Paik, Y.K. and K.C. Sung. Hanyang University, Seoul, Korea. Chromosome inversions in Korean populations of D. melanogaster.

The natural populations of D. melanogaster were sampled at 17 different localities in Korea from 1977 to 1978. The results to be reported below include a portion of the present study, which was done in 1977. Fifty-eight different inversions were detected from nine local populations on examination of 1875 wild-caught females; four inversions were found in Chromosome X; ten in Chromosome 2R and 17 in the 2L; 15 in Chromosome 3R and 12 in the 3L. Of these inversions, six were common cosmopolitan types, four were semicosmopolitan, seven were new and common endemic, and 41 were new and rare endemic. Of this last group there were five overlapping inversions occurring in Chromosome 3. In a population sampled four times, the frequency changes of some of the cosmopolitan inversions followed a seasonal trend; some of the common endemics remained stable in frequency from month to month. Coefficients of similarity obtained based on the types and frequencies of inversions found appear to illustrate distinctiveness of each population rather than similarity between populations tested. In the following list the approximate breakpoints of the present series of inversions are given in terms of Bridges' salivary maps.

Chromosome	Break points	Chromosome	Break points	Chromosome	Break points
X	1D; 3F	2L	31F; 36F	3L	66D; 73B
	8C; 18B	(cont'd)	37A; 40A	(cont'd)	69C; 77C
	10B; 12B		37E; 39E		71E; 75E
	13F; 16E	2R	42A; 60A		72F; 78B
2L	22A; 26B		42D; 60F	3R	83C; 85B
	22A; 33B		42E; 43A		86D; 88E/F**
	22B; 25C		43B; 46E		86F; 96A
	22D/E; 34A*		47C; 54D		87B; 92F
	23B; 25E/F		47E; 55E		87F; 90F
	23E; 33E		51F; 60D		88C; 98F
	24A; 31F		52A; 56F*		88C/D; 93C
	25B; 28C		54B; 59C		88D; 90F
	26A; 31A		56D; 59B		88D; 94A
	26A; 34E	3L	61F; 67E		89C; 96A*
	37A; 40A		62A; 63C		91C; 93B
	30A; 34A**		63C; 72E*		92D/E; 100F*
	31B/C; 34E/F**		65E; 67D		93D; 98F*
	31F; 35D		66D; 71D**		

* denotes cosmopolitan types; ** denotes semicosmopolitans.

Note: Three overlapping inversions on the 3L and two overlappings on the 3R are not included in the list.

Pinsker, W. University of Tübingen, Germany. Relation between effective population size and allozyme polymorphism in D. subsilvestris and D. subobscura.

Wild flies of the Drosophila obscura-group were collected in a forest near Tübingen (West Germany) during September 1975, 1976 and 1978. Using the malt bait method recommended by Prof. Lakovaara (Oulu, Finland), flies of six different species could be trapped. The numbers of specimens are given in Table 1.

Table 1. Number of flies collected in a forest near Tübingen.

	Sept. 75	Sept. 76	Sept. 78	Total
D. subobscura	157	392	201	750
D. obscura	15	44	75	134
D. subsilvestris	5	23	34	62
D. helvetica	-	3	3	6
D. ambigua	1	-	-	1
D. tristis	-	1	-	1

According to these collection data, D. subobscura seems to be 12.1 times more frequent than D. subsilvestris in this area. Kimura and Crow (Genetics 49: 725-738) have postulated a correlation between the effective population size and the genetic variability for selectively neutral alleles. In the formula

$$H = \frac{1}{4N_e u + 1}$$

the average heterozygosity H is described as a function of the effective population size N_e and the mutation rate u. To prove this theoretical concept the allozyme polymorphism of both species, D. subobscura and D. subsilvestris, was studied by means of horizontal starch gel electrophoresis. Fourteen loci were investigated: Adh, Ao, Aph-3, αGpdh-3, Hk-1, Hk-3, Idh, Mdh-2, Me, Odh, 6Pgdh, Pgm, Phi and Tpi. In D. subobscura 78.6% of the loci turned out to be polymorphic; the corresponding percentage in D. subsilvestris was 28.6%. The average heterozygosity was determined with 13.1% for D. subobscura and 1.5% for D. subsilvestris. Thus allozyme variation is actually much higher in the common species than in the rare species which is in accordance with the prediction of Kimura and Crow mentioned above. Using the experimental data for H and assuming a constant mutation rate of 10^{-6} for both species, the effective population size can be calculated. The result is a number of 37,687 individuals for D. subobscura and 3,801 for D. subsilvestris. These fictitious population sizes are quite dubious because of the inaccuracy of the parameter u. The proportion between the two values, however, does not depend on u. Hence the result that the population of D. subobscura is 9.9 times larger than the population of D. subsilvestris seems reliable.

In this study information about the proportion between the population sizes of D. subobscura and D. subsilvestris has been obtained from two completely different sources: from the number of flies trapped in malt baits and from the analysis of allozyme variation. Both methods yield surprisingly similar results of 12.1:1 and 9.9:1 respectively. A χ^2 test reveals that the deviation is not statistically significant ($\chi^2=2.3$; df=1). This conformity of the data leads to the conclusion that the average heterozygosity represents a suitable basis for the estimation of population sizes.

Pinsker, W. University of Tübingen, Germany. Sterility in D. subobscura males homozygous in a rare allele at the αGpdh-locus.

The allozyme variant $\alpha Gpdh^{90}$ was detected in a sample of wild flies collected in Tübingen. $\alpha Gpdh^{90}$ has an extremely slow electrophoretic mobility in starch gels of pH 7.1 compared to the common variant $\alpha Gpdh^{100}$ and was not found again in samples from natural populations, although about 2500 D. subobscura flies from several geographic regions had been screened. Since rare alleles were needed for other experiments, single pair crosses were set up in order to obtain a strain homozygous for $\alpha Gpdh^{90}$. This trial, however, failed completely. It turned out that a considerable proportion of the single pair cultures did not yield offspring. Among the fertile pairs, only some females were homozygous for $\alpha Gpdh^{90}$ but no males of this genotype could be detected.

To investigate this phenomenon in detail, two different experiments were carried out. In both of them homozygous 90/90-females were crossed with heterozygous 90/100-males. From the F_1 offspring, where the parental genotypes are expected to be present in the ratio of 1:1, single couples were set up in small culture vials. After three weeks the cultures which still contained both partners alive were separated into fertile and sterile pairs and the genotypes of the flies were determined electrophoretically. In the first experiment flies with the original chromosomes were used. For the second experiment the genetic background of the $\alpha Gpdh^{90}$-allele was recombined and substituted to a large extent by means of a marker strain. The results are given in Tables 1 and 2.

Table 1. Number of $\alpha Gpdh^{90/90}$ and $\alpha Gpdh^{90/100}$ genotypes in sterile and fertile cultures.

	Males		Females	
	90/90	90/100	90/90	90/100
sterile cultures	21	5	4	22
fertile cultures	--	56	14	42
	21	61	18	64
	$\chi^2=60.8$ df=1 $p<0.001$		$\chi^2=1.0$ df=1 n.s.	

In both experiments 90/90-males were only found in the sterile cultures and never among the fertile pairs, whereas the females were randomly distributed. The changing of the genetic background had no influence on the sterility of the males. In this connection it should be noticed that in the first experiment 90/90-homozygotes occurred significantly less frequently in the offspring of 90/90-females and 90/100-males than expected ($\chi^2=45.1$; df=1; $p<0.001$),