

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_{σ}) 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).