COMPARISON OF THE CONCEALED VARIABILITY IN DROSOPHILA WILLISTONI WITH THAT IN DROSOPHILA PROSALTANS

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NATURAL populations of every *Drosophila* species which has been studied carry genetic loads, consisting of deleterious genetic variants which are mostly recessives and are usually concealed in heterozygous condition. Many chromosomes in wild populations are lethal, semilethal, or subvital in double dose, or they cause sterility of females or of males, slower development rates, visible morphological changes, or other variations. Quantitative estimates and comparisons of the magnitudes of the genetic loads have been attempted for two pairs of closely related species of the subgenus *Sophophora*, namely *Drosophila pseudoobscura* and *D. persimilis* (DOBZHANSKY and SPASSKY 1953), *D. willistoni* (PAVAN, CORDEIRO, N. DOBZHANSKY, T. DOBZHANSKY, MALOGOLOWKIN, SPASSKY, and WEDEL 1951) and *D. prosaltans* (DOBZHANSKY and SPASSKY 1954). Among these, *D. pseudoobscura* seems to carry a somewhat heavier genetic load than *D. persimilis*, although the mutation rates for autosomal lethals are lower in *pseudoobscura* than in *persimilis* at similar temperatures. *D. pseudoobscura* is geographically more widely distributed, more common, successful, and ecologically more versatile than is *D. persimilis*. As for the other pair, *D. willistoni* carries more lethal, semilethal, and sterility-inducing chromosomes than *D. prosaltans*. Again, *D. willistoni* is much commoner, more successful, and ecologically more versatile than is *D. prosaltans* (DOBZHANSKY and PAVAN 1950). The published data on *D. willistoni* do not, however, give reliable information concerning the frequencies of chromosomes with recessive subvital effects in the natural populations of this species. The reason is that no satisfactory method for estimation of the frequencies of subvital chromosomes were available when PAVAN *et al.* (1951) made their study of this species. A method was evolved by WALLACE and MADDEN (1953), and was used by DOBZHANSKY and SPASSKY (1953, 1954) for making estimates of these frequencies in *D. pseudoobscura*, *D. persimilis*, and *D. prosaltans*. The chief purpose of the study reported in the present article has been to obtain comparable data for *D. willistoni*.

MATERIAL AND METHODS

A total of 177 second chromosomes of *D. willistoni* have been used in this study. They were obtained from samples of the natural populations collected in the following ten localities:

(1) Cubatão, Sao Paulo, (2) Angra dos Reis, Rio de Janeiro, (3) Mafra, Santa Catarina, collected by PROF. C. PAVAN and his collaborators, (4) Palmira, Co-

lombia, (5) Llanos near Villavicencio, Colombia, (6) Buenaventura, Colombia, collected by PROF. TH. DOBZHANSKY, (7) Panama, (8) Jamaica, (9) Trinidad, collected by PROF. M. WHEELER and DR. M. WASSERMAN, of the University of Texas, and (10) Tikal, Guatemala, collected by MRS. SOPHIE DOBZHANSKY COE (shown in Table 2).

The wild flies, or their offspring (the culture being continuously intercrossed to avoid inbreeding) were kept at temperature 15°C before being used for the experiments. No culture was kept for more than four months (about four generations).

The series of crosses used in the present experiments for analysis of the genetic contents of the second chromosomes of *D. willistoni* were the same as those used by PAVAN *et al.* (1951). One or more wild males were crossed to females homozygous for the recessive marking genes abbreviated and brown (*abb bw*). A single male from each F_1 culture (heterozygous for *abb bw*) was crossed to several females which had dominant Star (*S*) and Hook (*Hk*), recessive *abb bw*, an inverted section in one second chromosome to suppress crossing over, and a balancing recessive lethal in the other second chromosome. In the next generation (F_2), six to ten females, and a small number of males, showing *S* and *Hk* were selected and inbred. These parental flies were transferred three times to obtain oviposition in fresh culture bottles. The cultures were kept at 25°C. When the F_3 flies began to hatch, four counts were made at three-day intervals, in all the cultures. The wild type (non-*S*, non-*Hk*) flies appearing in these cultures carry in duplicate (are homozygous for) certain second chromosomes derived from the natural populations.

About simultaneously with the above series of crosses, another series of "control" crosses were made. For the controls, *S Hk*/++ females and males from *different* cultures but of similar geographic origin were intercrossed. The wild type flies hatching among the progenies are heterozygous for two different second chromosomes, derived from different wild progenitors. The control crosses were handled exactly like those which were used to produce homozygous wild type flies.

Control crosses—normal viability

Seventy intercrosses producing heterozygous wild type flies were made. The results are reported in the upper line of Table 1. A total of 35,491 flies were counted in the control crosses, and 15,555, or 43.83 percent, of them were wild type. The viability of these wild type flies is normal by definition (cf. PAVAN *et al.* 1951; DOBZHANSKY and SPASSKY 1953, 1954). Since the expected Mendelian ratio of the wild type: *S Hk* flies is 33.33:66.67, it follows that the presence of the dominant marking genes *S* and *Hk* decreases the viability of the flies which carry these genes. Table 1 shows also that the mean number of flies per control culture was 221.35.

The control experiment of PAVAN *et al.* (1951) gave results slightly different from the present one, since those investigators obtained 39.91 percent of wild type flies in the cultures. This is not surprising since PAVAN *et al.* used banana-

TABLE 1

Percentages of wild type flies, average number of flies per bottle, chromosomes or combinations tested in controls, quasinormal homozygotes and lethal plus semilethal ones, as well as in all homozygotes

		Flies counted	Percent wild	Average no. of flies per bottle	Chromosomes tested	Percentage of normal viability
Controls		35,491	43.83	221.35	70	100.0
Homozygotes	quasinormal	46,764	35.19	147.98	107	80.28
	lethal	11,837	1.19	134.51	65	2.71
	Total	58,601	22.91	142.88	172	52.27

agar food in their experiments, which is probably more favorable for *D. willistoni* than is SPASSKY's cream-of-wheat—molasses medium used in the present experiments.

The average percentages of wild type flies in the four counts made in the control cultures were 47.54, 46.56, 43.71, and 40.03. These are slightly higher than the series of values obtained by PAVAN *et al.* (1951), which were 43.37, 39.01, 35.33, and 38.76 percentage.

Lethals and semilethals

As stated above, a total of 177 wild chromosomes were involved in the experiments. Of these, 172 experiments were completed successfully. The results are summarized in Table 1 and in Figure 1.

The mean percentage of wild type flies in the control (heterozygous) cultures is taken as the standard for normal viability under our experimental conditions. This percentage is, as shown in Table 1, 43.83.

In those cultures in which the wild type flies were homozygous for certain wild second chromosomes, the frequency of the wild type class varied from zero to 48

FIGURE 1.—Distribution of viability frequencies of the wild type class in homozygotes cultures (black) and in heterozygotes (crosshatched).

percent (i.e., from zero to 110 percent of normal viability). As can be seen in Figure 1, the distribution of the viability frequencies is sharply bimodal. The distribution seems to be more or less continuous from zero to 13 percent (zero to 30 percent of the normal viability). No chromosomes have been found with viabilities between 30 percent and 43 percent of normal (producing between 13 and 19 percent of wild type flies in the cultures). For viabilities from 19 to 48 percent, the observed distribution is again continuous and normal. For our purposes we have defined as semilethals those chromosomes which in homozygotes cause viability of less than 30 percent of normal. This is somewhat different from the conventional definition, in which 50 percent of the normal viability is used as the dividing line between semilethal and subvital chromosomes.

Using these criteria we found that 65 out of 177 chromosomes in our material were lethal or semilethal when homozygous (Table 2). No significant heterogeneity between different geographic localities is observed. The percentage of lethal and semilethal chromosomes in our material was 36.7 ± 3.6 , which is not significantly different from 41.2 ± 1.1 given by PAVAN *et al.* (1951).

Subvital, normal and supervital chromosomes

The total number of quasinormal chromosomes adequately tested in our material was 107. Although the observed distribution is continuous, one may distinguish subvital, normal and supervital chromosomes. The estimates of the relative frequencies of these three classes were made following the method devised by WALLACE and MADDEN (1953) and used by DOBZHANSKY and SPASSKY (1953, 1954) for *D. pseudoobscura*, *D. persimilis* and *D. prosaltans*, and by DAWOOD (1958) for natural populations of *D. melanogaster*.

The observed variance (σ^2_{τ}) of the viabilities of the $+/+$ class in the experimental cultures has evidently three main components. The sampling component (σ^2_s) is estimated very easily from the numbers of flies counted in the cultures. The environmental component (σ^2_e) is estimated from the results in the three

TABLE 2
Number of chromosomes tested

Locality	Lethals and semilethals	Quasnormals	Total
Palmira	13	10	23
Llanos	9	22	31
Angra dos Reis	11	33	44
Cubatão	18	30	48
Buenaventura	2	7	9
Mafra	—	2	2
Panama	3	—	3
Guatemala	—	1	1
Jamaica	3	3	6
Trinidad	6	4	10
	65	112	177

replicate cultures which were raised to test each chromosome or chromosome combination. Subtracting the sampling and the environmental variance from the total variance observed, we obtain the residual, or genetic, variance, σ_g^2 . The estimates obtained for the experimental cultures in which the +/+ class was homozygous, and for the control cultures, in which this class was heterozygous, are listed in Table 3.

The observed total variance is greater for the homozygotes than for the heterozygotes, and the difference is due largely to the real or genetic variance which is more than twice as large for the homozygotes. Following WALLACE and MADDEN, the subvital chromosomes are defined as those with viabilities less than the normal one minus $2\sigma_g$ for the control distribution. Correspondingly, the supervital chromosomes exceed the normal viability by more than $2\sigma_g$ for the control distribution. Applying these definitions to our data, the frequency of subvital chromosomes among the quasinormal array turns out to be 71.9 percent, of the normal 28.0 percent, and of the supervital chromosomes 0.1 percent.

Table 4 shows a comparison of the available estimates of the frequencies of subvital chromosomes among the quasineormals in different species of *Drosophila*. It should be noted that the third chromosome of *D. prosaltans* is homologous to the second chromosome of *D. pseudoobscura* and *D. persimilis*, while the second chromosomes of *D. prosaltans*, *D. willistoni* and *D. melanogaster* are homologous to the sum of the third and fourth chromosomes in *D. pseudoobscura* and *D. persimilis* (DOBZHANSKY and SPASSKY 1953, 1954). Despite the experimental errors

TABLE 3

Estimates of the components of the variance of viabilities

	σ_τ^2	σ_s^2	σ_e^2	σ_{es}^2	σ_g^2	σ_g
Homozygotes	32.35	6.21	6.79	13.00	19.35	4.40
Controls	19.18	5.63	5.80	11.43	7.75	2.78

TABLE 4

Percentage frequencies of subvital chromosomes in five species

Species	Chromosome	Subvital
<i>prosaltans</i>	third	14.5
<i>pseudoobscura</i>	second	93.5
		89.6
<i>persimilis</i>	second	84.4
<i>prosaltans</i>	second	33.4
<i>willistoni</i>	second	71.9
<i>pseudoobscura</i>	third + fourth	97.3
		98.5
<i>persimilis</i>	third + fourth	99.5
<i>melanogaster</i>	second	26.1-66.6

being very considerable, it is evident that *D. prosaltans* carries fewer subvital variants in its chromosomes than do the other species.

Variability and viability

As indicated above, the quasinormal homozygotes and controls were tested generally in three replicate cultures. The variation between the percentages of the wild type class in the replicate cultures is due to sampling errors and to micro-environmental variations. The question arises whether the variance due to the environmental variations (σ_e^2 in Table 3) shows any relationship to the observed viabilities of the chromosomal heterozygotes and homozygotes.

The coefficients of variation, $C.V. = 100 \sigma_e/m$, were computed for each chromosome or chromosome combination, using the mean viability, m , which is the mean percentage of wild type flies in the cultures. Coefficients of correlation were calculated between the C.V. and the m values. Similar calculations were made for the second chromosome of *D. prosaltans* using the data of DOBZHANSKY and SPASSKY (1954), kindly furnished by them for this purpose. The values obtained are shown in Table 5. It can be seen that for the homozygotes the correlation is negative, i.e., the chromosomes which lower the viability tend to show a higher variability. The correlation coefficient is however not significant for *D. prosaltans*, while it is significant for *D. willistoni*. The correlation coefficients obtained for the control experiments (heterozygotes) are not significant.

Viability effects of the chromosomes in homozygous and heterozygous condition

One of the disputed problems in population genetics at present is to what extent the genetic loads in Mendelian populations are maintained by recurrent mutation and by balanced polymorphism. If the genetic load is chiefly mutational, one would expect a positive correlation between the viabilities of the heterozygotes and those of the homozygotes for the respective chromosomes. If the genetic load is balanced, one expects no correlation or even a negative one.

Figure 2, constructed as a correlation table, shows the viabilities of the heterozygotes on the ordinates and of the homozygotes on the abscissae. (The viabilities of the homozygotes entered in this figure are the arithmetic mean of the viabilities of the two chromosomes involved). The coefficients of correlation, computed for the second chromosomes of *D. willistoni* and *D. prosaltans*, are as follows:

$$\begin{array}{ll} D. willistoni & -0.02 \pm 0.12 \\ D. prosaltans & +0.25 \pm 0.12 \end{array}$$

TABLE 5

Coefficients of correlation between coefficients of variation and viabilities

	Quasinormal homozygotes	Heterozygotes
<i>D. willistoni</i>	-0.28 ± 0.09	$+0.15 \pm 0.11$
<i>D. prosaltans</i>	-0.08 ± 0.08	$+0.10 \pm 0.11$

FIGURE 2.—Correlation between viabilities of the wild type class in heterozygotes and corresponding homozygotes cultures. Further explanations in the text.

A significant, though small, positive correlation is observed in *D. prosaltans*, but no correlation in *D. willistoni*. Taken at face value this would mean that the genetic load is mainly mutational in *D. prosaltans* and mainly balanced in *D. willistoni*.

DISCUSSION

Table 6 summarizes the available data concerning the frequencies of lethal, semilethal, subvital, and sterility-producing homologous chromosomes in several species. The data for *D. melanogaster*, which is a commensal species, have been omitted. It is easy to see that the population of *D. willistoni* from the central part of its geographic distribution, and those of *D. pseudoobscura* and *D. persimilis* carry heavier genetic loads than the marginal populations of *D. willistoni* and those of *D. prosaltans*.

MORTON, CROW and MULLER (1956) tried to distinguish between the mutational and the balanced genetic load with the aid of the following method. They assume that the unfixed genes are represented in the populations usually by only two alleles. If the genetic load is balanced, the adaptive values of the homozygotes are $1 - s$ and $1 - t$, while that of the heterozygote is unity. On these as-

TABLE 6

Percentage frequencies of lethal plus semilethal, subvital, sterility-inducing chromosomes in different species of the subgenus *Sophophora*

Species	Locality	Lethal and semilethal	Subvitals	Sterile females	Sterile males
<i>D. willistoni</i> *	Central (Brazil)	41.2 ± 1.1	—	12.6	20.1
<i>D. willistoni</i> †	Central (Brazil)	36.7 ± 3.6	71.9	—	—
<i>D. willistoni</i> ‡	Marginal (La Plata)	33.4 ± 2.6	—	—	—
<i>D. willistoni</i> ‡	Marginal (Rio Grande do Sul)	32.2 ± 1.6	—	—	—
<i>D. willistoni</i> §	Marginal (Florida)	31.1 ± 4.4	—	10.2 ± 3.4	70.9 ± 5.1
<i>D. willistoni</i> §	Marginal (Cuba)	36.0 ± 9.5	—	small number of flies tested	
<i>D. prosaltans</i>	Brazil	32.6 ± 2.7	33.4	9.2 ± 2.2	11.0 ± 2.4
<i>D. pseudoobscura</i> ¶	California	44.4 ± 8.2	97.3—98.5	17.3 ± 5.8	21.1 ± 6.8
		42.9 ± 7.8			
<i>D. persimilis</i> **	California	48.0 ± 6.7	99.5	30.0 ± 6.5	22.8 ± 5.6

* PAVAN *et al.* 1951.

† KRIMBAS (present study).

‡ CORDEIRO *et al.* 1958.

§ TOWNSEND 1952.

|| CAVALCANTI 1950; DOBZHANSKY and SPASSKY 1954.

¶ DOBZHANSKY and SPASSKY 1953, and DOBZHANSKY *et al.*, unpublished.

** DOBZHANSKY and SPASSKY 1953.

sumptions, the population at equilibrium suffers a loss of fitness approximately $st/(s+t)$, whereas if the population is made completely homozygous the loss of fitness becomes $2st/(s+t)$. The ratio of the two values is two. Since the few data for human populations lead to estimates of a ratio of 10 to 25, MORTON *et al.* infer that the genetic load is in the main mutational. This inference is not justified if the variable genes are represented by more than two alleles per locus. Suppose that a locus is represented in a population by n alleles, with equilibrium frequencies $\bar{p}_1, \bar{p}_2, \dots, \bar{p}_i, \dots, \bar{p}_n$, where $\sum_{i=1}^n \bar{p}_i = 1$. Assuming that all the heterozygotes have a fitness equal to unity, and the fitnesses of the homozygotes are respectively $1 - s_1, 1 - s_2, \dots, 1 - s_n$, ($0 \leq s_i < 1$) we will have the equilibrium condition:

$$(1) \quad \frac{\bar{p}_1^2 s_1}{\bar{p}_1} = \frac{\bar{p}_2^2 s_2}{\bar{p}_2} = \dots = \frac{\bar{p}_i^2 s_i}{\bar{p}_i} = \frac{\bar{p}_n^2 s_n}{\bar{p}_n} = \frac{\bar{p}_i^2 s_i}{\bar{p}_i} = \sum_{i=1}^n \bar{p}_i^2 s_i$$

which is the genetic load in the panmictic population. On the other hand it is clear that

$$(2) \quad \frac{\bar{p}_i^2 s_i}{\bar{p}_i} = p_i s_i = \bar{p}_1 s_1 = \bar{p}_2 s_2 = \frac{n \bar{p}_i s_i}{n} = \frac{\sum_{i=1}^n \bar{p}_i s_i}{n}$$

From (1) and (2)

$$\sum_{i=1}^n \bar{p}_i^2 s_i = \frac{\sum_{i=1}^n \bar{p}_i s_i}{n} \quad \text{or}$$

$$n = \frac{\sum_{i=1}^n \bar{p}_i s_i}{\sum_{i=1}^n \bar{p}_i^2 s_i}$$

The ratio of these genetic loads is equal to the *number of alleles* n . If we consider more than one locus the treatment is difficult, because of the epistatic interactions. The test proposed by MORTON *et al.* gives accordingly ambiguous results.

It has been pointed out by several investigators (DOBZHANSKY and WALLACE 1953; DOBZHANSKY, PAVLOVSKY, SPASSKY and SPASSKY 1955) that the heterozygotes for "wild" chromosomes tend to be better buffered against changes in environmental conditions than the corresponding homozygotes. Indeed, our data for *D. willistoni* give a mean coefficient of variation for the survival rates of the homozygotes equal to 10.20 ± 1.09 ; the corresponding mean for the heterozygotes is 7.34 ± 0.87 ; the difference, 3.36 ± 1.40 , is significant at between the 5 percent and 2 percent levels. It should be noted that, as shown above, the mean viability of a homozygote is negatively correlated with the coefficient of variation of its viability in different environments. The mean viability of the quasinormal homozygotes is lower than that of the control heterozygotes. If we compare the coefficients of variation in the homozygotes producing more than 34 percent of wild type flies in the cultures, with that for the heterozygotes, the difference is no longer significant (9.85 and 7.34 respectively, a difference of 2.51 ± 1.51). The situation in *D. prosaltans* is as follows: the mean coefficient of variation for the quasinormal homozygotes is 7.32 , and for the heterozygotes 6.30 , an insignificant difference of 1.02 ± 1.03 .

It is interesting to compare the population structures in *D. willistoni* and in *D. prosaltans*, as revealed by our data. As shown above, the genetic load is greater in the former than in the latter species. In *D. willistoni*, the viability and the variability of the quasinormal homozygotes are negatively correlated; in *D. prosaltans* there is no correlation. In *D. willistoni*, the viability of a heterozygote shows no correlation with the viabilities of the corresponding homozygotes, but in *D. prosaltans* an apparently significant positive correlation is observed. These differences are consistent with the supposition that the genetic load in *D. willistoni* is predominantly a balanced load, and in *D. prosaltans* a mutational load. In turn, this is consistent with what is known concerning the reproductive biology of these species (DOBZHANSKY and PAVAN 1950; DOBZHANSKY and SPASSKY 1954). *D. willistoni* is, in South America, an ecological dominant, while *D. prosaltans* is a rare and specialized form. In the former species, close inbreeding is probably much less frequent than in the latter. Natural selection would, then, be expected to act differently in the two species. In *D. willistoni* the genetic contents of chromosomes are selected according to the fitness they confer on heterozygous individuals, while in *D. prosaltans* the fitness of the homozygotes is also important. Studying the allelism of autosomal lethals found in natural populations, PAVAN and KNAPP (1954) concluded that the genetic population sizes in *D. willistoni* (excepting certain island populations) may be considered

effectively infinite. Corresponding data are, unfortunately, not available for *D. prosaltans*, but the known features of its ecology suggest that the genetically effective size of its population may, on the average, be small. We can conclude that the genetic structure of the population in *D. willistoni* is closer to that postulated by the balance theory, while in *D. prosaltans* it is closer to what the classical theory of the genetic structure leads one to expect. The genetic population structure is interrelated with the reproductive biology of the respective populations.

SUMMARY

The concealed genetic variability in natural populations of *Drosophila willistoni* has been examined. The frequencies of chromosomes which are lethal, semilethal or subvital when homozygous, or which produce sterility of females or of males, are much higher in *D. willistoni* than in *D. prosaltans*. In *D. willistoni*, the viability of quasinormal homozygotes shows a negative correlation with the environmental sensitivity of these homozygotes; such a correlation is absent in *D. prosaltans*. On the other hand, the correlation between the viabilities of the heterozygotes and the corresponding homozygotes does not differ from zero in *D. willistoni*, while it is positive in *D. prosaltans*. These differences may be related to the differences in the reproductive biology of the two species, since *D. willistoni* is a common, successful, and ecologically versatile form, while *D. prosaltans* is rare and probably specialized ecologically. It may be inferred that the relative importance of the mutational component of the genetic load is greater in *D. prosaltans* than in *D. willistoni*, while that of the balanced component is greater in *D. willistoni* than in *D. prosaltans*.

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