Gvozdev, V.A., S.A. Gostimsky, T.I. Gerasimova and E.M. Gavrina. Kurchatov Institute of Atomic Energy, Moscow, and Department of Genetics of Moscow State University. Complementation and fine structure analysis at the 2D3-2F5 region of the X-chromosome of D. melanogaster.

The 2D3 region of the X-chromosome was saturated with the lethals induced by the treatment of males with ethyl methane-sulphonate (EMS) or nitrosomethylurea (NMU). This region contains the pn and kz loci and is deleted in the deficiency Df(1)Pgd-kz[1]. The Df(1)Pgd-kz and the 2F5-3C5 deficiency, obtained from Prof. M. Green complement each other, thus indicating that the 2F6 band is possibly included in the former chromosome.

The lethals in the 2D3-2F5 region were located by mating 1/Muller-5 females to Df(1)Pgd-kz/w$^+$Y males. In this region, which includes no more than 12 bands of the nearly 1000 bands of the whole X-chromosome 0.5-1.2% (independent series of expts.) of the induced X-linked lethals were mapped.

64 lethals located in 2D3-2F5 region were divided into two groups by deletion mapping with the use of Df(1)64c18, 2E1.2-3C2, obtained from Dr. G. Lefevre: 1) lethals located to the left of the 2E1.2 doublet, in the 2D3-2D5.6 region, containing 3-4 bands; 2) lethals located in the 2E1.2-2F3.5 region, containing 7-10 bands.

The Pgd locus coding for 6-phosphogluconate dehydrogenase (6PGD) was mapped in the 2D3-6 region (1). The Pgd^A and Pgd^B loci determine the electrophoretically fast and slow forms of 6PGD respectively (2). Seven lethal and semilethal mutations in the Pgd^A locus were selected by the absence of the fast (A) and hybrid (AB) or only the fast PGD isozymes in the extract of the Pgd^B/l females produced from a cross of ♀ Pgd^B/Pgd^B x ♂ 1/w$^+$Y.

To detect the complementation between the lethals, matings of ♀ l_1/FM4 x ♂ l_2/w$^+$Y were performed (see Table, asterisks indicate the lethals induced with NMU). Two vital loci, in addition to the well known non-vital pn locus, were revealed in the 2D3-6 region: the Pgd and the locus mapping between the Pgd and pn (lethals 3, 25, 29 etc.) whose function is unknown.

Table. Saturation of the 2D3-2F5 region with lethals.

Complementation groups	Bands	Number of bands in region	Lethals	Number of lethals
1 (Pgd)			11,35,39,45,50,71,109	7
2	2D3-5.6	3-4	3,25,29,33,37,38,40,44,48,49,52,56	12
3 (pn)			-	-
4			1*	1
5			20	1
6			70	1
7			69*	1
8	2D6-2F3.5	7-10	2,8,30,51,59	5
9			14,15,19,42,64	5
10			23,26,31,53,60,105*	6
11			16,18,22,24,28,57,58*,64,102,108	10
12			4,5,17,21,32,34,36,41,47,55,61,63,67,71	15
			Total	64

Nine complementation groups were revealed in the 2E1.2-2F3.6 region containing 9 bands. Thus a good correlation between the number of bands and functional units was demonstrated for the whole 2D3-2F5 region as well as for the adjacent 3A1-3C3 region (3).

This type of investigation allows us to determine whether lethal mutations are situated in the structural region of Pgd locus coding for its product or are scattered in a nearby, possibly regulatory, region.

References: 1) Gerasimova, T.I. and E.V. Ananiev 1972, DIS 48:93; 2) Young, W.J. 1966, J. Hered. 57:58; 3) Judd, B.H., M.W. Shen, T.C. Kaufman 1972, Genetics 71:139.