Bischoff, W.L. University of Toledo, Ohio. Fine structure mapping of three lethal mutants within the deep orange gene of Drosophila melanogaster.

Fourteen mutants of independent origin have been assigned to the deep orange locus (1 - 0.3 ±) in Drosophila melanogaster. The absence of complementation between all possible combinations of these mutants and the failure of five of them (dor, dor^{66g}, dor^{61e}, dor^{169f}, and dor^{69L1}) to map in a manner compatible with predictions based on the operon model have permitted the conclusion that this locus best fits the single cistron model of genetic organization (1). The present study was undertaken to determine the topographical relationships between three more of the original fourteen mutants (dor^{169L1}, dor^{169L2}, and dor^{169L3}) and to assign them appropriate positions on the fine structure map of the dor gene. All crosses utilized a crossover selector system which is based on the unique sterility phene of deep orange females and involved mating y dor/Y tester males with females heterozygous for the appropriate pair of dor mutants. Under these conditions such females will produce no progeny unless an event occurs yielding a dor$^+$ gene which will allow the zygote receiving it to survive. Crosses were performed in 1/2 pint bottles on standard cornmeal-molasses-agar medium at 25 ± 1°C. An estimation of the total number of zygotes sampled for each cross was obtained by counting the number of eggs present in 5% of all cultures ten days after set-up. The mutants yellow (y, 1-0.0) and prune (pn, 1-0.8) were used as outside markers lying to the left and right of dor respectively. A summary of all fine structure crosses, dor$^+$ chromosomes recovered, and recombination frequencies is given in Table 1. A revised genetic fine structure map incorporating the

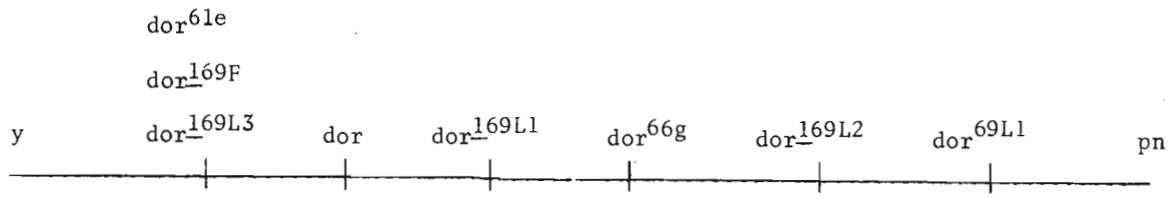
Table 1. Summary of fine structure crosses and surviving progeny.

	Experimental cross	dor$^+$ recombinant chromosomes	dor$^+$ exceptions	Frequency of dor$^+$ alleles
(1)	y dor pn/+ 169L1 + x y dor/Y	2 + + pn	0	2/511,000
(2)	y 66g +/+ 169L1 pn x y dor/Y	1 y + pn	3 + pn	5/890,000
(3)	y dor pn/+ 169L2 + x y dor/Y	2 + + pn	2 + +	4/319,000
(4)	y 66g +/+ 169L2 pn x y dor/Y	3 + + +	0	3/602,000
(5)	y 69L1 +/+ 169L2 pn x y dor/Y	1 y + pn	1 + pn	2/491,200
(6)	y dor pn/+ 169L3 + x y dor/Y	2 y + +	2 + +	4/650,500
	TOTALS	11	9	20/3,463,700

relative positions of the above three mutants is shown in Figure 1. The localization of the lethal mutant dor^{169L1} to the region between the viable mutants dor and dor^{66g} and of the lethal mutant dor^{169L2} to the region between the viable mutants dor^{66g} and dor^{69L1} strengthens earlier conclusions (1) that the various dor alleles do not represent polarity mutants in

Figure 1

Genetic fine structure map of the deep orange locus



several adjacent cistrons of a gene cluster. No attempt was made to determine the relative positions of dor^{61e}, dor^{169L3}, and dor^{169F}, all of which lie to the left of dor since the various heterozygous combinations of these mutants are either lethal or show greatly reduced viability and are therefore not readily adaptable for use in the present selector system. The dor$^+$ exceptions listed in Table 1 represent the products of events which are not associated with outside marker exchange. The possible origins of these exceptions are discussed in detail elsewhere (1).

Reference: (1) Bischoff, W.L. and J.C. Lucchesi 1971, Genetics 69:453-466.