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Estimation of the effective size in
D. experimental populations.

In a previous experiment the author (1963) estimated the effective population size by measuring the random fluctuation of frequencies of a mutant gene in competition with its wild type allele in *D. melanogaster*, obtaining the ratio

of effective (N) to apparent size (N') (N/N' ratio) 35-62% when $N' < 10$ and 22-30% when $N' > 10$. These values seemed to be too small in comparison with the experimental results of Kerr and Wright (1954a and b), Wright and Kerr (1954), Crow and Morton (1955) and Buri (1956), all of which gave the N/N' ratio 56-83%. A new experiment was carried out in order to obtain a more accurate estimate of effective size in relation to change in parental population density. In this experiment the effective numbers of female and male parents were estimated separately by using sex-linked marker genes.

Females of Muller-5 stock ($w^a B/w^a B$) were mated with the Oregon wild type males (+/Y). Ten F_1 females ($w^a B/+$) were mated with the mixture of 5 F_1 males ($w^a B/Y$) and 5 wild type males (+/Y). In the next generation (F_2) three kinds of female genotype, $w^a B/w^a B$, $w^a B/+$ and +/+, and two kinds of male genotype, $w^a B/Y$ and +/Y, appeared and were counted, so that the frequencies of $w^a B$ chromosomes in the female (q_f) and male (q_m) flies were calculated. One, 4, 10, 20 or 50 pairs of females and males which were sampled randomly from the F_2 population were allowed to breed in a culture bottle of 3 cm. diameter which contained corn-meal agar media added with 0.2 cc. of 5% suspension of dry yeast (manufactured by Oriental Co.). The F_3 flies emerged from the culture bottle were counted and the frequencies of $w^a B$ chromosomes in the female (q'_f) and male (q'_m) flies were obtained. All the F_2 and F_3 flies emerged were counted in each culture bottle.

From the above chromosome frequencies, the values of variables $\delta Q_f = [(q'_m - q_f) - (\overline{q'_m} - \overline{q_f})] / \sqrt{q_f(1-q_f)/2N'_f}$ and $\delta Q_m = [(2q'_f - q_f - q_m) - (2\overline{q'_f} - \overline{q_f} - \overline{q_m})] / \sqrt{q_m(1-q_m)/N'_m}$ were calculated, where N'_f and N'_m were the numbers of female and male F_2 flies, respectively, used in the matings for obtaining F_3 populations. Being fixed the values of N'_f and N'_m , the groups of values of δQ_f and of δQ_m were expected to form approximate normal distribution with mean 0 and standard deviation $\sigma_{\delta Q_f}$ and $\sigma_{\delta Q_m}$, respectively. Then, the average effective numbers of female (\overline{N}_f) and male (\overline{N}_m) parents were estimated as $N'_f / \sigma_{\delta Q_f}^2$ and $N'_m / \sigma_{\delta Q_m}^2$, respectively.

Table 1 shows the results of experiments. From this table it can be seen that the effective numbers of female and male parents enlarge along with the increase in parental popu-

Table 1. Estimations of effective numbers of female (A) and male (B) parents.

(A) No. of female F_2 flies (N'_f)	No. of culture bottles (n)	$\overline{\delta Q}_f$	$\sigma_{\delta Q_f}$	Effective no. of female parents ($\overline{N}_f = N'_f / \sigma_{\delta Q_f}^2$)	\overline{N}_f / N'_f (%)
1	215	-.018±.130*	.965±.092*	1.073(.895 ~ 1.312)**	107
4	335	-.013±.110	1.008±.076	3.937(3.404 ~ 4.605)	98
10	109	+.011±.212	1.117±.150	8.015(6.229 ~ 10.695)	80
20	73	+.004±.410	1.756±.290	6.486(4.777 ~ 9.306)	32
50	325	-.020±.290	2.626±.206	7.247(6.234 ~ 8.537)	14
(B) No. of male F_2 flies (N'_m)	No. of culture bottles (n)	$\overline{\delta Q}_m$	$\sigma_{\delta Q_m}$	Effective no. of male parents ($\overline{N}_m = N'_m / \sigma_{\delta Q_m}^2$)	\overline{N}_m / N'_m (%)
1	215	-.005±.158*	1.164±.112*	.738(.614 ~ .903)**	73
4	335	-.007±.128	1.172±.090	2.912(2.396 ~ 3.416)	72
10	109	+.017±.224	1.173±.158	7.267(5.644 ~ 9.704)	72
20	73	+.038±.380	1.672±.276	7.154(5.270 ~ 10.262)	35
50	325	+.097±.274	2.470±.192	8.189(7.055 ~ 9.635)	16

* 95% confidence limit.

** In parenthesis a range of effective number corresponding to the 95% confidence limit of $\sigma_{\delta Q}$ is given.

lation density when the number of parental pairs is less than 10, but that the effective numbers are almost constantly between 7 and 8 irrespective of the parental density when the number of parental pairs is more than 10. Therefore, it is suggested that in the *Drosophila* mating population kept in a closed culture bottle the effective population size has a certain maximum level which would be determined by the volume of bottle, area of culture media and/or amount of food for larvae. This result means also that the N/N' ratio can be reduced indefinitely by increasing in the parental population density. Any statistically significant difference could not be observed between the effective numbers of female and male parents allowed to breed in a culture bottle.

References: Nozawa, K. 1963, Japan. Jour. Genet. 38: 6; Kerr, W.E. and Wright, S. 1954a, Evolution 8: 172; Kerr, W.E. and Wright, S. 1954b, Evolution 8: 293; Wright, S. and Kerr, W.E. 1954, Evolution 8: 225; Crow, J.F. and Morton, N.E. 1955, Evolution 9: 202; Buri, P. 1956, Evolution 10: 267.

Bos, M. University of Groningen, Genetics Institute, Haren (Gn.), The Netherlands. The influence of disruptive selection on body size in *D. melanogaster*.

In a previous report (DIS 44: 105, 1969) it was shown that stabilizing selection (S) on thorax length in *D. melanogaster* did not have an effect on the phenotypic variance, calculated as squared coefficients of variation ($c.v^2$). In both S-lines the mean thorax

length decreased about 6% below the control level (C). In the two D⁻-lines (disruptive selection with compulsory mating of opposite extremes) $c.v^2$ increased considerably. In D⁻² no change of mean size occurred, in D⁻¹ there was only a slight increase after G 23 (Table 1).

Table 1. The effects of stabilizing and disruptive selection on phenotypic variance and mean.

	$c.v^2$							mean size females (1/100 mm.)			
	G 0	5	10	15	20	25	30	G 0	10	20	30
C 1	6.50	6.10	9.24	7.78	12.18	7.78	6.15	108.7	109.1	110.7	111.3
C 2	6.50	5.15	5.95	9.36	7.51	----	8.41	108.7	108.6	105.3	108.4
S 1	6.50	4.12	5.38	11.56	8.64	10.56	----	108.7	106.9	102.2	-----
S 2	6.50	3.76	17.30	10.43	13.40	5.43	----	108.7	107.1	105.3	-----
D ⁻¹	6.50	8.82	15.84	13.40	28.62	31.47	18.32	108.7	107.9	108.6	112.6
D ⁻²	6.50	7.78	12.39	20.79	20.70	19.98	24.31	108.7	108.2	109.4	108.1

Progeny tests (table 2) show that the increase in the phenotypic variance in D⁻¹ is a consequence of an increase in the residual variance (environmental variance and/or genetic interaction). The increase of the phenotypic variance in D⁻² is a consequence of an increase in additive genetic variance.

Table 2. Heritabilities and the composition of the phenotypic variances ($c.v^2$) in the base population (B), the control lines (C) and in the stabilizing (S) and disruptive (D⁻) selection lines.

	B	C 1		C 2		S 1	S 2	D ⁻¹	D ⁻²
	G 0	G 19	G 30	G 19	G 30	G 19	G 19	G 30	G 30
Phenotypic variance	6.50	12.46	6.15	7.08	8.41	8.01	7.02	18.32	24.30
Heritability	0.53	0.34	0.24	0.25	0.18	0.32	0.31	0.19	0.81
Additive genetic variance	3.45	4.24	1.48	1.77	1.51	2.56	2.18	3.48	19.68
Residual variance	3.05	8.22	4.67	5.31	6.90	5.45	4.84	14.84	4.62

The difference between the two D⁻-lines is corroborated by the result of divergent directional selection started from G 32. After four generations divergence (σ_p) between the high and the low line is 18.9 units in D⁻² and only 8.1 units in D⁻¹ (1 unit = 1/100 mm).