Portin, P. and M. Ruohonen. University of Turku, Finland. A new type of allelic interaction at the Ax locus in Drosophila melanogaster.

A sex linked mutant showing an Abruptex phenotype was found in April, 1971, in a "Muller-5" test of F_1 females of X-irradiated (1000 r) wild-type males. The mutant is dominant and homozygous viable and fertile both in females and males. The mutant gene was localized at or close to the Ax locus by means of crossing-over test. To test the allelism the mutant was crossed to the original Ax. The cross yielded only male offspring, i.e. the heterozygous females were lethal. Thus, the results suggest that the new mutant is allelic to Ax, and accordingly, it was named Ax^{71d}.

The lethality of the heterozygous combination of two viable alleles (Ax/Ax^{71d}) shows a new type of allelic interaction which has been recently observed also by Foster (1972, Genetics 71 Suppl. s:18) likewise at the Ax locus. According to Foster, Ax^{E1}/Ax^{E2}, Ax^{E1}/Ax^{16172}, Ax^{9B2}/Ax^{E2}, and Ax^{9B2}/Ax^{16172} combinations are lethal. From the alleles involved, at least three (Ax^{9B2}, Ax^{16172}, and Ax^{E2}) are homozygous viable and fertile (Welshons, personal communication). It is suggested that the lethality of the heterozygotes is due to an active process, probably some kind of interaction between two different mutant gene products, but not due to lack of function.

This type of allelic interaction is tentatively called contracomplementation.

Lefevre, G.Jr. California State University, Northridge, California. The distribution of X-ray-induced sex-linked lethals.

The distribution of X-ray-induced sex-linked lethals among ten cytologically defined intervals of the X chromosome has been investigated by using a series of duplications to "cover" random lethals. The results are recorded in the accompanying table. Each interval is characterized by a specific band length, which can also be expressed as a percent of the total number of X-chromosome bands. The percent of tested lethals falling in each interval can be compared with the percent of bands. In general, the

Region	# of bands	% of bands in interval	% lethals covered	Coefficient of mutation: % lethals/% bands
1A1 - 1B2	10	0.99%	6/778 = 0.77%	0.78
1B3 - 2C2	54	5.34	42/522 = 8.05	1.51
2C1 - 3C5	44	4.35	34/522 = 6.51	1.50
3C2 - 3E8	25	2.47	13/778 = 1.67	0.68
6C12 - 7C9	52	5.14	13/228 = 5.70	1.11
9E1 - 9F13	23	2.27	9/778 = 1.16	0.51
10A1 - 10A11	11	1.09	8/1098 = 0.73	0.67
10B1 - 11A7	59	5.83	58/1098 = 5.28	0.91
18F1 - 20A2	39	3.85	39/778 = 5.01	1.30
20A3 - 20F4	17	1.68	33/778 = 4.24	2.52
TOTALS	334	33.00%	39.12%	1.19

correlation is rather poor. Band number appears to be an inappropriate measure for estimating the frequency of induced lethal mutations, as it is also for estimating the distribution of chromosome breaks. A more useful measure is the relative DNA content of a region, which is reflected in the size of bands, not simply their number. Allelism tests of lethals falling in each different interval must be completed before a final assessment of the results can be made and should permit the identification of mutational "hot" and "cold" spots. Cytological analysis of all lethals, covered or not, is being carried out in order to permit a comparison of the distribution of lethals arising from mutation with that of those associated with chromosome rearrangement.