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

Table 3. Estimation of P_∞ between Crete-Parnes populations.

	O_{ST} / O_{3+4+8} x O_{ST} / O_{3+4+8}	O_{3+4} x O_{ST} / O_{3+4+8}	O_{3+4} x O_{3+4}	Total
total no. of crosses	174	913	417	1553
no. allelic crosses	1	2	0	3
allelism frequency	0.00575 ±0.00573			0.0019 ±0.0011

Table 4. Estimation of Q, P, P_∞, p, p_∞, n and N_em in Crete-Parnes population.

		Q	P	P_∞	p	p_∞	n	N_em
Crete	uncorrected Q, P, P_∞	0.187	0.00540	0.00190	0.00505	0.00155	645	344
	corrected Q, P, P_∞	0.242	0.00704	0.00575	0.00568	0.00439	228	573
	corrected Q, P	0.242	0.00704	0.00190	0.00659	0.00145	689	175
Parnes	uncorrected Q, P, P_∞	0.248	0.00950	0.00190	0.00904	0.00144	694	115
	corrected Q, P	0.284	0.01449	0.00190	0.01396	0.00137	730	59

Diamantopoulou-Panopoulou, E. and H. Bacoulas. Agricultural College of Athens, Votanicos, Greece. "Sex ratio" in D. obscura.

One isofemale line of D. obscura from a Greek natural population (Mt. Parnes) produced offspring of only female sex; this continued for many generations (the male parent was taken from an obscura stock). A treatment was undertaken to clarify if this condition was similar to that of "sex ratio" in D. bifasciata. After penicillin G was given "per os" for one or two generations, the culture produced both sexes (males and females vs. females only) progressively to fifty-fifty percent. After enough time the culture began to produce again only female flies.

An attempt to find the causal factor, spirochaete in the haemolymph of the female fly, gave no results.

Doane, W.W. Arizona State University, Tempe, Arizona. Midgut amylase activity patterns in Drosophila: nomenclature.

A control gene for tissue specific expression of α-amylase in the adult posterior midgut (PMG) in D. melanogaster was located at 2-80± by Abraham and Doane (1976, 1978). This gene, called map for midgut activity pattern, lies approximately two crossover units to the right of the structural gene(s) for the enzyme (Amy). Strain specific differences in the regional expression of amylase in the PMG were attributed to allelic differences at the map locus. Three spatially different PMG patterns were found in an initial survey of isogenic laboratory strains. These patterns, which reflect the cellular dis-