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University of California, Davis, California. Gene order and cytological localization of several X-linked mutants of Drosophila melanogaster.

The su(w^a) locus is known to be in the su(s)^2 - dor interval (M. M. Green, unpublished). As an initial step in two independent studies of genetic fine structure in this region of the X chromosome, it was felt that ambiguities and inconsistencies in the published reports of gene order and cytological localization ought to be cleared up. Utilizing several previously described duplications and a set of seventeen Dp(1;Y) chromosomes synthesized in this laboratory, it was possible to order the mutants sta, 1(1)EN2, and tw with respect to each other and to the other mutants mentioned above (Table 1).

Cytological determination of the breakpoints of the duplications utilized (and several additional duplications and deficiencies) has provided rather precise salivary gland chromosome map locations for tw, su(w^a), sta and dor (Table 2). The mutant hfw (Rayle, Genetics 56: 583) could not be ordered with respect to dor on the basis of the data of Table 1. Additional tests with hfw, the dor alleles and dor-variegating duplications differing in the direction from which the variegation is exerted (to be described in detail elsewhere) suggested that hfw is to the right of dor. The outside markers present in the single wild type recombinant so far recovered from dor/hfw females are consistent with this interpretation.

Several other observations made during this study should be mentioned, since they support the conclusions reached here. Df(1)sta was found to be deficient for the su(w^a) locus. Dp(1;3)sta carries su(w^a)$^+$. The left breakpoint of Dp(1;f)1337 was found to be as described by Krivshenko, as opposed to the description by Gersh. Dp(1;f)101 was found not to cover any of the dor alleles. Its left breakpoint was shown to be at 1F4-2A2 rather than at 2A2-B1. T(1;Y)2E (Clancy, Genetics 50: 241) was found to differ from the original Dp(1;Y)2E (Masterson, DIS 43) by a loss of the wild type alleles of su(s)^2 (first noted by Clancy, personal communication), tw, su(w^a) and sta. Wild type alleles of sc, dor and hfw are still present in T(1;Y)2E.

Table 1. Results of tests for the presence (+) or absence (-) of wild type alleles (y^+ and y^2 both scored as y^{1+}) in duplications used to order mutants in the su(s)^2 - 1(1)EN2 interval.

Duplication tested	Loci tested (arranged in correct order)								
	y^1	sc	su(s)^2	tw	su(w^a)	sta	dor	hfw	1(1)EN2
Dp(1;3)w^{Vco}	-	-	-	-	-	-	-	-	+
Dp Type A	+	+	+	+	+	+	+	+	-
Dp Type B	+	+	+	+	+	+	-	-	-
Dp Type C	+	+	+	+	+	-	-	-	-
Dp(1;f)3	+	+	+	+	-	-	-	-	-
Dp Type D	+	+	+	-	-	-	-	-	-

Dp Type A = seven Dp(1;Y) chromosomes and Dp(1;f)1337.
Dp Type B = two Dp(1;Y) chromosomes.
Dp Type C = six Dp(1;Y) chromosomes, Dp(1;f)18 and Dp (1;f)101.
Dp Type D = two Dp(1;Y) chromosomes.
Note: Df(1)sta;Dp(1;3)sta = sta. Tests for coverage of Df(1)sta lethality in absence of Dp(1;3)sta gave results identical to those for coverage of the visible phenotype.

Table 2. Localization of tw, su(w^a), sta, dor and hfw on the salivary gland X-chromosome map.

Longest and shortest of each duplication type	Genetic coverage	Left breakpoint	Map location of mutant
Dp(1;f)3	y - tw	1D3-1E1	tw in 1C5-1D4*
Dp(1;Y)60e17.4-3	y - su(w^a)	1E2-4	su(w^a) in 1D4-1E3
Dp(1;f)101	y - su(w^a)	1F4-2A2	
Dp(1;Y)59k9-1	y - sta	2A2-B1	sta in 2A1-4
Dp(1;Y)68h20	y - sta	2B3-5	
Dp(1;f)1337	y - dor, hfw	2B8-9	dor, hfw in 2B4-8

*Based on cytology of Dp(1;f)3 and on the published location of tw in 1C5-2C10 (Lindsley and Grell, 1968).