COMPETITION INVOLVING DOMINANT MUTANTS IN EXPERIMENTAL POPULATIONS OF *DROSOPHILA MELANOGASTER*¹

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EARLIER papers (MERRELL 1953a, b; MERRELL and UNDERHILL 1956) explored the effects of competition between sex-linked and autosomal recessives and their wild-type alleles in experimental populations of *Drosophila melanogaster*. FALCONER (1960) has used data from one of these papers (1953b) to show the change in gene frequency under selection of a sex-linked gene, commenting that "there is no well documented case of an autosomal gene." Actually, there were a few cases (e.g. WIEDEMANN 1936; L'HERITIER and TEISSIER 1937; NIKORO and GUSSEV 1938; MERRELL and UNDERHILL 1956) but the comment is still, to a large extent, valid. Relatively little experimental work has been done on the adaptive value of specific genes compared to the amount on polygenic traits. Inasmuch as the pioneering theoretical work of FISHER, HALDANE, and WRIGHT on the genetics of populations dealt initially with effects at single loci, this is rather surprising. Furthermore, the number of known cases of genic polymorphism in natural populations (melanism in moths, blood groups in man, burnsi-kandiyohi polymorphism in leopard frogs, etc.) suggests that further work on the adaptive role of individual genes may be of considerable significance. This report deals with the competitive relationship between autosomal and sex-linked dominant genes and their wild-type alleles.

METHODS

The dominant mutants studied were Lobe-2 (L^2 ; 2-72.0) and a spontaneous Lobe mutant; Beadex-3 (Bx^3 ; 1-59.4); the Bar duplication (B ; 1-57.0); and brown-dominant (bw^D ; 2-104.5), also apparently a duplication. Because of its phenotypic resemblance to bw^D , the recessive brown allele (bw) was also used. Of these genes, only bw^D was completely dominant to the wild type, so that $bw^D/+$ is indistinguishable from bw^D/bw^D (and bw/bw). The other dominants were partial dominants, with the heterozygotes less extreme in expression than the homozygous dominant type.

The procedures were similar to those of MERRELL and UNDERHILL (1956). All of the populations and experiments were run in constant light at $21 \pm 1^\circ\text{C}$ and 50% relative humidity. The competition in the population bottles was started by adding a single homozygous wild-type Lausanne Special male to a well established population (200 to 400 adults) homozygous for one of the mutants. The initial gene frequency of the wild type was, at most, about 0.005. This procedure permits study of the course of selection over virtually the entire range of gene frequencies. No effort was made to achieve isogeneity at the other loci. The variability in the populations at the outset was probably not nearly so great as might be found in a wild population,

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however, because of prior inbreeding in the Lausanne Special stock and because the usual methods of maintaining mutant stocks lead to some inbreeding. The experiments lasted so long that isogeneity would have been lost anyway owing to spontaneous mutations. Estimates for mutation rates per chromosome for lethals in *D. melanogaster* are of the order of 0.5% per generation, or more (see DOBZHANSKY, SPASSKY and SPASSKY 1952). With this estimate, it can be calculated that after 30 generations only 85% of the chromosomes would still be free of lethals. If the rate included semilethals, subvitals, etc., the proportion of chromosomes untouched by spontaneous mutation would be still further reduced.

SUSMAN and CARSON (1958) introduced only a single haploid set of wild-type autosomes into their populations. However, these autosomes, as they increase in frequency, can not be expected to remain identical in genic content in view of the known mutation rates and the possibility of recombination between the + and sesro chromosomes. Therefore, their procedure is not too different from that reported here. However, if the single introduced wild-type chromosome happens to carry deleterious genes, the results could be considerably modified.

One set of populations was established in which three alleles were placed in competition with one another, bw^D , bw , and bw^+ . In three of these populations the initial frequencies were $bw^D = 0.25$, $bw = 0.50$, and $bw^+ = 0.25$. In three other populations the initial frequencies were $bw^D = 0.50$, $bw = 0.25$, and $bw^+ = 0.25$.

Since the dominance relations are $bw^D > bw^+ > bw$ with each allele completely dominant to the ones below it, bw^D/bw^D , $bw^D/+$, bw^D/bw and bw/bw are phenotypically indistinguishable. The gene frequencies were obtained by determining the genotypes of a random sample of 50 males from each population at each count. The brown males ($bw^?/?$) were individually crossed to virgin wild-type females. The expected results were:

$$\begin{array}{lcl} +/+ \text{ } \text{f} \times bw^D/bw^D \text{ } \text{m} & \text{All brown} \\ +/+ \text{ } \text{f} \times bw^D/+ \text{ } \text{m} & \text{ } \\ +/+ \text{ } \text{f} \times bw^D/bw \text{ } \text{m} & \left. \begin{array}{l} \\ \end{array} \right\} 50\% \text{ brown} : 50\% + \\ +/+ \text{ } \text{f} \times bw/bw \text{ } \text{m} & \text{All } + \end{array}$$

Thus with this test it was not possible to distinguish $bw^D/+$ males from bw^D/bw males. Hence for the males found to be $bw^D/?$, half of the unknown alleles were arbitrarily assigned to + and the other half to bw . Since bw^D declined rapidly in frequency, the bias introduced in this way was relatively minor, was confined primarily to the earlier estimates, and probably led to an overestimate in the frequency of bw .

The wild-type males from the populations were crossed to bw/bw females with the following results expected:

$$\begin{array}{lcl} +/+ \text{ } \text{m} & \longrightarrow & \text{All } + \\ +/bw \text{ } \text{m} & \longrightarrow & 50\% \text{ brown} : 50\% + \end{array}$$

From these crosses, therefore, estimates of the frequencies of the three alleles in the populations could be made.

The population experiments showed the dominant genes to be deleterious and to be rapidly eliminated in the populations. When only wild-type flies were found in a population for several counts (usually three), that population was then discarded. In Bx^3 populations 6 and 8, and in all populations with bw , the experimental populations were discontinued before the mutants had been completely eliminated.

In an effort to gain information about the various components of fitness, four traits were tested: rate of development, viability, longevity, and mating success. For these tests flies were taken from the populations and cultured separately. Then from these cultures, typically, three crosses of ten virgin females heterozygous for a dominant mutant were made to ten wild-type males in half pint bottles. In order to estimate relative viabilities and rates of development, the progeny from these crosses were counted from the 15th to the 27th day. These progeny, after being counted, were then used in the experiments on mating success and longevity. In each separate test comparing mutant and wild-type flies, the flies used were the progeny of the same set of parents and were reared in the same culture bottle. In this way, the possible effects of environ-

mental heterogeneity or of heterogeneity for genes other than those under study were minimized. However, no further effort was made to achieve isogeneity for the residual genotype.

Previous work (MERRELL 1949) has shown that males of *D. melanogaster* placed with two types of females (male "choice") tend to mate at random whereas females placed with two kinds of males (female "choice") frequently do not mate at random. For this reason, except with Bar, only female "choice" mating experiments were conducted. The procedure was to place ten females of a given type in a creamer with ten males of each of two types for 48 hours. Each female was then placed in a separate creamer and her progeny scored to determine the genotype of the male parent. For the male "choice" tests with Bar, ten males of one type were placed with ten females of each of two types for 48 hours.

Tests of longevity were made by putting groups of 50 flies into half pint bottles and transferring them without etherization to fresh food bottles approximately once a week. The number of dead flies was counted at each transfer. 50 males and 50 females of each genotype were tested separately. The longevity of heterozygous or hemizygous dominant mutant flies was compared with that of wild-type males and females. For *bw*, the longevity of *bw/bw* flies was compared with that of *+ / bw*. Flies heterozygous for the dominant mutants rather than the homozygous dominant types were used in the tests on longevity and mating success because the critical competition between the mutant and wild-type alleles seemed most likely to involve the heterozygous dominant genotype versus the homozygous wild type.

RESULTS

Table 1 shows that in 56 of 92 populations the wild type became the predominant phenotype; in all but a few cases more than 90% wild type was reached. These results give a striking demonstration of the adaptive superiority of the wild type over these mutants despite the fact that all are considered to have excellent viability (BRIDGES and BREHME 1944), except perhaps *gl*. The spontaneous *L* mutant is unranked but appeared to have good viability.

Table 2 and Figures 1 to 6 show the changes in gene frequency for the various mutants. For *B*, *Bx*³, *L*, and *L*² gene frequencies were calculated directly from the samples since all genotypes had recognizably different phenotypes. For *bw*^D and

TABLE 1

Establishment of wild-type alleles in mutant populations. The initial gene frequency of + alleles is estimated as less than 0.005

Mutant	Number of populations	Number with + predominant
<i>B</i>	10	6
<i>Bx</i> ³	10	6
<i>L</i>	9	6
<i>L</i> ²	5	5
<i>bw</i> ^D	9	1
<i>bw</i>	10	5
<i>vg</i> *	10	10
<i>gl</i> *	10	9
<i>ras</i> ² *	10	5
<i>γ</i> *	9	3
	92	56

* MERRELL and UNDERHILL (1956).

TABLE 2—Continued
Competition between mutant and wild-type alleles

Genes	Day	Population							
		1	5	6	8	9	10		
<i>L</i> and <i>L</i> ⁺	0	200+	200+	200+	200+	200+	200+	200+	(99.5+)
	22	76 (97.4)	22 (90.9)	38 (98.7)	20 (100.0)	36 (100.0)	37 (100.0)	37 (100.0)	
	58	14 (92.8)	57 (86.0)	14 (89.3)	..	36 (76.4)	33 (100.0)	33 (100.0)	
	87	20 (52.5)	70 (46.4)	41 (57.3)	..	80 (41.9)	21 (100.0)	21 (100.0)	
	119	57 (36.0)	46 (35.9)	51 (39.2)	..	52 (40.4)	12 (95.8)	12 (95.8)	
	143	50 (26.0)	41 (18.3)	100 (28.0)	38 (100.0)	87 (30.5)	21 (78.6)	21 (78.6)	
	176	6 (41.7)	22 (20.4)	13 (15.4)	128 (60.4)	40 (20.0)	83 (36.1)	83 (36.1)	
	207	37 (14.9)	..	35 (15.7)	45 (24.4)	37 (18.9)	24 (12.5)	24 (12.5)	
	244	82 (20.1)	42 (14.3)	25 (10.0)	15 (6.7)	65 (2.3)	114 (6.6)	114 (6.6)	
	275	19 (15.8)	29 (19.0)	32 (15.6)	32 (9.4)	41 (2.4)	101 (4.5)	101 (4.5)	
	334	45 (25.6)	34 (13.2)	29 (11.3)	48 (2.1)	62 (0.0)	57 (7.9)	57 (7.9)	
	371	15 (23.3)	27 (7.4)	41 (7.3)	17 (0.0)	41 (0.0)	54 (2.8)	54 (2.8)	
	400	35 (10.0)	95 (6.8)	42 (6.0)	53 (0.0)	61 (0.0)	91 (3.8)	91 (3.8)	
	480	63 (0.0)	86 (2.9)	64 (1.6)	30 (0.0)	91 (0.0)	199 (4.0)	199 (4.0)	
	522	10 (0.0)	46 (2.2)	31 (0.0)	30 (0.0)	80 (0.0)	89 (4.2)	89 (4.2)	
	570	..	177 (0.0)	..	..	72 (0.0)	216 (0.9)	216 (0.9)	
	618	..	65 (0.0)	..	..	..	122 (0.6)	122 (0.6)	
	730	..	84 (0.0)	..	..	..	103 (2.4)	103 (2.4)	
	884	..	..	..	..	..	188 (0.0)	188 (0.0)	
	1033	..	..	..	..	..	138 (0.0)	138 (0.0)	
<i>L</i> ² and <i>L</i> ⁺	0	200+	200+	200+	200+	200+	200+	200+	(99.5+)
	35	113 (91.6)	100 (95.5)	96 (98.4)	45 (98.9)	62 (91.9)	62 (91.9)	62 (91.9)	
	58	53 (60.4)	41 (56.1)	19 (71.0)	48 (71.9)	51 (53.9)	51 (53.9)	51 (53.9)	
	79	156 (30.3)	95 (53.7)	61 (69.7)	142 (54.9)	116 (50.0)	116 (50.0)	116 (50.0)	
	102	60 (37.5)	52 (52.3)	46 (53.3)	70 (42.8)	56 (42.0)	56 (42.0)	56 (42.0)	
	125	80 (29.4)	103 (36.9)	122 (41.0)	120 (34.2)	89 (33.1)	89 (33.1)	89 (33.1)	
	160	34 (14.7)	52 (23.1)	34 (36.8)	51 (20.6)	46 (23.9)	46 (23.9)	46 (23.9)	
	192	64 (31.2)	63 (21.4)	27 (18.5)	73 (19.2)	69 (21.0)	69 (21.0)	69 (21.0)	
	230	42 (21.4)	72 (16.0)	54 (13.9)	100 (7.0)	57 (9.6)	57 (9.6)	57 (9.6)	
	261	38 (6.6)	35 (18.6)	6 (0.0)	53 (15.1)	57 (10.5)	57 (10.5)	57 (10.5)	
	317	91 (1.1)	44 (15.9)	..	53 (4.7)	64 (1.6)	64 (1.6)	64 (1.6)	
	390	71 (0.0)	66 (0.0)	..	75 (5.3)	68 (0.0)	68 (0.0)	68 (0.0)	
	420	108 (0.0)	79 (0.0)	..	104 (1.9)	77 (0.0)	77 (0.0)	77 (0.0)	
	456	56 (0.0)	48 (0.0)	..	137 (1.9)	10 (0.0)	10 (0.0)	10 (0.0)	
	496	108 (0.0)	111 (0.0)	..	173 (0.0)	56 (0.0)	56 (0.0)	56 (0.0)	
	546	..	..	..	43 (0.0)	..	..	..	
	594	..	..	..	..	..	..	..	

TABLE 2—Continued
Competition between mutant and wild-type alleles

B. The size of each sample is followed by the percentage of phenotypically brown flies in parentheses

Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population
<i>bw^D</i> and <i>bw⁺</i>	0	200+ (99.5+)	<i>bw</i> and <i>bw⁺</i>	0	200+ (99.5+)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (99.5+)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (99.5+)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (99.5+)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (99.5+)
	36	148 (100.0)		36	143 (99.3)		36	102 (97.0)		36	109 (97.0)		36	142 (100.0)		36	105 (96.2)
	65	44 (100.0)		65	66 (83.3)		65	61 (80.3)		65	92 (85.9)		65	113 (100.0)		65	62 (45.2)
	88	57 (100.0)		88	72 (90.0)		88	76 (95.0)		88	64 (64.1)		88	50 (100.0)		88	78 (37.2)
	112	45 (91.2)		112	49 (49.0)		112	54 (55.6)		112	55 (41.8)		112	65 (98.5)		112	66 (31.8)
	138	85 (89.4)		137	120 (27.5)		137	102 (26.5)		137	107 (45.8)		137	153 (86.3)		137	142 (31.0)
	178	53 (34.0)		165	27 (25.9)		165	44 (9.1)		165	19 (10.5)		165	37 (54.0)		165	31 (12.9)
	221	41 (56.1)		196	47 (8.5)		196	56 (7.1)		196	53 (41.5)		196	47 (55.3)		196	54 (18.5)
	258	91 (20.9)		263	152 (17.8)		263	56 (3.6)		263	132 (31.8)		263	47 (42.5)		263	...
	319	50 (12.0)		321	90 (15.6)		321	127 (4.7)		321	119 (22.7)		321	86 (16.3)		321	...
	384	57 (5.3)		354	88 (4.5)		354	103 (13.6)		354	119 (6.7)		354	54 (11.1)		354	...
	464	128 (0.0)		397	43 (11.6)		397	112 (6.2)		397	253 (6.3)		397	39 (2.6)		397	...
	554	106 (0.0)		477	27 (0.0)		477	111 (15.3)		477	...		477	...		477	...
	602	90 (0.0)		518	22 (9.1)		518	93 (11.7)		518	...		518	...		518	...
	...	...		567	166 (36.7)		567	199 (5.0)		567	...		567	...		567	...
	...	...		615	48 (33.3)		615	89 (3.7)		615	...		615	...		615	...
	...	...		728	...		728	41 (0.0)		728	...		728	...		728	...

Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population
<i>bw^D</i> , <i>bw⁺</i> and <i>bw</i>	0	200+ (50.0)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (50.0)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (50.0)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (50.0)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (50.0)	<i>bw^D</i> and <i>bw⁺</i>	0	200+ (50.0)
	30	198 (68.7)		30	154 (53.0)		30	217 (80.2)		30	201 (65.7)		30	115 (73.9)		30	124 (60.5)
	67	131 (51.9)		67	115 (53.0)		67	141 (61.0)		67	99 (33.3)		67	139 (70.5)		67	108 (33.3)
	119	129 (33.3)		119	164 (27.4)		119	129 (42.6)		119	135 (24.4)		119	98 (50.0)		119	117 (51.3)
	147	118 (46.6)		137	137 (22.6)		137	129 (29.4)		137	77 (19.5)		137	105 (36.2)		137	134 (40.3)
	177	79 (31.6)		117	79 (31.6)		117	119 (19.3)		117	92 (8.7)		117	81 (16.0)		117	47 (34.0)
	224	100 (36.0)		83	83 (12.0)		83	109 (11.0)		83	117 (7.7)		83	131 (9.2)		83	146 (17.1)
	336	160 (17.5)		270	270 (11.8)		270	362 (2.5)		270	281 (2.1)		270	315 (10.8)		270	346 (17.0)
	365	142 (6.3)		158	158 (4.3)		158	157 (2.5)		158	183 (3.8)		158	178 (6.7)		158	188 (12.8)
	373	263 (5.3)		664	664 (9.6)		664	599 (2.3)		664	556 (2.2)		664	477 (9.2)		664	473 (8.0)

C. Gene frequency estimates from male tests.

Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population	Genes	Day	Population
<i>bw^D</i> , <i>bw⁺</i> and <i>bw</i>	0	25.0	<i>bw^D</i> and <i>bw⁺</i>	0	25.0	<i>bw^D</i> and <i>bw⁺</i>	0	25.0	<i>bw^D</i> and <i>bw⁺</i>	0	25.0	<i>bw^D</i> and <i>bw⁺</i>	0	25.0	<i>bw^D</i> and <i>bw⁺</i>	0	25.0
	30	28.3		30	26.1		30	24.3		30	20.7		30	31.2		30	28.0
	73	2.8		73	37.5		73	16.2		73	39.2		73	23.2		73	13.2
	230	...		230	37.2		230	...		230	60.0		230	74.2		230	7.4
	366	...		366	77.6		366	...		366	79.4		366	75.6		366	1.4

FIGURE 1.—(Top) Competition between Bar and wild type. Gene frequency of Bar plotted against time in days. Numbers indicate the different populations. Dark line shows the expected change when $s_m = 0.9$.

FIGURE 2.—(Middle) Competition between Beadex-3 and wild type.

FIGURE 3.—(Bottom) Competition between Lobe and wild type.

FIGURE 4.—(Top) Competition between Lobe-2 and wild type.

FIGURE 5.—(Middle) Competition between brown-Dominant and wild type. Comparison between gene frequency and phenotype frequency for autosomal complete dominant.

FIGURE 6.—(Bottom) Competition between brown and wild type.

FIGURE 7.—Theoretical changes in gene frequency under selection (s assumed equal to 0.9). Curves numbered according to corresponding equations in text.

- (2) Selection against homozygotes and intermediate heterozygotes (autosomal). (For comparison with L and L^2 .)
- (3) Selection against sex-linked genes with intermediate effects in females. (For comparison with B and Bx^3 .)
- (4) Selection against an autosomal dominant. (For comparison with bw^D .)
- (5) Selection against an autosomal recessive. (For comparison with bw .)

bw populations gene frequencies were estimated from the frequency of the homozygous recessives: $(+/+)^{1/2}$ in the bw^D population and $(bw/bw)^{1/2}$ in the bw populations.

Theoretical curves have been plotted in Figure 7 for purposes of comparison with the data and with each other. The curves are numbered according to the equations given below. For sex-linked genes such as B and Bx^3 , selection is equivalent to gametic selection in the males and zygotic selection in the females.

For gametic selection against a deleterious gene whose frequency is p :

$$(1) \quad \Delta p = -spq/(1-sp)$$

Both $B/+$ and $Bx^3/+$ females are intermediate in appearance to the two homozygous types. The appropriate zygotic selection equation for the females would therefore seem to be (with p the frequency of the harmful allele):

$$(2) \quad \Delta p = -spq/[2(1-sp)]$$

When the sexes are equal in number, one third of the sex-linked genes is carried by the males and two thirds by the females. The combination of (1) and (2) then gives the appropriate selection equation for B and Bx^3 :

$$\Delta p = \frac{1}{3}[-s_m pq/(1-sp)] + \frac{2}{3}[-s_f pq/2(1-sp)]$$

where s_m = selection coefficient in males and s_f = selection coefficient in females. This equation simplifies to:

$$(3) \quad \Delta p = [(s_m + s_f)/3] [-pq/(1-sp)]$$

The similarity in form of equations 1, 2, and 3 is worth noting.

Since L and L^2 heterozygotes are intermediate in expression to the two homozygotes, equation (2) seems appropriate for these mutants.

The bw^D mutant was the only dominant that acted as a complete dominant to the wild type. For such unfavorable autosomal dominant genes (of frequency p):

$$(4) \quad \Delta p = -spq^2/[1 - s(1 - q^2)]$$

For unfavorable autosomal recessive genes such as bw

$$(5) \quad \Delta q = -spq^2/(1 - sq^2)$$

where q is the frequency of the recessive.

The selection coefficient for each theoretical curve in Figure 7 has quite arbitrarily been assumed to be 0.9 and the generation length 20 days. If generation length in the populations were also 20 days, the curves would be directly comparable. This duration seems reasonable for the existing conditions, but no data are available to support the assumption (however, see MERRELL, 1953b and BARKER 1962).

Curves 2, 3, and 5 in Figure 7 are very similar in the early generations but very different from 4. In other words, selection against sex-linked and autosomal genes without dominance and against deleterious autosomal recessives can be expected to be relatively effective at high frequencies of the harmful gene. This expectation is borne out by the results with B , Bx^3 , L , L^2 , and bw shown in Figures 1, 2, 3, 4, and 6. The assumed value of 0.9 for s is obviously too high, for the actual rate of decline in frequency of the mutants is slower than is shown in the theoretical curves of Figure 7.

On the other hand, selection against a completely dominant deleterious gene is expected to be very slow at high frequencies of the deleterious gene (Curve 4, Figure 7) because so few of the favorable recessives are then exposed to selection. However, once the recessive starts to be expressed in homozygotes, its frequency increases very rapidly. The results with bw^D (Figure 5) conform to the expectations based on equation 4. The eight bw^D populations showing no wild-type flies were sampled at monthly intervals over periods of 138, 258, and for the remaining six populations, more than 460 days. Not only were no wild-type flies found, but direct tests by crosses of 123 bw^D flies from six of the populations to $+/+$ flies failed to reveal any $bw^D/+$ heterozygotes. Therefore, it seems reasonable to assume that the wild type had not become established in these populations even at a low frequency.

The rapid elimination of bw^D in one population indicates that it, like the other dominants, is definitely adaptively inferior to the wild type. The failure of the wild-type allele to become established in the other bw^D populations must then have been due to the fact that it was completely recessive to bw^D , had very little chance to be expressed in the homozygous condition where selection could favor it, and hence suffered random loss.

The wild-type alleles had a better chance of becoming established in the populations when they were not completely recessive. Chance loss of the wild type at low frequencies did occur in the other populations, but the probability of extinction was greatest when the wild type was completely recessive. With the dominants other than bw^D the wild type was partially expressed and subject to favorable selection in heterozygotes as well as homozygotes.

FIGURE 8.—(Top) Comparison between gene frequency and phenotype frequency for autosomal recessive (*bw*).

FIGURE 9.—(Bottom) Comparison between gene frequency and phenotype frequency for autosomal incomplete dominant (*Lobe*).

The rate of elimination for all of the dominant genes was more rapid than for the recessive *bw*, as expected from Figure 7. However, in Figures 5, 8, and 9, illustrative comparisons are shown between the change in gene frequency and the change in phenotype frequency. Figure 5 represents the single *bw^D* (complete dominant) population and Figures 8 and 9 the totals for the *bw* (recessive) and *L* (incomplete dominant) populations in which the + allele became established. It can readily be seen that the phenotypic selection curves are quite similar in form.

The genic selection curves for the dominants differed from that for the deleterious *bw* recessive (and also from *vg* and *gl* [MERRELL and UNDERHILL 1956]). The general trend is clearly downward for these autosomal recessives, but they lingered on in the populations at reduced frequencies. On the other hand, selection against the dominants continued to be effective at low gene frequencies, in

most cases leading rather quickly to the complete elimination of the deleterious dominant mutant.

As in the case of the sex-linked and autosomal recessives, selection against sex-linked and autosomal dominants appeared to be most effective at intermediate gene frequencies. However, B (Figure 1) showed the usual sigmoid-type curve, but Bx^3 (Figure 2) had an initial rapid drop in gene frequency followed by a more gradual decline. It seems possible that the selection pressure against the Bx^3/Bx^3 females was considerably greater than that against the less extreme Bx^3 males or $Bx^3/+$ females. The increase in frequency of the wild-type gene reduced the frequency of the homozygous Bx^3/Bx^3 females quite rapidly so that the selection pressure against the Bx^3 gene may actually have lessened as it became less frequent in the populations.

Figures 10 and 11 and Table 2 give the results of competition among three alleles, bw^D , bw , and bw^+ . In all six populations, bw^D was virtually eliminated in a year, bw^+ increased from 25% to between 70% and 80% in frequency, and

FIGURE 10.—(Top) Competition among three alleles: brown-Dominant, brown, and wild type.
FIGURE 11.—(Bottom) Phenotypic selection in populations with three alleles: bw^D , bw , bw^+ .

TABLE 3
Viability and longevity tests

Genotype	Males	Females	Relative viability	Day of 50% mortality (interpolated)	
				Males	Females
+	1070	1117	1.000	86	29
<i>B</i> (<i>B</i> /+)	1041	1126	.991	79	29
+	610	644	1.000	43	84
<i>Bx</i> ³ (<i>Bx</i> ³ /+)	608	572	.941	54	82
+/+	428	409	1.000	72	63
<i>L</i> /+	425	410	.998	85	69
+/+	764	788	1.000	70	75
<i>L</i> ² /+	709	687	.899**	60	60
+/+	744	775	1.000	30	35
<i>bw</i> ^D /+	680	676	.893**	32	36
+/ <i>bw</i>	635	704	1.000	37	35
<i>bw</i> / <i>bw</i>	671	592	.943	36	..

** Statistically highly significant.

bw declined somewhat in frequency to the vicinity of 20% to 30%. Despite this frequency of *bw*, the phenotypes in the population, of course, were more than 90% wild type.

The results of the tests for the various components of fitness are given in Tables 3 and 4. Where the mutant had a deleterious effect on viability (Table 3), it appeared to be greater in the females than in the males. When the totals for sexes were combined, only two mutants, *bw*^D and *L*², significantly reduced the viability of the heterozygotes, in each case only about 10%. Even though only two of the differences in viability were significant, in all cases there were more wild-type than mutant flies.

The data on daily emergence revealed no appreciable differences between mutants and wild type in rate of development. No striking differences in longevity were observed (Table 3), and the data suggest that chance environmental factors played a considerable role in mortality in these experiments. In nearly all experiments, a few flies survived beyond 100 days so that the conditions appear to have been very favorable to survival. For both rate of development and longevity, less favorable conditions might have revealed differences between mutant and wild type.

In the female "choice" mating tests (Table 4) the *B*, *L*²/+, and *bw*/*bw* males were significantly less successful in mating than the wild-type males. The *bw*^D/+ and *bw*/*bw* males, though indistinguishable phenotypically, differed significantly in mating success. The *L*²/+ and *L*/+ males also differed, but in this case the *L*² mutant had a more extreme effect.

Since the *B* mutant had the greatest effect on mating success, male "choice" experiments were conducted with this mutant. Either *B* or + males were used with both *B*/*B* and *B*/+ females, the latter, with many more facets, being quite

TABLE 4
Tests of mating success

A. Female "choice"								
Females	Mated		Unmated	Females	Mated		Unmated	Females
	Successful male				Successful male			Successful male
	+	B			+	Bx ³		+/+ L/+
B/B	30	5	8	Bx ³ /Bx ³	16	13	0	L/+
B/+	85	11	8	Bx ³ /+	40	39	0	+/+
+/+	94	7	7	+/+	50	35	1	27 27 2
	209	23	23		106	87	1	58 53 4
M _m [*]		0.11**				0.82		0.91
L ² /+	+/+ L ² /+			+/+ bw ^D /+	24 26	3		+/bw bw/bw
+/+	44 13	0		bw ^D /+	32 26	2		41 30 4
	43 17	0		+/+	56 52	5		94 57 6
M _m [*]		0.34**				0.93		0.61**

B. Male "choice"						
Males	B/+ females		B/B females		Total	
	Mated	Unmated	Mated	Unmated	Mated	Unmated
+	22	6	20	9	42	15
B	10	20	6	19	16	39
	32	26	26	28	58	54
M _f [†] = 0.88						

** Statistically highly significant.
* Male mating ratio (MERRELL 1950).
† Female mating ratio (MERRELL 1950).

different from the B/B females. The males mated at random, but the wild-type males, as might have been expected from the female "choice" tests, inseminated a greater proportion of the females to which they were exposed.

If the components of fitness are independent of one another, the overall fitness equals the product of the separate components. The selection coefficient then equals one minus this product. For example, the *s* for L² was obtained as follows; where M_m = male mating ratio, and W_m and s_m = fitness and selection coefficient in males, based on M_m. M_m = .34 = W_m = 1 - s_m; s_m = .66. s_{mating} = 1/2 s_m = .33. W_{mating} = 1 - .33 = .67. W_{viability} = .9. W = .67 × .9 = .60 = 1 - s; s = .4.

With the information available from the separate tests, the following selection coefficients have been estimated:

Mutant	Selection coefficient	
B	s _m = .9	s _f = 0
Bx ³	s _m = .2	s _f = .2
L	s = .05	
L ²	s = .4	
bw ^D	s = .15	
bw	s = .25	

Calculations with these selection coefficients and the appropriate equation from

those listed above showed that the rate of elimination of the deleterious mutants in the populations was more rapid than could be accounted for by these values of s . The only case in which the expected curve approximated the observed was with B . The difference between expected and observed could be due either to a more drastic deleterious effect by the mutants under the crowded conditions and intense competition in the populations, or to the effect of additional components of fitness not measured in the separate tests.

The expected change in frequency of B based on $s_m = 0.9$ is shown in Figure 1. With the selection coefficients estimated above, however, ten generations of selection (about 200 days) would be expected to reduce the frequency of Bx^3 only to 0.977 (from an initial frequency of 0.995), of L^2 to 0.917 and of bw to 0.926. A comparison of these values and those in Figure 7 with the observed data indicates that the selection coefficients for all of these mutants are somewhat greater than those given above, but somewhat less than 0.9. In other words, in the populations these mutants were acting essentially as semi-lethals.

DISCUSSION

The effects of selection: The genic selection curves involving the autosomal and sex-linked dominants are all rather similar in form (Figures 1 to 5). The decrease in frequency of the mutants was fairly rapid, and usually they were completely eliminated from the populations.

The phenotypic selection curves are rather similar for both dominant and recessive mutations (Figures 5, 8, 9; also MERRELL and UNDERHILL 1956), but the changes in gene frequency are quite different. The deleterious dominants go to extinction, but the rate of decrease for the deleterious autosomal recessives becomes asymptotic as their frequency declines toward zero. The fact that they do not continue rapidly to extinction need not be explained by a change in s with a decrease in q or by the establishment of balanced polymorphism.

In the case of bw , an equilibrium does seem possible. However, in the $bw-bw^+$ populations the frequency of the brown phenotype declined from 100% to 11.3% in 615 days. In the six bw^D-bw^+-bw populations the brown phenotype fell from 50 or 100% to below 10% in a year. Thus, selection clearly favored the wild phenotype as compared to the brown phenotype. Furthermore, the independent tests of fitness suggest that bw/bw individuals were not subjected to nearly as strong selection pressure as were the vg/vg or gl/gl homozygotes. The gene-frequency estimates of bw show rather large fluctuations. These must be due in part, at least, to sampling errors, to errors in estimating q from bw/bw , and possibly to random shifts in gene frequency associated with small population size. The following shows the expected changes in bw frequency due to selection in the range of frequencies found toward the end of the population experiments. The value of s was assumed to be 0.25, as seems reasonable.

q	q^2	Δq
.3	.09	— .016
.2	.04	— .008
.1	.01	— .002

Thus, it is clear that the expected changes in gene frequency due to selection against the *bw* gene are small in comparison with the observed fluctuations in the gene-frequency estimates. The populations would have to be run considerably longer before a decision could be reached as to whether an equilibrium did, in fact, exist or whether the *bw* gene was still gradually going toward extinction. The results at the higher gene frequencies suggest that the latter possibility is somewhat more plausible. The sex-linked recessives *y*, *ct*, *ras*, and *f*, (MERRELL 1953b), where one third of the mutants were exposed to selection each generation, did not behave like the autosomal recessives, but went to, or close to, extinction (see also WIEDEMANN 1936).

Polymorphism and overdominance: Mutants with effects as obvious as those used in these experimental populations are very rarely observed in natural populations. It seems safe to conclude, therefore, that they are selected against under virtually all circumstances in nature. Nevertheless, for a number of recessives balanced polymorphism has been reported in experimental populations (e.g. L'HERITIER and TEISSIER 1937, and KALMUS 1945 for *e*; TEISSIER 1947 for *se*; LUDWIN 1951 for *ras* and *f*; BUZZATI-TRAVERSO 1952 for *lt*; SUSMAN and CARSON 1958 for *ro* and *se*; and FRYDENBERG 1962 for *cn*). The balanced polymorphism in these cases has been attributed to the superiority of the heterozygote over both homozygotes. Superiority of the heterozygote over the homozygous wild type has also been reported for recessive lethals (e.g. MASING 1938, 1939a, b for 2nd-chromosome lethals from wild populations of *D. melanogaster*; MUKAI and BURDICK 1959 for *l(2)55i*; FRYDENBERG 1963 for *Sb^w*; KARPER 1930 for an albina mutant in Sorghum; NABOURS and KINGSLEY 1934 for an autosomal lethal in the grouse locust; and GUSTAFSSON 1946, 1947 for lethals in barley). Although the authors may express some reservations, the tendency in all of the reports cited is to attribute the balanced polymorphism in the populations (or the heterozygote superiority in viability tests) to single-locus heterosis involving the deleterious recessive and its wild-type allele, or, as it is often called, to overdominance at the mutant locus.

In view of the frequency with which balanced polymorphism has been reported in populations with mutant and wild-type alleles in competition, it is perhaps rather surprising that among the 62 such populations on which data are available (Tables 1, 2) none has reached what must unequivocally be regarded as an equilibrium (see also POLIVANOV 1964). Rather, the mutants appear to be replaced by their wild-type alleles at different rates depending on their relative fitness and their dominance relations. Consequently it seems appropriate to raise the question whether the cases of balanced polymorphism cited above are, in fact, balanced, and if so, whether they are actually due to overdominant effects at the mutant locus.

In some cases (e.g. LUDWIN 1951 for *ras* and *f*) the slow rate of elimination of the mutants may give the appearance of an equilibrium. Repetition of the experiments with the same stocks over longer periods of time showed that the mutants were, in reality, gradually being eliminated from the populations (MERRELL 1953b). Similarly, although L'HERITIER and TEISSIER (1937) postulated an equi-

librium, the initial frequency of *e* was 99.9% and the final frequency after 610 days was 14.1%. At that time only about 2% of the flies were homozygous for *e*, and any further decrease in frequency of *e* would take place very slowly (see discussion of *bw* above).

KALMUS (1945) found that heterozygotes for *e* were apparently favored under all conditions and that at low temperatures the frequency of *e* was so high that *e/e* flies must have been favored over *+/+* flies. However, ten generations of inbreeding preceded the establishment of the populations, and each population came originally from a single pair mating (*+/+* ♀ × *e/e* ♂). Under the circumstances it is not surprising to find heterosis, but it is problematical whether it is single-gene heterosis at the *e* locus. If the wild-type chromosomes carried a deleterious gene closely linked to the *e*⁺ locus, a definite possibility (see MERRELL 1963), it might require more than the 14 months the population was run before this balanced system was broken up. FRYDENBERG (1964b) reported that after an initial period of apparent equilibrium, *e* tended to be eliminated in populations run for more than 1000 days (see also DAWOOD and STRICKBERGER 1964; PARSONS 1963).

BUZZATI-TRAVERSO (1952) also obtained an apparent balanced polymorphism for *lt*. He used 16 *lt* and 16 wild-type flies to start one population, which was run only 20 generations. A series of six populations, run for 15 generations with different initial gene frequencies, all reached the same apparent equilibrium point with a mutant frequency of about 0.6, indicating the homozygous mutant to be superior to the homozygous wild type. It would have been of interest to know more about the previous history of the flies used to initiate the populations, and about the outcome after a longer period of time, but apparently no further report has been made. NOZAWA (1958) found that *bw* in competition with wild type increased in frequency to 0.8 or higher, apparently owing to the unusually low viability of the wild-type stock used. Only 58.5% of the eggs from his Oregon wild stock gave rise to adult flies, as compared to 72.8% and 79.7% for the *bw* stocks used.

The importance of the genic content of the wild chromosome is particularly clear in the work of SUSMAN and CARSON (1958) with *se*, *ro*, and *ss*, for they introduced only a single wild third chromosome derived from a wild male. Some information of the effect of this chromosome when homozygous would have been of considerable interest, but was apparently not obtained. The available information about chromosomes taken directly from wild populations (see e.g. DOBZHANSKY and SPASSKY 1954) suggests that it might be expected to carry some deleterious mutants. This argument takes on added force because in several instances what appeared to be single-locus heterosis later diminished or disappeared (MASING 1938, 1939b; HEXTER 1955; PIPKIN 1962). The latter two authors suggested that they were dealing not with single-locus heterosis or overdominance but with "multilocus" heterosis (HEXTER) or "strain" heterosis (PIPKIN) that later broke down owing to recombination. Furthermore, SMATHERS (1961), continuing the work of SUSMAN and CARSON (1958), reached the conclusion that the heterosis observed in connection with *se*, *ss*, and *ro* was not single-locus heterosis, in contrast to the earlier conclusion of SUSMAN and CARSON. Recently, CANNON (1963a,

b) has reported balanced polymorphism with "apl" and "sesro" multiple mutant stocks in experiments similar to CARSON's. The methodology and relatively short duration of the experiments make it possible that this system might still break down if continued for a longer period.

NOVITSKI and DEMPSTER (1958), after analyzing HEXTER's data, state that "the assumption that heterosis is responsible for the increased frequency of the heterozygotes is unwarranted, and that a reduced viability of homozygous classes will equally well explain such data." This may very well be true, but unless there is some absolute standard of viability, to say that there is an excess of heterozygotes or a deficiency of homozygotes is to say the same thing in two different ways. Since the comparisons of viability between different genotypes are always relative, it is not possible to distinguish between these alternative explanations despite their quite different implications. This problem, of course, is the crux of many of the difficulties in the attempts to establish or refute the concept of overdominance.

A very interesting experiment by HOCHMAN (1958) with two wild-type isoalleles revealed that one of the wild alleles was replacing the other with no indication of heterosis in the isoallelic heterozygote. In this experiment, in which the likelihood of single-locus heterosis might be considered greater than in any of the experiments mentioned thus far, none was observed. In a later experiment HOCHMAN (1961) did find balanced polymorphism associated with wild-type isoalleles. However, the equilibrium later broke down so that single-gene heterosis was not a satisfactory explanation, and he suggested that the degree of heterozygosity in the genetic background was an important factor in the origin of the balanced polymorphic system.

FRYDENBERG (1962) reported that in one series of populations, *cn* was rapidly eliminated, but in two other series balanced polymorphism became established. It seems significant that the two wild stocks giving rise to balanced polymorphism had both been inbred. The history of the third stock was not given, but the contrasting results suggest that different degrees of inbreeding and different gene contents of the wild-type chromosomes involved may have been of more significance to the outcome than a simple overdominant effect at the *cn* locus.

The reports on single-gene heterosis for the autosomal lethal *l(2)55i* (MUKAI and BURDICK 1959; SCHNICK, MUKAI, and BURDICK 1960; and MUKAI and BURDICK 1960) illustrate some of the problems involved. In 1959, the equilibrium frequency of lethal heterozygotes was reported to be 0.42 after 16 generations. During subsequent generations the frequency of lethal heterozygotes dropped to about 0.2 (MUKAI and BURDICK 1960). Thus, postulation of an equilibrium seems to have been premature since the lethal was, in fact, slowly being eliminated. The authors (1960) suggested, apparently without direct evidence, that the decline was due to "random spontaneous mutational changes of modifying genes" affecting the lethal heterozygote. This conclusion seems to vitiate their argument for single-gene heterosis.

Furthermore, recombination appears to be another possible explanation for their results. Even though they stated (1959) that their experimental procedure

had eliminated the contributions of the genetic background and of the interaction between the lethal gene and the genetic background, it may not have done so. Although the other chromosomes were made homozygous in the "homozygous" populations, it appears that the lethal-bearing second chromosome might no longer have been isogenic at all other loci with the nonlethal-bearing second chromosome by the time the experiments began. Moreover, in the "heterozygous" populations only one additional type of second chromosome was introduced. Therefore, the comparison was between populations with two types of second chromosomes and populations with three types of second chromosomes. The use of the CMI technique and of single-pair matings in getting flies with which to start both types of populations must have greatly reduced the amount of available variability as compared to wild populations. For this reason recombination could have been slower to take effect.

The work of FRYDENBERG (1963) with Sb^w , lethal in homozygous condition, is similar in many respects to that of MUKAI, BURDICK, and SCHNICK. Unlike their results, however, these populations did not all behave alike. In one series Sb^w was eliminated in three populations and reached an apparent equilibrium in seven. However, they were only run for 18 or fewer generations, and a downward tendency seemed present at the time the experiments were terminated. In the next five populations, run for only 13 generations, Sb^w clearly decreased (from 0.5 to 0.05 to 0.15) although the author postulated an equilibrium. In the last five populations, the frequency increased from 0.025 to about 0.10 and then appeared to be declining again at the 12th and final generation. In all of these experiments the results might have been less equivocal if the populations had been continued for a longer period. Furthermore, each population was started from but a single pair of flies. Thus, the amount of variability was obviously low, and no information was given about the characteristics of the wild-type chromosomes against which Sb^w was matched. A more recent report (FRYDENBERG 1964a) has confirmed that the apparent equilibrium with Sb^w did break down eventually owing to recombination, even though in some cases 60 generations passed before the breakdown occurred.

FRYDENBERG (1963) used the term "functional overdominance" to describe the maintenance of the mutant apparently due to overdominance in fitness. The expression "associative overdominance" is proposed to designate overdominance "due to nonrandomized linkage between the observed pair of allelic units and the entire remainder of genetic alternatives present in the same chromosome pair." "Intrinsic overdominance" is used for single-gene heterosis inherent in the alleles themselves. The results are then interpreted as being due exclusively to associative overdominance, which seems in accord with the facts, and is the same sort of phenomenon observed by HEXTER (1955) and called by him "multilocus heterosis."

The use of the expressions "functional overdominance" and "associative overdominance" to describe the phenomena observed in these populations seems unfortunate. Overdominance, as defined by HULL (1945, 1946, 1952), referred specifically to allelic interaction such that $AA < Aa > aa$, a concept earlier called

superdominance by FISHER (1918) and elaborated by EAST (1936). Although heterozygotes often appear superior to the homozygotes, the evidence available from the *Drosophila* populations discussed above suggests that overdominance in the original sense is not involved. "Multilocus heterosis," "strain heterosis," and "associative overdominance" seem rather to be interpretable in terms of the dominance theory of JONES (1917) and interlocus (epistatic) interactions of the sort observed by POWERS (1944) in tomatoes. Therefore, to call these cases "overdominance" is apt to be misleading with respect to the actual mechanisms involved (see e.g. PARSONS and BODMER 1961). Many of the instances of heterosis in inversion heterozygotes are also probably due to multilocus heterosis even though they too are often referred to as cases of overdominance. In general, the cases reported as single-gene heterosis in laboratory populations of *Drosophila* appear to be due to linkage disequilibrium (LEWONTIN and KOJIMA 1960) rather than overdominance.

FRYDENBERG in an argument similar to that of MUKAI and BURDICK (1960) stated that "intrinsic overdominance" is not solely a property of the alleles involved but may be altered by "gene frequency changes in the remainder of the gene pool, though it can also be brought about by the release of modifiers from balanced complexes." This statement seems reasonable, but it also skirts perilously close to his definition of associative dominance. "Intrinsic overdominance" would seem to imply an interaction between alleles that would produce heterosis on a variety of genetic backgrounds. If it is as readily altered as implied above, it seems more dependent on interlocus interaction than on interallelic interaction.

LEWONTIN (1964) has written that there is increasing evidence that if heterosis at the locus level is important in natural populations, the degree of heterosis at each locus is a function of the amount of heterozygosity at other loci. In other words, epistatic or interlocus interactions are important in heterosis. The crucial question then becomes whether there is any heterosis when there is no heterozygosity at other loci. If not, then all of the heterosis observed is dependent on interlocus interactions or on dominance. The difficult problem experimentally, of course, is to get heterozygosity at a single locus on a homozygous background.

There has been a strong tendency to call any case in which the heterozygotes exceed both homozygotes an example of overdominance. While such cases involve heterosis in the unencumbered sense of SHULL (1948), this heterosis can not uncritically be regarded as due to overdominance in the original sense of the word. Direct evidence concerning the nature of the allelic interaction leading to heterozygote superiority would seem the surest way to establish overdominance. However, the increasingly sophisticated knowledge of the nature of the genetic material seems to pose some conceptual problems as to just what constitutes allelic interaction.

The greater fitness in malarial regions of the heterozygotes (Hb_1^S/Hb_1^A) for the sickle cell gene seems clearly dependent on the properties of the hemoglobin controlled by the Hb_1 locus itself. This example seems to be a clear-cut case of overdominance, but such well established cases are rare. Even in this case selection will tend to favor those wild-type isoalleles (STERN and SCHAEFFER 1943)

that when homozygous match the heterozygote in fitness. In this way the existing "wild-type" alleles would be replaced, and the population would no longer suffer the loss of fitness entailed in this heterozygosity (HALDINE 1939; MULLER 1959). Such reasoning would lead to the conclusion that the sickle cell polymorphism will become transient if and when a more efficient genetic mechanism for resistance to malaria appears. (Where malaria is controlled or absent, of course, the gene is already decreasing in frequency [ALLISON 1955]).

No attempt will be made to review all reported cases of single-gene heterosis. HAGBERG (1953) has a discussion dealing with cases in plants. Another paper of particular interest is that of JONES (1945). The postulated single-gene heterosis was later (1952, 1957) shown to involve more than an interaction between the degenerative mutants and their normal alleles, and instead seemed due to non-allelic interactions. Results such as these suggest that in plants, too, considerable caution is desirable before instances of heterosis are attributed to overdominance.

Components of fitness: The tests of three of the components of fitness, viability and longevity (Table 3), and mating success (Table 4), warrant some comment. The most striking differences showed up in the mating competition between B and $+$ males and between $L^2/+$ and $+/+$ males. It is thus of interest that in the populations, B was eliminated more rapidly than the other sex-linked dominant, Bx^3 , and L^2 more rapidly than the spontaneous L allele. These results tend to support an earlier conclusion (MERRELL 1949, 1953b; MERRELL and UNDERHILL 1956) that selective mating is a major component of fitness in higher species of animals. This conclusion has apparently been misunderstood (MORPURGO and NICOLETTI 1955, 1956; NICOLETTI and SOLIMA 1956, 1958; PETIT 1958; THOMSON 1961) as suggesting that selective mating was the only selective factor operating in the experimental populations. Since some mutants (f , Bx^3 , L , bw^D) have not significantly affected mating behavior in tests but have declined in frequency, these mutants obviously must have other deleterious effects in the populations. Even though differences in viability, fecundity, longevity, fertility, etc. undoubtedly were present in varying degrees in all of the populations, the fact remains that the most rapid elimination of mutants generally took place in those populations in which mutants with a strongly adverse effect on mating success were present (γ , ct , vg , gl , B , and L^2). It hardly seems likely that coincidence alone could be responsible for this parallelism in so many cases.

NICOLETTI and SOLIMA (1958) measured a number of components of fitness for Bar and found it to be inferior to the normal. However, they did not measure the effect on selective mating. Since PETIT (1958) with Bf vs. B^+f found a value of M_m (MERRELL 1950) of 0.47, and Table 13 showed M_m for B vs. B^+ (without forked) equal to 0.11, the effect of B on mating success is obviously a major component of its effect on fitness, no matter what other effects it may have.

MORPURGO and NICOLETTI (1955, 1956), working with white, reported that changing the sex ratio from 2 males: 1 female to 2 males: 2 females caused strong selective mating to become random. That this is not generally true is indicated by the results of comparable experiments of REED and REED (1950), also with w , or of GEER and GREEN (1962) with several w alleles, or of BARKER (1962) with γ ,

or MERRELL (1954) in experiments with *D. persimilis* and *D. pseudoobscura*.

Some of the differences in results with mating tests are not surprising, for as noted (MERRELL 1949, 1953b) courtship and mating are very complex and sensitive processes, apt to be easily influenced by both genetic and environmental effects. Seemingly trivial differences in experimental conditions could therefore lead to decided differences in the outcome of what appear to be comparable experiments. However, the conditions that would cause *w* males to be twice as successful in mating as *w*⁺ males (PETIT 1958) should be explored further. The *w* males were more successful than wild-type males at frequencies below 40% or above 80%, but only in some of the tests. Certainly, PETIT's finding that changes in the relative proportions of the two male types lead to significant changes in the "coefficient of sexual selection" is not generally true (e.g. her own results with *B* and those of MERRELL and UNDERHILL [1956] with *vg* and *gl*).

MORPURGO and NICOLETTI (1956) also suggested that double insemination of the females would eliminate the effect of selective mating in populations. It is true that virtually all females in a population will be inseminated, and will probably mate repeatedly. However, LEFEVRE and JONSSON (1962) have shown that when an inseminated female remates, "sperm from the second male displace the majority of sperm previously stored in her ventral receptacle and spermathecae." Thus, even though double inseminations occur regularly in populations of *D. melanogaster*, the male types that mate more frequently will tend to leave more progeny than the other males. MORPURGO and NICOLETTI also argued that since double inseminations occur, female "choice" could not be a factor in the populations. However, even though all females may be inseminated repeatedly, under the conditions described above the relative success of the males could be determined by their ability to win acceptance from the females.

SUMMARY

Competition was studied between the following dominant mutants and their wild-type alleles: *L*² (Lobe-2); *L* (spontaneous Lobe mutant); *Bx*³ (Beadex-3); *B* (Bar); and *bw*^{*p*} (brown-dominant). Also studied were *bw* (recessive brown) and populations with three alleles in competition, *bw*^{*p*}, *bw*⁺ and *bw*. From initial frequencies of more than 99%, the dominants declined rather rapidly in frequency and usually went on to extinction in a relatively short time as compared to the recessives reported in this and earlier papers. Four components of fitness were tested separately: rate of development, viability, longevity, and mating success. The separate tests of fitness indicated that mating success was a significant factor, but not the only factor involved, in the decline in frequency of the mutants. Attempts to estimate the magnitude of the selection coefficient in the populations indicate that these mutants act as semi-lethals.

Failure to find a case of balanced polymorphism in 62 populations having mutant and wild type in competition contrasts with previous reports, in which the polymorphism is usually attributed to overdominance at the mutant locus. It is concluded that the heterosis previously observed is not, in fact, generally due to single-gene heterosis or overdominance, but rather to linkage disequilibrium.

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