vae of our stock carry an extra Y chromosome, with the two Y's identical to each other in all respects. The females may also carry a supernumerary Y, but that condition occurs less frequently than in the males.

The species from western Canada proves to have a rod-shaped X, a submetacentric Y, one pair of small metacentrics, one large metacentric pair, one pair of larger rods and one pair of small rods. With the exception of the small rods in place of dots, this karyotype is very similar to that published for the European D. littoralis. We are grateful to Dr. E. Momma for providing us with the stock of the new Japanese species and to the National Drosophila Species Resource Center, the University of Texas, for providing us with a strain of the new species from Canada. This work was supported in part by National Institute of Health grant GM 23007 to L. H. Throckmorton.

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Dewees, A.A. Sam Houston State University, Huntsville, Texas. Lethal-bearing genomes from a Texas population of D. melanogaster.

Second and third chromosomes were sampled directly from a natural population near Huntsville, Texas, and analyzed simultaneously for the presence of lethal genes. The A_1B_{18} marker stock, supplied by Dr. Bruce Wallace, was used to produce flies isogenic for both second and third chromosomes (Wallace, Zouros and Kimbras 1966). This stock contains two reciprocal translocations, designated (Cy L; Ubx)/(Pm; Sb), and allows second and third chromosomes to be handled simultaneously. The mating scheme was initiated by crossing single wild-caught males to virgin (Cy L; Ubx)/(Pm; Sb) females in shell vials. From each parental mating a single F_1 male (Cy L; Ubx)/(+;+) was mated with a (Cy L; Ubx)/(Cy; Pm) female. Virgin F_2 (Cy L; Ubx)/(+;+) brothers and sisters were mated in half pint bottles to produce an F_3 generation (in some F_2 matings (Pm;Sb)/(+;+) flies were used). The expected proportion of viable F_3 flies, assuming lethal-free wild type chromosomes, is 2 (Cy L; Ubx)/(+;+): 1 +/+;+/+.

Second and third chromosomes, "genomes", from a total of 78 wild-caught males were carried through to the F_3 generation. An average of 105 F_3 flies was examined for the 78 genomes. The distribution of genomes into viability classes is presented in Table 1 for each of two collecting periods. The results from a 2x4 contingency chi-square analysis ($\chi^2_3 = 0.42$; $0.9 < P < 0.975$) indicate no difference in distributions over the two months. The total percentage of lethal plus semilethal genomes was 89.7% (70/78), based on pooling the three lowest viability classes. These results are similar (2x2 contingency $\chi^2_1 = 3.4$; $0.05 < P < 0.1$) to genome lethal plus semilethal frequencies reported by Wallace et al. (1966). Using the same balancer stock for the detection of viability differences in a Bogota, Colombia, population, they reported 79.8% (95/119) lethal plus semilethal genomes. Although no effort was made in the present study to localize the lethal effects of a genome to the individual chromosomes, some predictions can be made based on the findings of Wallace et al. (1966). They reported that their genome lethals were nearly equally distributed between second and third chromosomes. Band and Ives (1963) also reported similar lethal plus semilethal frequencies for these two chromosomes tested separately. Under the assumption of equal chromosome frequencies, lethal plus semilethal frequencies in the Huntsville, Texas, population can be individually determined for the second and third chromosomes as follows: Let p = frequency of lethal plus semilethal chromosomes; then $(1-p)^2$ = expected frequency of genomes having both second and third chromosomes free of lethal and semilethal genes. Eight of 78 genomes were in this category; therefore, the estimate of p is $1-\sqrt{8/78} = 0.68$.

Ives (1945) reported second chromosome lethal plus semilethal frequencies from 34% to 67% for eastern U.S. populations of D. melanogaster, with the highest frequencies obtained for Florida populations. The southeast Texas population sampled in the present study appears to be quite similar in its frequency of lethal plus semilethal chromosomes to Florida and Colombia populations.

Table 1. Observed (and expected) numbers of genomes in different viability classes.

Collecting Period	Relative Frequency of Wild-Type F_3 Flies				Total Number Genomes
	0.0	0.01-0.083	0.084-0.166	0.167-0.333	
May 1977	22 (23.2)	9 (8.8)	7 (6.6)	5 (4.4)	43
June 1977	20 (18.8)	7 (7.2)	5 (5.4)	3 (3.6)	35
Totals	42	16	12	8	78

References: Band, H.T. and P.T. Ives 1963, Can. J. Genet. Cytol. 5:351-357; Ives, P.T. 1945, Genetics 30:167-196; Wallace, B., E. Zouros and C.B. Kimbras 1966, Am. Naturalist 100: 245-251.

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Estimation of N_em by allelism method in D. subobscura.

In an attempt to estimate the effective population size, N_e, by the allelism method (Wright, Dobzhansky and Howanitz 1942) the parameters Q, P, and P_{∞} have been determined in two Greek natural populations of D. subobscura from Mt. Parnes and Crete. (Q = frequency of lethal chromosomes; P and P_{∞} = frequencies of lethal chromosomes in and between populations.)

For Parnes 145 and 218 O chromosomes, collected at different times, were analyzed by the Va ch cu/Ba $O_{3+4+X+4}/O_{ST}$ balanced strain, and for Crete 150 and 261, respectively. The frequency Q had no significant difference in two samples for each population, so they have been considered as one.

Table 1. Estimation of Q in Crete-Parnes population.

Population	Total Q	Corrected Q	
		O_{3+4}	O_{ST} & O_{3+4+8}
Crete	0.187 ± 0.032	0.136 ± 0.073	0.242 ± 0.037
Parnes	0.248 ± 0.036	0.284 ± 0.042	0.414 ± 0.073

The underlined data were considered as more representative of each population.

The two populations differ at O chromosome inversions. The O_{3+4} and $O_{3+4+\varphi}$ (where φ = 1,22, 2,7) are the most common in the Parnes population, while in Crete the most common is the O_{3+4+8} inversion. Because the balanced strain (it has been analyzed) does not cover the O chromosome near the O_{3+4} end, all the estimated frequencies were corrected with reference to O inversion (Tables 1, 2, 3). By some relations of the method, it was possible to estimate the parameters: p, frequency of allelism of lethal genes' O chromosomes in a population; p_{∞}, frequency of allelism of lethal genes' O chromosomes between two populations; n, number of genes subject to lethal mutation. Then the quantity N_em was estimated, where m = migration rate (Table 4).

Table 2. Estimation of P in Crete-Parnes population.

	$O_{3+4} \times O_{3+4}$		$O_{3+4} \times \begin{Bmatrix} O_{ST} \\ O_{3+4+8} \end{Bmatrix}$		$\begin{matrix} O_{ST} \\ O_{3+4+8} \end{matrix} \times \begin{Bmatrix} O_{ST} \\ O_{3+4+8} \end{Bmatrix}$		Total	
	Crete	Parnes	Crete	Parnes	Crete	Parnes	Crete	Parnes
total no. of crosses	3	138	71	67	284	5	358	210
no. allelic crosses	0	2	0	0	2	0	2	2
allelism frequency	0	0.0145 ±0.0102			0.0070 ±0.0049		0.0054 ±0.0038	0.0095 ±0.0069