THE GENETIC STRUCTURE OF NATURAL POPULATIONS OF *DROSOPHILA MELANOGASTER*. VIII. NATURAL SELECTION ON THE DEGREE OF DOMINANCE OF VIABILITY POLYGENES¹

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SINCE the destinies of mutant genes in a large, random-mating population are decided almost entirely by selection on heterozygotes much attention has been paid to the degrees of dominance of mutant genes. It has been pointed out that the average degree of dominance in an equilibrium population ($\bar{h}_E$) is different from that of newly-arising mutants ($\bar{h}_N$), (e.g., MORTON, CROW and MULLER 1956; DOBZHANSKY 1964), and this difference will be discussed here for polygenes affecting viability.

An apparent coupling-repulsion difference was discovered in *Drosophila melanogaster* by MUKAI and YAMAZAKI (1964, 1968) with respect to the heterozygous effects of newly-arising, mutant, viability polygenes in a homozygous genetic background; namely, they show overdominance when located in the same chromosome, but when located heterozygously in both homologous chromosomes, they are not only deleterious, but their degree of dominance is surprisingly high ($\bar{h} \approx 0.4$). They have tentatively concluded that the manifestation of overdominance is rare in equilibrium natural populations for the following reasons: 1. Most of the chromosomes carry mutants of viability polygenes and many of them are in repulsion; coupling heterozygotes being rare; 2. There is an optimum level of heterozygosity in the coupling phase (MUKAI 1969a). This report concerns only viability polygenes; lethal genes are not considered. Furthermore, overdominance will be ignored since its manifestation might be very low in equilibrium populations.

If the average degree of dominance of viability polygenes is 0.4, inbreeding depression due to these polygenes is scarcely expected. However, experimental results suggest there is an appreciable amount of inbreeding depression due to viability polygenes (e.g., Table 6 of Crow 1968). A reasonable explanation for this phenomenon is that, among polygenes, there is genetic variation in the degrees of dominance and that the average degree of dominance of mutant, viability polygenes in an equilibrium population is smaller than that among newly-arising mutants.

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Employing the experimental results of MUKAI and YAMAZAKI (1968), genetic variances of the degrees of dominance of newly-arising, mutant, viability polygenes were calculated for repulsion heterozygotes and attempts were made to predict the average degrees of dominance in equilibrium populations. The result is presented in this article.

MATERIALS AND METHODS

Mating scheme: Starting with a single normal second chromosome from an Erie, Pennsylvania population of *Drosophila melanogaster*, 104 replicate lines were established in the form: Cy/Pm (♀ ♀) $\times$ $Pm/+_i$ (1 ♂), where i indicates line number ($i = 1, 2, \dots, 104$). In each of these lines spontaneous mutations were allowed to accumulate for many generations during which the chromosome was maintained in heterozygous condition with minimal selection pressure. The viability of homozygotes was estimated by the Cy method (WALLACE 1956), i.e. $Cy/+_i$ (5 ♀ ♀) $\times$ $Cy/+_i$ (5 ♂ ♂). The expected ratio of wild-type progeny to total progeny was 33.3%. The percentage of wild-type flies was employed as the viability index throughout.

The viability of heterozygotes between lines having successive line numbers ($1 \times 2, 2 \times 3, \dots$) (in generations 32 and 52) and that between lines carrying alternate line numbers ($1 \times 3, 2 \times 4, 3 \times 5, \dots$) (in generation 52), were estimated by $Cy/+_i \times Cy/+_{i+1}$ (RS cross) and $Cy/+_i \times Cy/+_{i+2}$ (RA cross), respectively. Five pair-mating were made as in the case of homozygotes. In each line or cross, eight replicated observations were made in generation 32 and six in generation 52. Details of the experimental procedure can be seen in MUKAI (1964) and MUKAI and YAMAZAKI (1968).

Estimation of the degree of dominance and its variance: The following parameters are defined:

v_o = original viability (or control viability of homozygotes and heterozygotes (expected value is 33.3))

$v_{i(k)}$ = the homozygote viability of the k -th observation of line i .

$v_{ij(m)}$ = the viability of the m -th observation of the heterozygote between lines i and j .

s_l = selection coefficient against a mutant homozygote at locus l with fitnesses (1, 1- s , 1- s).

h_l = the degree of dominance of a mutant polygene at locus l .

Assume (a) a mutant, viability polygene at locus l ($l = 1, 2, \dots, n$); (b) n_1 mutant-carrying loci in line i and n_2 ($=n-n_1$) such loci in line j and they are not allelic; and (c) additivity over loci.

The degree of dominance of mutant polygenes on a chromosome pair basis (H) can be expressed as follows:

$$\begin{aligned}
 H &= \frac{v_o - v_o \left(1 - \sum_{l=1}^n s_l h_l \right)}{2v_o - v_o \left(1 - \sum_{l=1}^{n_1} s_l \right) - v_o \left(1 - \sum_{l=n_1+1}^n s_l \right)} \\
 &= \frac{\sum_{l=1}^n s_l h_l}{\sum_{l=1}^{n_1} s_l + \sum_{l=n_1+1}^n s_l} = \frac{\sum_{l=1}^n s_l h_l}{\sum_{l=1}^n s_l} .
 \end{aligned} \tag{1}$$

That is, H is the average h value weighted by s , and if there is no correlation between s and h , then,

$$H = \frac{\bar{h} \Sigma s}{\Sigma s} = \bar{h} . \tag{2}$$

Using the following formula, dominance of mutant, viability polygenes on a chromosome pair basis can be estimated for each group of $v_{i(k)}$, $v_{j(k')}$, $v_{ij(m)}$, where $k = k' = m$ and the errors of $v_{i(k)}$, $v_{j(k)}$, and $v_{ij(k)}$ are not correlated with each other:

$$H_{ij(k)} = \frac{v_o - v_{ij(k)}}{2v_o - (v_{i(k)} + v_{j(k)})} \quad (3)$$

For a group of lines i and j , we have 8 estimates of $H_{ij(k)}$ in generation 32 and 6 in generation 52. Thus, with analysis of variance, it is possible to estimate the genetic variance of H (σ^2_H) among cross combinations. Using $\hat{\sigma}^2_H$, we are able to estimate the genetic variance of the degree (σ^2_h) of dominance.

Heterozygotes can be classified into groups, each of which contains individuals which carry the same number of mutant genes per individual in heterozygous condition. In this calculation we exclude heterozygotes carrying less than a mutants. The genetic variance of the degree of chromosomal dominance (σ^2_H) can be expressed as follows:

$$\sigma^2_H = \sigma^2_{H(\text{within groups})} + \sigma^2_{H(\text{among group means})} \quad (4.1)$$

where $\sigma^2_{H(\text{within groups})}$ is the genetic variance of the degree of chromosomal dominance within groups pooled over all groups and $\sigma^2_{H(\text{among group means})}$ is the genetic variance among groups with respect to $\bar{H}$ values within groups. From formula (2), it can be expected to be approximately zero in a large population (in an infinite population $\sigma^2_{H(\text{among group means})}$ is exactly zero). Thus, if $f(i)$ is the frequency of heterozygotes carrying i mutant genes ($\sum_{i=a}^{\infty} f(i) = 1.0$), the following formula can be obtained for a large population:

$$\begin{aligned} \sigma^2_H &\approx \sum_{i=a}^{\infty} \frac{1}{i} \cdot \sigma^2_h \cdot f(i) \\ &= \sigma^2_h \cdot \overline{(1/i)} \end{aligned} \quad (4.2)$$

where $\overline{(1/i)}$ stands for the inverse of the harmonic mean number of mutant polygenes per chromosome pair.

From (4.1), σ^2_h can be expressed as follows:

$$\sigma^2_h \doteq \sigma^2_H \cdot 1/\overline{(1/i)} \quad (4.3)$$

We estimate σ^2_h using formula (4.3).

RESULTS AND ANALYSIS

Heterozygotes showing overdominance were not employed in the present analysis.

Generation 32: The basic statistics and genetic parameters for homozygotes and heterozygotes were reported in Table 4 of MUKAI and YAMAZAKI (1968). The outline is as follows: Since the crosses involving lethal lines and deleterious lines (lines 13, 53, 66, and 76) were not employed, the number of crosses was 63 and the number of lines which were constituents of these crosses was 72. The average viability of the homozygotes was 27.54 and that of the heterozygotes was 28.36. The harmonic mean number of flies counted in a single observation is about 650 for both homozygotes and heterozygotes.

The degrees of chromosome dominance [$H_{ij(k)}$] and their average values within crosses [$H_{ij(\cdot)}$] were estimated. The distribution pattern of $H_{ij(\cdot)}$ is presented in Figure 1. In generation 32, the reduction of homozygote viability

FIGURE 1.—Distribution of the degrees of dominance on the chromosome pair basis.

and heterozygote viability is relatively small. Thus, the error of estimated $H_{ij(k)}$ sometimes becomes extraordinarily large, and the corresponding observation shows a large or small H value which is separated from the other observations of the same cross. This type of abnormal observation could cause biased estimation. For that reason, the observations showing $H_{ij(k)}$ larger than 1.9 or less than -1.1 were not employed in the present analysis. Nine out of 504 observations were disregarded for this reason.

In order to obtain an unbiased estimate of the genetic variance σ^2_h , it is necessary that the viability and the degree of dominance are not correlated. In Figure 1, in the two crosses showing the lowest $H_{ij(\cdot)}$ value, the viability of one of the constituent homozygote lines showed viability index higher than 30.0. Since there might be a correlation between the viability of the heterozygotes or constituent homozygotes and the H value, the following two correlation coefficients were calculated using the data of generations 32 and 52: (1) The correlation coefficient between the homozygous viability of the more viable homozygote with chromosomal dominance [$H_{ij(\cdot)}$] in the corresponding heterozygote and (2) the correlation coefficient between the average viability of two homozygotes and the degree of chromosomal dominance in the corresponding heterozygotes [$H_{ij(\cdot)}$]. The results are presented in Table 1. The pooled estimates are -0.30 (the former) and -0.07 (the latter). The former figure is highly significant, implying that the

TABLE 1

Correlation coefficients between viability and degree of chromosomal dominance

Correlation coefficient between	All crosses			Excluding exceptional crosses		
	G32 RS (63)	RS (56)	G52 RA (53)	G32 RS (59)	RS (51)	G52 RA (48)
Homozygous viability of the more viable chromosome in a heterozygote and the degree of dominance ($H_{ij(.)}$)	-0.19	-0.43**	-0.27*	0.04	-0.02	-0.10
	[-0.30***]			[-0.02]		
Average homozygous viability of two homologous chromosomes in a heterozygote and the degree of dominance ($H_{ij(.)}$)	0.17	-0.12	-0.15	0.17	0.11	0.11
	[-0.07]			[0.11]		

RS—stands for heterozygotes between two successively numbered lines.

RA—stands for heterozygotes between two alternately numbered lines.

The figures in parentheses indicate the numbers of crosses.

The figures in brackets indicate the pooled correlation coefficients.

* significant at the 5% level.

** Significant at the 1% level.

*** Highly significant.

degree of dominance is small when the homozygous viability of the more viable chromosome in a cross is large. Thus, we excluded any heterozygotes carrying the chromosome (homozygously more viable than its homologue) which, in the homozygous condition, showed a viability index greater than 31.78 in generation 32 and 29.88 in generation 52. The numbers of excluded crosses are 4 in generation 32, and 5 in the RS and RA experiments, respectively, in generation 52. The correlation coefficients mentioned above were again calculated, and are presented in Table 1. None of the correlation coefficients is significantly different from zero. Thus, the analyses used 59 crosses in the RS of generation 32, 51 and 48 in the RS and RA, respectively, of generation 52.

An analysis of variance was conducted for the data in generation 32 (Table 2).

TABLE 2

Analysis of variance of degree of chromosomal dominance for mutant viability polygenes in generation 32

Source of variation	df	Mean square	F	Expected mean square
Between crosses	58	0.14401	1.38*	$\sigma_e^2 + 7.86 \sigma_H^2$
Error	405	0.10444		σ_e^2
Total	463			

σ_e^2 stands for the error variance.

$\hat{\sigma}_H^2 = 0.00504 \pm 0.00350$.

* Significant at the 5% level.

It can be seen from the table that there is a significant difference among crosses with respect to the degree of chromosome dominance (H). ($P < 0.05$.) The estimated genetic variance of the degree of chromosome dominance (σ_H^2) is 0.00504 ± 0.00350 . In the next section this estimate will be converted to one for an individual locus. The grand mean degree of dominance is 0.47.

Generation 52: The basic statistics and genetic parameters were also described in Table 4 of MUKAI and YAMAZAKI (1968). In the present analysis, special attention was given to avoiding lines carrying lethal, semilethal, or deleterious genes. The criterion for deleterious genes in the present analysis is: If viability decreases more than 16.6 ($\frac{1}{2} \times 33.3\%$) in a homozygote by *a single mutation*, the gene is defined as deleterious (see MUKAI 1969a). There were three suspicious lines, but additional information indicated that these lines did not carry major genic semilethal mutations. Indeed, a mutation which would be semilethal when made homozygous on an otherwise normal chromosome (viability index about 33.3), would probably be lethal if several additional polygenic, viability mutations were present in homozygous condition, because of synergistic interaction (MUKAI 1969b). In describing statistics and genetic parameters on generation 52 RS and RA, the figures in parentheses correspond to those of RA. Fifty-six (53) crosses with 67 (64) constituent chromosome lines were first employed in the RS (RA) experiment. The average viability of the homozygotes was 19.97 (19.91) and that of the heterozygotes was 22.49 (23.51). The harmonic mean number of flies counted in a single observation is approximately 630 (630) in homozygotes and 680 (555) in heterozygotes. The control viability (v_0) was estimated as 33.12 (33.12). The distributions of $H_{ij(\cdot)}$ in the RS and RA experiments are pooled and graphically presented in Figure 1.

The grand mean of the degree of chromosomal dominance ($H_{\cdot(\cdot)}$) is 0.45 ± 0.012 in RS and 0.38 ± 0.012 in RA. These two values are significantly different from each other. Possibly, there are biological reasons for this significant difference. The grand mean values together with the estimate in generation 32 are

TABLE 3

Analysis of variance of degree of chromosomal dominance for mutant viability polygenes in generation 52

Source of variation	df	Mean square	F	Expected mean square
(a) The RS Experiment				
Between crosses	50	0.04315	1.70**	$\sigma_e^2 + 6 \sigma_H^2$
Error	255	0.02540		σ_e^2
Total	305			
(b) The RA Experiment				
Between crosses	47	0.04236	1.81*	$\sigma_e^2 + 6 \sigma_H^2$
Error	240	0.02334		σ_e^2
Total	287			

$\sigma_H^2 = 0.00296 \pm 0.00149$ (RS), 0.00317 ± 0.00150 (RA).

** Significant at the 1% level.

closer to each other than are the estimated degrees of dominance of lethal genes and polygenes. The analyses of variance were conducted independently for both the RS and RA crosses (Table 3). The estimated genetic variances of the degree of chromosome dominance ($\hat{\sigma}_H^2$) are 0.00296 ± 0.00149 in RS and 0.00317 ± 0.00150 in RA experiment. These two values are very close to each other.

Estimation of the overall mean value and the genetic variance of the degree of dominance: The overall means of the degree of dominance were estimated to be 0.47 (gen. 32), 0.45 (RS in gen. 52) and 0.38 (RA in gen. 52) and weighted by the inverses of their estimated variances. The resulting overall mean value is 0.43 ± 0.008 .

The genetic variance of the degree of chromosome dominance was estimated as described above to be 0.00504 in generation 32, 0.00296 in RS of generation 52 and 0.00317 in the RA experiment of generation 52. Since these estimates are on the basis of the average degree of dominance of mutant polygenes located in single chromosomal heterozygotes, these values should be approximately inversely proportional to the number of generations. The above estimates satisfy this requirement.

A spontaneous mutation rate of viability polygenes was estimated by MUKAI (1964) to be 0.1411 / second chromosome / generation. Based upon this estimate, it is possible to calculate the average number of polygenes per second chromosome in generations 32 and 52, including the chromosomes which do not carry any mutant viability polygene. The results are 4.52 in generation 32 and 7.34 in generation 52. Assuming that the numbers of mutant genes in heterozygotes (both homologous chromosomes) are distributed according to a Poisson distribution with means $4.52 \times 2 = 9.04$ in generation 32 and $7.34 \times 2 = 14.68$ in generation 52, the harmonic means of the number of heterozygous loci per heterozygous individual *employed for the final analysis* were calculated to be 8.53 for generation 32, and 14.56 for generation 52. Using formula (4.3), σ_h^2 can be estimated from $\hat{\sigma}_H^2$ and from the harmonic means obtained above. The results are 0.043 ± 0.030 in RS of generation 32, 0.043 ± 0.022 in RS of generation 52, and 0.046 ± 0.022 in the RA of generation 52. These estimates are remarkably close to each other. The mean variance, which is obtained by weighing each estimate by the inverse of its variance, was calculated to be 0.044 ± 0.014 —a markedly large value! All the above figures are presented in Table 4.

The variance of the selection coefficients against heterozygotes (σ_{sh}^2) can be calculated by using the following formula (GOODMAN 1960), assuming that *s* and *h* are not correlated.

$$\sigma_{sh}^2 = \sigma_s^2 [E(h)]^2 + \sigma_h^2 [E(s)]^2 - \sigma_s^2 \cdot \sigma_h^2 \quad (5)$$

where σ_s^2 is the variance of the selection coefficients against homozygotes (locus basis); $E(s)$ is the expected value of the selection coefficient, and $E(h)$ is the expected value of the degree of dominance. Having obtained estimates of the parameters in the right-hand side of formula (5) (see Table 8 of MUKAI (1964)), we then used these values to estimate the genetic variance of *sh*: $\hat{\sigma}_h^2 = 0.044$ is

TABLE 4

The degree of dominance of mutant viability polygenes and their variances

	Generation 32 RS	RS	Generation 52 RA
Grand mean of the degree of dominance [$\bar{H}_{..(.)}$]	0.47	0.45	0.38
(Overall mean)	± 0.018	± 0.012	± 0.012
	(	0.43 ± 0.008	)
Genetic variance of the degree of chromosomal dominance [$\hat{\sigma}^2_H$]	0.00504	0.00296	0.00317
	± 0.00350	± 0.00149	± 0.00150
Genetic variance of the degree of dominance [$\hat{\sigma}^2_h$]	0.043	0.043	0.046
	± 0.030	± 0.022	± 0.022
(Overall mean)	(	0.044 ± 0.014	)

Figures in parentheses indicate the means weighted by the inverse of their variances.

a minimum estimate, since this was estimated on the basis of a minimum mutation rate; $\hat{\sigma}_s^2 = 1/(33.3)^2 \cdot 0.1997 = 0.000180$ (a maximum estimate, see MUKAI (1964)); $E(h) = 0.43$ (probably an unbiased estimate), and $E(s) = 0.8937/33.3 = 0.027$ (a maximum estimate, see MUKAI (1964)). On the basis of these estimates, σ_{sh}^2 is estimated to be 0.0000567, a very small value.

Prediction of the average degree of dominance of viability polygenes in an equilibrium population: MORTON, CROW and MULLER (1956) showed that the average degree of dominance in an equilibrium population is approximately equal to the harmonic mean of the degrees of dominance of newly-arising mutants under the classical model. In the present analysis, we have estimated the arithmetic mean and the genetic variance of the degrees of dominance of newly-arising, mutant, viability polygenes. Assuming some distribution, we can estimate the harmonic mean of the degrees of dominance of newly-arising mutants. Since the distribution range is roughly 0 to 1 with an intermediate mean, a bell-shaped distribution, characteristic of many biological phenomena, may be assumed for the h values. First, we assumed a discrete distribution which was constructed on the basis of a normal distribution truncated at $h = 0$ and at its corresponding right-hand tail. The standard deviation of the normal distribution (before truncation) was determined by an iterative method so as to make the variance of the truncated normal distribution 0.044 (estimated value). The result was $\hat{\sigma} = 0.348$. In this truncation, approximately 10.3% was truncated at each tail. The region of h considered was divided into 10 to 100 subregions since the harmonic mean is changed according to the number of subregions in the discrete distribution, and the exactly intermediate value of h in each subregion was employed as the representative. The relative frequency of each subregion was calculated using the normal distribution and the harmonic mean of h values was calculated on the basis of the discrete distribution. The results are 0.235 (for the 10 subregions) to 0.173 (for the 100 subregions). Of course, it is known that if the number of subregions increases greatly, the harmonic mean approaches zero. However, since

this is not realistic, the above discrete distribution with a limited number of sub-regions was used as an approximation.

Secondly, we may assume some continuous distribution with a range of 0 to 1. A Beta distribution may be appropriate. This is completely determined by the mean and variance. The mean, variance, and harmonic mean are related according to the following formulae (KENDALL and STUART 1963):

$$\text{Mean} = \frac{q}{p+q} \quad (6)$$

$$\text{Variance} = \frac{pq}{(p+q+1)(p+q)^2} \quad (7)$$

$$\text{Harmonic mean} = \frac{q-1}{p+q-1} \quad (8)$$

where p and q are positive and real.

In the present analysis, the mean and the genetic variance were estimated to be 0.43 and 0.044, respectively. Equating these values to formulae (6) and (7), it is possible to estimate p and q . The results are: $p = 2.58$ and $q = 1.95$. Indeed, the shape of this beta distribution is very similar to the one constructed above on the basis of a normal distribution, except at the tails. Using formula (8), the harmonic mean of the degrees of dominance of newly-arising mutants was estimated to be 0.27. These estimates are consistent with the other predictions (CROW 1968; MUKAI 1969b) as well as the direct approximate estimates of WILLS (1966).

DISCUSSION

MORTON, CROW and MULLER (1956) first tried to estimate the genetic variance of the degree of dominance of newly-arising (N) lethal genes and to estimate the average degree of dominance in an equilibrium (E) population. In their case, the genetic variance of the degree of dominance of newly-arising, lethal genes appeared to be quite small, just as in the case of the degrees of dominance of lethal genes. In the present experiment, large values of $\bar{h}_N$ and of genetic variance were detected in mutant viability polygenes. This is probably the first time that a large genetic variance of h for newly-arising, mutant, viability polygenes has been reported. A large value of $\bar{h}_N$ could be expected from the works of GREENBERG and CROW (1960), TEMIN (1966), and MUKAI and CROW (in preparation) who showed that there must be a large $\bar{h}_E$ or $\bar{h}_N$ on the basis of the detrimental load to lethal load ratio ($D : L$ ratio). Detailed experimental results indicating a large $\bar{h}_N$ value have been described in MUKAI and YAMAZAKI (1968). WILLS (1966) estimated the average degree of dominance of mildly deleterious genes in probably equilibrium populations to be about 0.20–0.30 by the regression method in *D. pseudoobscura*. These estimates are probably underestimates (since the estimation formula of the regression coefficient contains error variance in the denominator, but not in the numerator), but they are consistent with the values inferred in the present experiment. MUKAI (1969b) estimated the $\bar{h}_E$ value to be 0.1–0.25

using the estimated $D : L$ ratio under the condition of synergistic interaction among mutant polygenes.

The fact that the predicted $\bar{h}_E$ is in good accord with the $\bar{h}_E$ estimated directly from an equilibrium population may indicate that the assumptions under which the genetic variance of h_N was estimated are approximately valid. Especially, a high mutation rate of viability polygenes (about 0.141/second chromosome/generation) may be said to be confirmed. In the process of estimating $\bar{h}_N$ we assumed no overdominance and no epistasis, and while these are not true assumptions, they did not affect the result significantly. This may imply (1), that overdominance is rare in equilibrium populations, although its manifestation is possible (MUKAI and YAMAZAKI 1968; MUKAI 1969a,b) and (2), that epistasis existing in equilibrium populations does not affect the dynamics of the degree of dominance significantly (cf. MUKAI 1969b).

The experimental material employed in the present investigation was extracted from an Erie, Pennsylvania population which would have experienced a long history of natural selection. It might be said from the present studies that the h value of the newly-arising, mutant, viability polygenes is approximately 0.4 on the average and its genetic variance is large. Natural selection rapidly eliminates the mutant genes whose h values are large and the mutant genes carrying small h values have been maintained for many generations. This process might have been repeated in natural populations. Assuming that mutation is a recurrent phenomenon and that h_N was approximately 0.5 at a primitive stage of the organism, we have little evidence of evolution of dominance in the repulsion phase. Indeed, it is difficult to understand how h evolved in two opposing directions (Figure 1). It is necessary to accumulate more data for the case of the coupling phase. Unfortunately, it is difficult to apply the present method for estimating the genetic variance of the degree of dominance to the coupling phase, since the h values change with the homozygous viability of one of the homologous chromosomes (MUKAI and YAMAZAKI 1968).

Finally, it might be necessary to note that the artifact due to the choice of a viability index which might not be appropriate is not disturbing. Viability may be expressed in two ways, i.e., the ratio of the wild-type flies either to the total or to the phenotypically *Cy* flies. The appropriate conditions for using these indices have already been discussed by MUKAI (1964, 1969b). For the sake of comparison, the $\bar{H}_{\dots(i)}$ and σ_h^2 were estimated on the basis of the latter index. The results are $\bar{H}_{\dots(i)} = 0.43 \pm 0.007$ and $\hat{\sigma}_h^2 = 0.034 \pm 0.011$. The former is almost exactly the same as the $\bar{H}_{\dots(i)}$ inferred in this experiment. The latter is slightly smaller. In addition the estimated H values of repulsion heterozygotes ($+i/+j$) are biased if, under the present method for estimating viability, the *Cy* chromosomes are not completely dominant over the homologous chromosomes. However, numerical examinations show that, if the H values in *Cy* heterozygotes are not large, the amount of bias is very small, especially when the true H is close to 0.5. Indeed, assuming that the selection coefficients against homozygotes of chromosomes carrying mutant polygenes are 0.2 ($+i/+i$) and 0.3 ($+j/+j$), that

the H values in the Cy heterozygotes are 0.1, 0.2, 0.3, 0.4, and 0.5, and that the true H value in repulsion heterozygotes is 0.5, then the estimated H values are 0.499, 0.499, 0.498, 0.498, 0.497, respectively. It is speculated on the basis of the data presented in MUKAI, CHIGUSA and YOSHIKAWA (1965) that the H values in Cy heterozygotes are, at most, of the order of h for lethal mutations. Thus, the effect of the degree of dominance of Cy chromosomes on the mean and the variance of estimated H values is not significant.

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SUMMARY

Spontaneous mutant polygenes controlling viability have been accumulated with minimal selection against them in 104 second chromosome lines which originated from a single, probably well-adapted, normal second chromosome. In generations 32 and 52, the heterozygous effects, as well as the homozygous effects of these newly-arising, mutant polygenes were examined in the repulsion phase. On the basis of observations consisting of 3952 vials (about 1.3 million flies), the average degree of dominance ($\bar{h}$ in WRIGHT's fitness model) and the genetic variance of the degree of dominance (σ_h^2) were estimated as $\bar{h} = 0.43 \pm 0.008$ and $\sigma_h^2 = 0.044 \pm 0.014$. The average degree of dominance in an equilibrium random-mating population was estimated using MORTON, CROW and MULLER's equation (1956), under the assumption of a discrete distribution constructed from a truncated normal distribution (about 10.3% of each tail was discarded) and from a Beta distribution with respect to the degrees of dominance of newly-arising, mutant, viability polygenes. The results are 0.24–0.17 and 0.27, respectively. These estimates are consistent with direct estimates in equilibrium populations. The implication of these findings in the evolution of dominance of viability polygenes is discussed.

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