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Hilliker, A.J.*, A. Chovnick and S.H. Clark. Univ. of Connecticut, Storrs, Connecticut. The relative mutabilities of vital genes in D. melanogaster.

In recent years, several chromosomal regions of D. melanogaster have been subjected to intensive analysis. Most of these studies have focused primarily on the identification of genes capable of mutating to a lethal or semi-lethal state within a short, defined chromosome segment. However, the screens employed were generally competent to detect genes whose mutant alleles exhibit a recessive alteration in visible phenotype.

If all vital genes in a given region were equally mutable, then it would be possible to employ the Poisson distribution to determine the number of unmutated genes remaining after completion of a mutagenesis study. Cohen (1960) has discussed such methods for truncated Poisson distributions. It is, however, generally appreciated that vital genes within a given chromosomal interval are not of equal mutability, a point we herein substantiate and document for several regions of the Drosophila genome that have been extensively analyzed.

Since the Poisson distribution has only one parameter, the mean (m), which is equal to the variance, it is possible to determine if a given distribution of counts differs from a Poisson distribution by use of the variance ratio, s^2/m, where the sample mean square, s^2, estimates the variance of the distribution, and where m has infinite degrees of freedom (see discussion in Gilbert 1973). The variance ratio test of significance for deviation from the Poisson distribution is preferable to the chi square test in that it is more readily applicable to smaller data samples. Moreover, even in situations where one can apply the chi square test, the variance ratio test is associated with a greater number of degrees of freedom. Where the variance ratio is not significantly different from one, indicating possible agreement with a Poisson distribution, it is possible that the count distribution does differ from a Poisson distribution. Such cases would be better revealed by the chi square test which examines the entire distribution. However, this issue is irrelevant with respect to the present analysis since (1) the sample counts are too small to employ the chi square test, and (2) none of the 11 data sets examined are in good agreement with a Poisson distribution by the variance ratio test.

Table 1 summarizes a series of mutagenesis experiments that are competent to determine if vital genes within a given region are equally mutable by a given mutagen. Each entry represents a mutagenesis screen in which lethal mutations for all genes within a region are detected following treatment of sperm with the indicated mutagen. The data for the regions defined by $Df(3R)ry^{614}$ (Df(3R)87D2-4; 87D11-14) and $Df(3R)ry^{619}$ (Df(3R)87D7-9; 87E12-F1) were obtained in this laboratory as part of a larger analysis of the chromosome interval adjacent to the rosy locus (Hilliker et al. 1980).

The six regions included in the analysis of Table 1 involve both euchromatic and heterochromatic segments of the Drosophila genome. In no instance are the vital genes within a segment of equal mutability. Of the 11 experiments examined in Table 1, only the analysis of fourth chromosome spontaneous mutations failed to show a significant deviation from the Poisson expectation. The P value for this count distribution is greater than 0.05 but less than 0.10.

On the basis of these data, we are led to conclude that Drosophila vital genes within a defined chromosome segment are not of equal mutability. Hence, one cannot use the Poisson distribution to estimate the number of remaining unmutated vital genes within such an extensively analyzed segment.

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Table 1. Variance ratio analyses for the 11 indicated mutagenesis experiments involving six chromosomal intervals in D. melanogaster.

Region analyzed	No. of lethal complementation groups	Mutagen	Mean no. of alleles per complementation group	Variance	Variance ratio	Reference
Chromosome 4	36	Spontaneous	0.806	1.190	1.477†	Hochman 1973
		X-rays	0.833	2.486	2.983***	
		EMS	3.111	18.273	5.873***	
		ICR-170	0.306	0.733	2.397***	
2R Heterochromatin	6	EMS	14.000	202.800	14.486**	Hilliker 1976
2L Heterochromatin	7	EMS	4.000	20.000	5.000**	Hilliker 1976
Df(3R)ry^{614}	9	EMS	3.778	23.444	6.206**	Hilliker et al. 1980
Df(3R)ry^{619}	15	EMS	4.933	20.210	4.097**	Hilliker et al. 1980
Zeste-white	15	EMS	5.533	53.552	9.678***	Lim & Snyder 1974
		TEM	1.800	10.029	5.571***	
		MMS	7.000	37.286	5.327***	Liu & Lim 1975

† $0.05 < P < 0.10$ ** $P < 0.01$ *** $P < 0.001$

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Hilliker, A.J.*, S.H. Clark, W.M. Gelbart** and A. Chovnick. University of Connecticut, Storrs, Connecticut. Cytogenetic analysis of the rosy micro-region, polytene chromosome interval 87D2-4; 87E12-F1, of D. melanogaster.

Figure 1 presents a summary of our cytogenetic analysis of the rosy micro-region. A total of 153 recessive lethals falling into this region were subdivided by inter se complementation, and complementation tests with rosy region deficiencies, into 20 lethal complementation groups. Adjacent complementation groups illustrated within parentheses in Fig. 1 have not been separated by deficiency from one another, hence their relative left-right order is unknown.

The recessive lethals employed in this study are listed in Table 1 according to complementation group (beginning with the most proximally located and continuing through to the most distal). Each listed recessive lethal mutation is accompanied by a description of its source, the mutagen used and, where possible, the isogenic third chromosome on which it was constructed (designated by the specific ry^{+} allele carried on that chromosome).

A majority of the 153 recessive lethals listed in Table 1 were synthesized by Hilliker and Clark (120) as lethal alleles of Df(3R)ry^{614} (34), Df(3R)ry^{619} (83) and Df(3R)ry^{75} (3) (see Table 2). These recessive lethals were recovered from the treatment of iso-3 males with either 0.025M EMS (Lewis and Bacher 1968) or gamma radiation (2000 to 4000 rads).

Since the majority of recessive lethals were synthesized as alleles of Df(3R)ry^{614} or Df(3R)ry^{619}, the region encompassed by these deficiencies, 87D2-4; 87E12-F1, defines the rosy micro-region.

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