Marzluf, G. and E. Mayer. Marquette University, Milwaukee, Wisconsin.
Aldolase of Drosophila melanogaster.

A wealth of biochemical information is available about the enzyme, aldolase, which suggests that it is a tetramer composed of two distinct subunits (cf. Chan, Morse, and Horecker, PNAS 57, 1013, 1967). We have examined this enzyme for genetic variability in D. melanogaster. After acrylamide gel electrophoresis of crude extracts of adult flies in Tris-borate buffer at pH 8.9, the enzyme is demonstrated by incubating the gel in a solution containing fructose-1,6-diphosphate, glyceraldehyde-3-phosphate dehydrogenase, NAD, phenazine methosulfate, and nitro blue tetrazolium. In this coupled system, glyceraldehyde-3-phosphate produced by aldolase in the gel serves as a substrate for the exogenously added dehydrogenase which is revealed by the standard dehydrogenase staining method. The activity "bands" obtained are relatively wide, probably because of the indirect method required for staining. The following strains which have been examined to date do not reveal any difference in electrophoretic mobility of their aldolase: Amherst, Canton S, Cockaponsett, Oregon R, Swedish B, Urbana, cn bw, cn bw e, Gl Sb H/Payne, and pr.
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Valencia, Ruby M. Atomic Energy Commission, Buenos Aires, Argentina.
A cytological study of recessive lethals.

In a study of total genetic damage induced in entire genomes of mature spermatozoa by 4000r of X-rays (Abstr. Eb-5, Rad. Res. Soc., May 1967), a total of 203 recessive lethals was collected in all chromosomes. Of these 21 were in the X, 82 in chromosome 2, 94 in chromosome 3 and 6 in chromosome 4. All were analyzed cytogenetically.

134 (66.0%) were point mutations, apparently agreeing quite well with expectation based upon an earlier cytological analysis (Valencia, Hered. Suppl. Vol., 1954) of 81 lethals induced by 700r (85.1% point mutations) and 122 lethals induced by 2800r (71.3% point mutations). This comparison, however, between the previous experiment and the present one, is not valid, due to the fact that lethals associated with 2-chromosome rearrangements were counted differently in the 2 cases. In the present experiment, since lethals were collected in all chromosomes of entire genomes, two "lethal" chromosomes were collected for each lethal translocation or complex rearrangement involving 2 chromosomes. If the results are corrected in order to be comparable to the previous experiment or any typical recessive lethal study, in which lethals are collected in a single chromosome of any particular genome, the results are as shown in the second column of the table. When treated in this way, the present results show an unexpectedly high proportion of point mutation lethals.

	No. "lethal" chromosomes	No. lethals, counting 1 lethal per transl.
Cytol. normal	134 (66.0%)	134 (75.7%)
Inversions	16	16
Translocations	40	20
Complex, 2-chrom.	12	6
Deletion	1	1
Total	203	177

The paucity of deletions is surprising but might be due to failure to detect very small deletions, since the lethals were not localized (as they were in the previous study). Larger deletions, as well as other deleterious rearrangements, might have been less likely to be recovered in this experiment, in which the flies were already quite heavily loaded with markers and rearrangements. This would explain the higher than expected proportion of point mutations.
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