produce heterozygous combinations of different viabilities that could not have been accurately predicted from a knowledge of the action of the chromosomes when homozygous.

Case 1 of population 3 is probably one of the few cases in which the divergent viabilities have occurred through chance error. Concurrent with these tests a search was made for "negative heterosis," cases in which heterozygotes had poorer viabilities than either of the two chromosomes involved in the heterozygous combination. No cases of negative heterosis were found; case 1 of population 3 was one of those that were tested further and the original wide divergence was not confirmed.



The unpredictability of viabilities of heterozygous combinations was demonstrated by still another method. Each chromosome was tested in two combinations and, consequently, it was possible to calculate a difference and a standard error of the mean for the viabilities of combinations sharing a common chromosome. Similarly, it was possible to calculate a mean difference and the standard error of the mean for viabilities of heterozygous combinations that did not share a common chromosome. (The original data are tabulated so that adjacent entries represent combinations with a common chromosome. Differences between adjacent entries were compared with differences between non-adjacent entries separated by one culture; symbolically, we compared  $(a/b - b/c)$  with  $(a/b - c/d)$ .) In a series of 301 differences calculated for combinations with a chromosome in common, the mean of differences without regard to sign was  $5.01\% \pm 0.23\%$ ; 312 differences between independent combinations gave  $4.74\% \pm 0.20\%$ . The knowledge of the viability of a particular chromosome in one combination, then, does not permit a more accurate prediction regarding its viability in a second combination than could be made for a combination of entirely different chromosomes. This situation would apply equally well if all chromosomes of a population were identical for then the distinction between the "same" and "different" chromosomes would be only apparent; the data in table 3 rule out this possibility, however, by showing that these chromosomes—and their combinations—are not identical.

Some of the complex interactions involved in the establishment of the adaptive value of a population through the action of selection on the genetic structure are now apparent. The manifestation of lethal or semilethal chromosomes in individuals of markedly poor viability has a minor influence on the population as a whole. These chromosomes exert a greater effect on the population through their action in "normal" individuals; within some populations, at least, individuals carrying lethal or semilethal chromosomes have demonstrably poorer viabilities, on the average than those that carry chromosomes giving higher viabilities when homozygous. It was also demonstrated, however, that the viabilities of individuals carrying only "normal" chromosomes varied from population to population and that these individuals were frequently the most influential determiners of the estimated adaptive values. It appears that the viability of a combination of two chromosomes is characteristic of the combination, not of either one of the two chromosomes. The action of selection, then, cannot be to retain this or that chromosome in a population because of its characteristics when homozygous or because of its characteristics when in any one of several possible combinations; rather, selection must act to retain within a population those chromosomes whose complex of combinations and recombinations gives, on the average, the highest adaptive value.

Dobzhansky<sup>5</sup> showed that the three cytologically distinguishable third

chromosomes (ST, AR and TL) of *D. pseudoobscura* were retained in a population only through the superiority of AR/TL heterozygotes and ST/AR heterozygotes. ST/TL heterozygotes were inferior to ST/ST homozygotes and, if it were not for the other, heterotic combinations, TL would have been eliminated by selection. The frequency of each chromosome finally established by selection was that which gave the highest average adaptive value to the entire complex. These three variables, then, lead to a fairly complicated situation; all the subtle interactions of the many individual AR, ST and TL chromosomes with one another is staggering.

It seems impossible to avoid the conclusion that an isolated population, within surprisingly few generations after its inception, achieves as a result of selection a characteristic and unique integration of its genetic pool. It develops a genetic personality. In the present studies, the differing histories of the populations have resulted in the establishment of gene pools identifiable by routine tests on frequencies of lethals and semilethals, average viabilities of non-lethal, non-semilethal chromosomes when homozygous, average viabilities of random combinations of second chromosomes, and to a limited extent, frequency of lethal and semilethal heterozygous combinations.

*Summary.*—An analysis of viabilities of individuals heterozygous for chromosomes sampled from a number of experimental populations of *D. melanogaster* has made it possible to identify the determinants of the adaptive values of the populations. Individuals of drastically reduced viabilities are so rare in populations that they have little effect in determining the adaptive values. Of the normal individuals, those carrying lethal or semilethal chromosomes have, in some populations, lowered average viabilities (1–3% lower than individuals carrying “normal” chromosomes). In these same populations, however, the individuals carrying two normal second chromosomes have viabilities that account for anywhere from 29 to 99% of the reductions in adaptive values.

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<sup>1</sup> Gause, G. F., *The Struggle for Existence*, Williams and Wilkins, Baltimore, 1934.

<sup>2</sup> Wallace, B., and King, J. C., “Genetic Changes in Populations Under Irradiation,” *The American Naturalist*, **85**, 209–222 (1951).

<sup>3</sup> Wallace, B., *Evolution* (in press).

<sup>4</sup> Cordeiro, A. R., *THESE PROCEEDINGS* **38**, 471–478 (1952).

<sup>5</sup> Dobzhansky, Th., “Genetics of Natural Populations. XVIII. Experiments on Chromosomes of *Drosophila pseudoobscura* from Different Geographic Regions,” *Genetics*, **33**, 588–602 (1948).