GENETIC LOADS IN CAGE POPULATIONS OF DROSOPHILA¹

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THE manners by which detrimental alleles are maintained in sexually propagating diploid populations have received considerable attention dating back to HALDANE (1937), and especially MULLER (1950). The two major hypotheses currently proposed in this connection are the gene frequency equilibrium theories based upon (1) mutation-selection balance and (2) heterozygote superiority. The genetic load imposed on a population by the mutation-selection balance is called the *mutational load* and that by the heterozygote superiority condition is referred to as the *segregational load*, which is one aspect of what DOBZHANSKY (1964) labels the *balanced load*.

The problem of the relative importance of the different loads in various populations has been the subject of several recent reports involving the effects of inbreeding [e.g. MORTON *et al.* (1956) and NEEL and SCHULL (1962) with human populations; DOBZHANSKY *et al.* (1963), STONE *et al.* (1963), and MALOGOLOW-KIN-COHEN *et al.* (1964), with *Drosophila* populations; and LEVENE *et al.* (1965) with *Tribolium*.]

The present study pursues the same vein of objectives as investigated by these workers, but it is distinguished from the others in considering (1) experimental populations of long-time standing and (2) populations with and without chromosomal polymorphisms. Materials consisted of cage populations of *D. pseudoobscura* and of two species of the repleta group, *D. arizonensis* and *D. mojavensis*, all of which had been maintained for a number of generations under fairly constant laboratory conditions.

MATERIALS AND METHODS

Each population was sampled by collecting a total of 200 virgins and 100 males from several culture cups randomly withdrawn from the cage. A series of crosses were made by separately placing one male together with two females. After insemination, the females were singly transferred into individual culture bottles. The 200 cultures each produced full-sib families, which could be paired according to the males involved in the crosses into 100 half-sib groups.

The second generation flies were outcrossed in pair matings in such a pedigreed fashion as to produce noninbred progeny (third generation) that were related as sibs within cultures and as double-first cousins, single-first cousins, half-first cousins, or unrelated between cultures, depending on the particular cultures. The third generation matings, equally represented with mates

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having the above five levels of relationships, were made by crossing males from one culture with females from the same or from a different culture. The eggs produced by these various matings had prescribed inbreeding coefficients of $F = 1/4, 1/8, 1/16, 1/32$, and 0 (progenies obtained from full-sib, double-first cousin, single-first cousin, half-first cousin, and unrelated matings, respectively).

Each of the third generation matings was made by using six males and six females; the 12 flies were placed together in one egg-laying bottle. Appropriate numbers of eggs, 25, 50, 100 or 200, depending upon the species of *Drosophila* used, were counted from each egg-laying bottle. The eggs were placed in a culture bottle containing a standardized amount of cream of wheat medium with water-suspended yeast for the *pseudoobscura* tests, and in standard vials (25×95 mm) with banana-agar-yeast medium for the *arizonensis-mojavensis* analyses. The cultures were randomized with respect to the different inbreeding groups and placed in constant temperature stockrooms (19°C for *pseudoobscura* and 23°C for the others).

The number of adults eclosed was scored from each culture, and the scores were converted into proportions of eggs yielding live adults. The cultures with contrasting egg densities (e.g. 50- and 200-egg densities per bottle for *pseudoobscura*) were set up simultaneously from the same set of egg-laying bottles. However, the scoring of eclosion came at different times due to a longer developmental time required under a higher density (e.g. there was about one week's difference between the 50- and 200-egg density tests in *pseudoobscura*).

RESULTS

Genetic loads in pseudoobscura cage populations: The progenitor lines of three *D. pseudoobscura* cage populations, called Gunnison, Lehman Cave, and Mono according to their origins, were originally collected by PROFESSOR TH. DOBZHANSKY and his associates at the locations indicated by the names given the strains; they were chromosomally monomorphic, having been screened for the Arrowhead arrangement of the third chromosome before they were caged. These three populations had been kept under 19°C stockroom condition for more than 80 generations prior to the initiation of this study. Consequently, it was considered that they were in a state of gene frequency equilibrium. The fourth population studied, AR/CH, was one of PROFESSOR DOBZHANSKY's cages kept at the Rockefeller Institute—a sample was kindly made available for this study. The AR/CH population contained the Arrowhead and Chiricahua arrangements of Chromosome 3 at equilibrium frequencies.

The character studied, egg-to-adult survival, which was measured by the proportion of eggs that ultimately gave rise to eclosed imagoes, will be referred to as eclosion proportion. Eclosion proportion is known to be highly sensitive to the degree of larval crowding in culture bottles. For this reason, all tests were conducted under two larval densities, which were obtained by placing either 50 or 200 eggs per culture bottle.

The data of eclosion proportion at the five levels of inbreeding are presented in Table 1. The table also includes the number of culture bottles (n) and the standard error for each datum. The other notations used are explained at the bottom of the table. The data in Table 1 are summarized according to the population cages in Figure 1. There is an overall tendency of viability depression with increased inbreeding under both densities.

The analysis proposed by MORTON *et al.* (1956) was performed with the data in Figure 1. This analysis consists of computing regression coefficient B and inter-

TABLE 1
Eclosion proportions averaged over cultures (n) at five levels of inbreeding for three chromosomally monomorphic cage populations and one chromosome 3 polymorphic population of D. pseudoobscura

Populations and egg densities	F=0		F=1/32		F=1/16		F=1/8		F=1/4	
	n	Eclosion	n	Eclosion	n	Eclosion	n	Eclosion	n	Eclosion
Gunnison I*										
50	44	.860 ± .015	37	.823 ± .030	59	.884 ± .012	34	.879 ± .022	51	.768 ± .027
200	60	.541 ± .020	60	.486 ± .024	60	.475 ± .020	60	.481 ± .026	60	.480 ± .027
Gunnison II*										
50	59	.790 ± .019	59	.730 ± .025	58	.807 ± .020	58	.794 ± .019	56	.693 ± .030
50†	59	.798 ± .021	59	.720 ± .029	58	.769 ± .025	59	.781 ± .025	58	.733 ± .027
50 + 50'	118	.794 ± .014	118	.725 ± .019	116	.788 ± .016	117	.788 ± .016	114	.713 ± .020
200	59	.679 ± .012	59	.686 ± .017	57	.700 ± .016	59	.699 ± .013	59	.646 ± .019
Lehman Cave I*										
50	54	.749 ± .024	55	.696 ± .031	59	.731 ± .021	53	.681 ± .032	58	.703 ± .024
200	59	.507 ± .018	57	.493 ± .020	59	.477 ± .016	55	.475 ± .019	58	.526 ± .022
Lehman Cave II*										
50	47	.854 ± .025	35	.861 ± .018	43	.848 ± .026	34	.826 ± .028	49	.698 ± .026
200	49	.707 ± .025	35	.751 ± .028	43	.697 ± .020	34	.742 ± .022	49	.634 ± .026
Mono										
50	63	.882 ± .015	53	.846 ± .022	...	†	54	.694 ± .020	58	.706 ± .020
200	62	.753 ± .015	53	.722 ± .016	53	.706 ± .018	54	.834 ± .018	63	.829 ± .021
AR/CH										
50	59	.882 ± .014	58	.920 ± .012	59	.928 ± .011	59	.912 ± .014	59	.826 ± .017
200	57	.796 ± .015	59	.780 ± .016	57	.802 ± .014	59	.765 ± .014	59	.743 ± .013

* I and II represent two independent samples from one cage.

† The printed and non-printed runs are duplicated observations from one sample.

‡ A technical error was found in obtaining this datum, and the value was discarded.

FIGURE 1.—The proportion of eggs giving rise to eclosed adults at five levels of inbreeding for four cage populations of *D. pseudo-obscura*.

FIGURE 2.—The proportion of eggs giving rise to eclosed adults at five levels of inbreeding for four cage population derived from *D. arizonensis* and/or *D. mojavensis*.

cept A in the linear regression equation of the form, $Y = A + BF$, where Y is $-\log_e$ (eclosion proportion) and F is the inbreeding coefficient. MORTON *et al.* suggested that the ratio of B to A could be used as a criterion for distinguishing

TABLE 2

The estimates of Morton-Muller-Crow's A and B statistics and the results of curvilinear regression analysis of $-\log$ (eclosion) on F values

	A	B	B/A	L*	Q†
<i>50-egg density</i>					
Gunnison	0.215 ± 0.035	0.306 ± 0.256	1.416 ± 1.353	1.43	0.78
L. Cave	0.244 ± 0.092	0.441 ± 0.086	1.806 ± 0.794	26.12	0.09
Mono	0.135 ± 0.020	0.200 ± 0.104	1.481 ± 0.830	3.80	1.93
AR/CH	0.081 ± 0.031	0.341 ± 0.195	4.193 ± 3.578	3.06	233.13
<i>200-egg density</i>					
Gunnison	0.511 ± 0.018	0.249 ± 0.081	0.488 ± 0.165	9.69	0.01
L. Cave	0.529 ± 0.040	0.123 ± 0.093	0.232 ± 0.057	1.72	2.22
Mono	0.315 ± 0.020	0.203 ± 0.141	0.645 ± 0.476	2.07	30.04
AR/CH	0.081 ± 0.031	0.341 ± 0.195	4.193 ± 3.578	3.06	233.13

* The values of the variance ratio (F) must be greater than 10.13 for the 5% statistical significance for this column.

† The values of the variance ratio (F) must be greater than 18.51 for the 5% statistical significance for this column.

segregational load *vs.* mutational load, provided that A measured purely the degree of genetic death at $F = 0$. From a theoretical consideration, it can be said that B/A takes the value 1 when all of the load involved is segregational, while the ratio takes a much higher value (e.g. mid-20's for mutational load caused by loci with near-lethal homozygous and slightly detrimental heterozygous effects) when the share of the mutational load is large.

The estimates of A and B for the four populations are listed in Table 2. Compared to the results of DOBZHANSKY *et al.*, 1963, who reported B 's ranging from 0.47 to 0.75 for natural populations of *D. pseudoobscura*, the estimates of B in Table 2 are rather small. Consequently, the ratios, B/A , are also small. Even under the 50-egg density, the ratios range between 1.42 and 4.19. The magnitude of these ratios is, however, in agreement with the report of TORROJA's (1964) cage population study.

The estimated ratios are lower still for the 200-egg density tests. This is due to the fact that B is slightly decreased and A is considerably increased under this density. The genetic death estimate at $F = 0$ (A) contains a high upward bias by including a large accidental death rate expected at a high larval density.

The following curvilinear regression equation was fitted to the data: $Y = A + BF + CF^2$, where C is the quadratic regression coefficient *adjusted for A and B* and the other quantities are as defined before. The variance ratios for the test of statistical significance of the sum of squares due to the linear regression (L) and of that due to the quadratic regression (Q) are presented on the right-hand side of Table 2. The underlined ratios are either statistically significant or nearing the significant level at the 0.05 level.

The values of lethal equivalents (inbred loads) can be computed by making $F = 1$ in the above regression equations. These estimates are listed in Table 3. It should be recognized that the true inbred load contains only the portion of A that is genetic, not the entire A ; but, since there is no estimate of this portion, the

TABLE 3
*Estimates of inbred loads (lethal equivalents) in cage populations
of D. pseudoobscura*

Population and egg densities	$A + B$	B	$A + B + C$
Gunnison			
50	0.521	0.306	3.011
200	0.760	0.249	0.678
Lehman Cave			
50	0.685	0.441	1.020
200	0.652	0.123	-0.600
Mono			
50	0.335	0.200	-0.970
200	0.518	0.203	-2.017
AR/CH			
50	0.422	0.341	3.898
200	0.509	0.283	0.782

values in column 1 of Table 3 include the entire A values. In the second column, the values of B estimates of Table 2 are relisted. The unbiased estimates of inbred loads in the respective populations revealed by the technique used should be located between the $(A + B)$ and B estimates.

The addition of the quadratic regression coefficient $(A + B + C)$ tends to increase the estimates of the inbred load in general, with the exception of the Mono population, in which the quadratic regression had the opposite effect. A large difference between the $(A + B)$ and $(A + B + C)$ estimates is an indication of the existence of synergism in gene action. However, comparing the statistical test of quadratic effects and the inbred load estimates, there is no clear-cut indication of synergism at such low levels of inbreeding. The strongest cases for the existence of possible synergism are the AR/CH and Mono populations (tested under the 50-density). But, even these cases are somewhat obscured by the behavior of the same populations under the 200-density.

Genetic loads in cage populations of D. arizonensis and D. mojavensis: Four cage populations (A , B , A/M and A/B) were analyzed by the inbreeding and viability testing procedures set forth above. Population A was started with flies from 15 isofemale lines of *arizonensis* established from collections made two years previously near Magdalena, Sonora, Mexico. The cage was sampled three months after its inception.

The closely related species, *mojavensis*, is found sympatric with *arizonensis* in several localities in Sonora, Mexico. It also occurs in Baja California and in the Mojave Desert. Flies of the Mojave Desert region constitute a northern race, called race M ; they are morphologically distinct and apparently geographically disjunct from those of the Baja California and Sonora populations, which make up race B . The one available stock of race M is chromosomally monomorphic, while several recently collected strains of race B are polymorphic for inversions in autosomes 2 and 3 (METTLER 1963). Cage population B was started two years prior to sampling with the progeny of several race- B females collected in Baja California. The population had reached an equilibrium with respect to the alternate chromosome sequences of both polymorphic autosomes.

Although *arizonensis* and *mojavensis* are apparently reproductively isolated in nature, they are related enough to produce some fertile offspring in the laboratory. The two species are known to differ cytologically by inverted segments in the X , 2 and 3 chromosomes. The third population, cage A/B , was initiated with F_1 hybrids from the cross of *mojavensis* (race B) females and *arizonensis* males. The interspecific "hybrid" population that ensued existed eleven generations before being sampled for this study. The population had reached genetic equilibrium not only for the race- B intraspecific polymorphisms but for the different interspecific chromosomal types as well.

The fourth cage, A/M , was started with *arizonensis* and *mojavensis* (race M) flies, which subsequently crossed to produce a "hybrid" population. This cage existed 75 generations prior to sampling. It was polymorphic and in equilibrium for the different species-specific arrangements of chromosomes 2 and 3. All four

TABLE 4
Eclosion proportions at five levels of inbreeding for a monomorphic population (D. arizonensis, Cage A), a polymorphic population (D. mojavensis, Cage B), and two interspecific polymorphic populations (Cages A/B and A/M)

Populations and egg densities	F=0		F=1/32		F=1/16		F=1/8		F=1/4	
	n	Eclosion	n	Eclosion	n	Eclosion	n	Eclosion	n	Eclosion
A	25	.772 ± .022	53	.764 ± .018	54	.751 ± .021	53	.663 ± .027	57	.662 ± .022
	25'*	.769 ± .018	53	.737 ± .019	54	.716 ± .024	53	.719 ± .022	57	.662 ± .022
	25 + 25'	.770 ± .014	106	.751 ± .013	108	.733 ± .016	106	.691 ± .018	114	.662 ± .016
	50	.766 ± .018	54	.705 ± .018	56	.746 ± .021	53	.693 ± .020	57	.682 ± .018
B	50	.624 ± .016	69	.571 ± .020	68	.461 ± .024	72	.484 ± .021	68	.441 ± .023
	100	.590 ± .013	70	.526 ± .016	69	.417 ± .022	72	.443 ± .019	68	.386 ± .020
A/B	50	.176 ± .022	47	.166 ± .019	65	.149 ± .016	44	.179 ± .024	86	.139 ± .013
100	48	.149 ± .015	47	.177 ± .018	63	.173 ± .018	42	.164 ± .018	83	.136 ± .011
A/M	25	.519 ± .024	45	.515 ± .027	52	.458 ± .029	48	.498 ± .030	52	.501 ± .022
	25'*	.514 ± .028	43	.477 ± .029	52	.465 ± .028	47	.491 ± .027	52	.472 ± .023
	25 + 25'	.516 ± .018	88	.496 ± .019	104	.461 ± .019	95	.497 ± .019	104	.487 ± .016
	50	.418 ± .018	42	.450 ± .022	52	.424 ± .024	46	.454 ± .019	52	.462 ± .021

* The primed and non-primed runs are duplicated observations from one sample.

populations were maintained under similar and rather constant (23°C) stock-room conditions.

The eclosion proportions at the five levels of inbreeding for the four populations are given in Table 4. Although there were some differences in viability according to egg density in the B and A/M test cultures, no drastic effects of larval crowding occurred for any of the egg densities chosen (25, 50, or 100 eggs per vial). This is particularly true of the A/B cultures because so few eggs hatched. For convenience, since all the tests were performed within or near the optimal density range, the data were pooled by calculating the means of the different tests, weighted by the number of cultures in each test. These average eclosion proportions are presented in Figure 2.

Two striking features of the results are immediately apparent. First, the outbred viability loads of the four populations are extremely different, being the highest in the two "hybrid" populations, A/M and A/B. A cage population of *mojavensis* (race M) was not available for comparisons with A and A/M. A stock of this race, however, had been maintained under laboratory conditions for over 20 years. Eggs produced by a random sample of impregnated females from the stock were tested (50 eggs per vial) under the same conditions of the population studies. Race M gave an "outbred" egg-to-adult survival value of about 90 percent, which is much higher than that of either race B or *arizonensis*. Secondly, as may be surmised intuitively from the values in Figure 2, the genetic load ratios are moderately low in the case of *arizonensis* ($B/A = 1.77$) and race B (2.32); they are extremely low for the "hybrid" populations, because of the lack of any significant B regression and the very high A values.

DISCUSSION

The face values of B/A estimates obtained apparently favor the conclusion of predominant segregational loads and little mutational loads in most of the populations of this study. However, there are some objections to accepting the face values of B/A as the criterion. The first objection comes from the fact that the estimate of A usually contains an upward bias due to nongenetic deaths in the type of experiment conducted. Secondly, egg hatchability, a component of egg-to-adult viability, is known to be affected by maternal and possible paternal influences. The failure of eggs to hatch owing to parental causes also results in an upward bias of the estimate of A . Every upward bias of the A estimate will lower the estimate of the B/A ratio, and this may in turn lead one to conclude erroneously in favor of predominant segregational loads (CROW 1958). Thus, it is necessary to scrutinize the situation by a criterion other than the B/A or $(A + B)/A$ ratio.

Of the quantities estimated in this study, the regression coefficient, B , is least likely to have large biases, particularly from the sources already mentioned. Under the fitness model of $AA:Aa:aa = 1:1-h:1-s$ for locus A , the expected regression value, b , from this locus is $b_o = \frac{-h(-h+s)}{(1-h)(-2h+s)}$ at the overdominance

TABLE 5

*Expected b_0 values for one overdominant locus at equilibrium with vary amounts of s and h .
The number of loci required to yield the overall regression values of 0.32 and
0.21 are given within the parentheses*

s	h				
	0.00	0.01	0.05	0.10	0.90
—0.01	0.00495 (65;42)	0.00660 (48;32)	0.00849 (38;25)	0.00908 (35;23)	0.00979 (32;21)
—0.05	0.01428 (23;15)	0.02597 (12; 8)	0.03175 (10; 7)	0.03571 (9; 6)	0.04524 (7; 5)
—0.10	0.04545 (7; 5)	0.04762 (7; 4)	0.05455 (6; 4)	0.06061 (5; 3)	0.08264 (4; 3)

equilibrium, when h is negative and s is positive, and $b_m = [(s/h)-2]\mu$ at the mutation-selection equilibrium, when h and s are positive and μ is the mutation rate for $A \rightarrow a$. The case of complete dominance will be excluded from the present discussion. The values of b_0 for various combinations of s and h are given in Table 5, and those of b_m for varying s/h values with $\mu = 10^{-5}$ in Table 6.

When gene action is multiplicative (i.e., additive on a logarithmic scale) between loci and when loci have equal effects, the overall B for n loci is nb . In the case of the *pseudoobscura* data in this study, B is in the neighborhood of 0.32 for the 50-density test and 0.21 for the 200-density test. The numbers of loci required to yield these B values are entered in the parentheses in Table 5 and 6. For the overdominance cases, n ranges from 65 to 4 for $B = 0.32$, and from 42 to 3 for $B = 0.21$. On the other hand, simultaneous heteroallelism at more than several hundred loci, possibly several thousand loci, are needed to account for the value of B obtained if all the genes involved are maintained solely by the balance between mutation and selection pressures. Such a situation is quite unlikely to exist in the kind of populations studied.

A more likely situation is that a large portion of the B regression is caused by a relatively small number of loci with overdominance while the remainder is due to segregations at a relatively large number of loci maintained by mutation and selection pressures. However, at present there is no quantitative way to partition the total B value into the two parts.

The values of B for *pseudoobscura* from cage population data (e.g. this study

TABLE 6

*Expected b_m values for one locus at mutation-selection equilibrium
with varying s/h and $\mu = 10^{-5}$*

	s/h			
	50	20	10	5
b_m	0.00048	0.00018	0.00008	0.00003
For $B = 0.32$	(667)	(1178)	(4000)	(10667)
For $B = 0.21$	(438)	(1167)	(2625)	(7000)

and TORROJA, 1964) tend to be substantially smaller than those from natural population data (e.g. DOBZHANSKY *et al.* 1963). The range of B values obtained by DOBZHANSKY *et al.* is 0.74 to 0.47 with a mean of 0.66 under a 50-egg density condition. The corresponding range for the *pseudoobscura* data of this study is 0.44 to 0.20 with a mean of 0.32 ± 0.08 . The reduction from 0.66 to 0.32 is probably significant, and the cause of this reduction is of some interest.

The low values of B probably reflect the partial loss of the genetic variability in cage populations from the level of variability existing in natural populations. This is obvious in that cage populations are subjected to a far more stable environmental condition than those in nature. The "closed" nature of cage populations and the uniformity of laboratory conditions are known to eliminate or reduce the genetic variability which is maintained in balance under natural environments (LEWONTIN 1958; MAYR 1963). During the period of more than 80 generations in cages, the populations of *pseudoobscura* used in this study must have lost a considerable amount of genetic variation that had been maintained in nature by overdominance or other balancing mechanisms. Since the genetic variability due to recurrent mutation is likely to be continued under the laboratory conditioning, the difference in genetic variability between DOBZHANSKY's populations and the populations of this study probably represents, to a great extent, the loss of variability due to the fixation of balanced polymorphic loci.

This conclusion is supported by the results of the *arizonensis-mojavensis* cage populations. Cage A/M expresses the lowest B regression of any in this report ($B = -0.095$); the lack of any inbreeding depression is quite apparent in Figure 2. This population was established with flies from stock cultures of *mojavensis* (race M) and *arizonensis*, both of which have been maintained since the early 1940's. Furthermore, the experimental population itself existed more than six years before the inbreeding tests were conducted. Much larger B values, on the other hand, are found for cages, A, B, and A/B ($B = 0.503, 1.369$, and 0.697 , respectively). These cages were initiated with flies from strains of the two species that were collected only three years prior to the study; presumably, they have retained more of the "open" variability.

The B/A ratios of populations A, B, and A/B may be compared to determine if they reflect the differences in the genetic structures of related monomorphic and polymorphic populations. These cages represent two closely related sibling species that exist sympatrically under similar ecologies over a large portion of their ranges. Cage A (*arizonensis*) is chromosomally monomorphic, while cage B (*mojavensis*, race B) is polymorphic for coadapted inversion sequences. These populations give comparable B/A ratios (1.79 and 2.32, respectively), but both the A and B values of cage B are significantly greater than cage A. This emphasizes the point made earlier that in some cases B/A ratios are not as informative as the A and B values considered separately.

The results of the "hybrid" population A/B are of even greater interest in this respect. As might be expected, the B regression is nearly intermediate between those obtained for the parental forms. But the A value of the "hybrid" population (1.76) is nearly six times that of Cage A (0.28) and three times that of cage B

(0.59). The tremendous inflation of the expressed viability load is due largely to low egg hatchability, which has been found to be caused by the high sterility of the post-F₁ recombinant males. Male sterility is also known to be largely responsible for the large *A* (0.75) found for cage A/M. Population B also has an inflated *A* value, but not to the extent of the "hybrid" populations. It is suspected that this increase is also due to prezygotic selection factors associated with a balanced load, and that the effect is weaker than in the "hybrid" cases because of the co-adapted nature of its polymorphisms. In any event, it appears that the polymorphisms contribute heavily to the expressed load and only little to the *B* regression, since prezygotic components of fitness are not considered in these analyses.

SUMMARY

The genetic load (viability at five levels of inbreeding) was estimated for eight cage populations of *Drosophila*: four of *pseudoobscura*, and four involving *arizonensis* and *mojavensis*. The Morton-Crow-Muller *A* and *B* criteria were calculated for each set of inbreeding datum. The *B/A* ratios were found to be low for all populations. However, considering the *B* regression alone, it was concluded that the inbreeding depression is due to a relatively small number of overdominant loci and the rest to a comparatively larger number of heteroallelic loci maintained by mutation-selection balance. The contribution of the overdominant loci to the *B* value, however, is presumably much greater than that of the "mutational" loci of these populations.—The *A* value of interspecific polymorphic populations was greatly increased over that of the parental forms owing to prezygotic selection factors, particularly male sterility, which do not appreciably affect the inbreeding regression. This effect on the expressed load was not nearly as exaggerated when the polymorphisms were coadapted.

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