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Canada. A test system for studies on
the mechanism of reverse mutation.

Demerec (PNAS 48:1696, 1962) proposed that
reverse mutations might arise by an un-
equal crossover following a mistake in
pairing at the molecular level. Demerec
(Genetics 48:1519, 1963) later found this
hypothesis would not explain the "selfer"

phenomenon in Salmonella but Magni (PNAS 50:975, 1963) proposed a similar mechanism in yeast.
He found a high reversion rate of a homozygous allele associated with an exchange of outside
markers that was greatly depressed when the allele was hemizygous in a deficiency heterozy-
gote. Baylor et al. (Genetics 52:539, 1965) with phage T2 and Strigini (Genetics 52:759,
1965) with phage T4 have suggested a similar mechanism.

In order to determine whether reversion by unequal crossing over might occur in
Drosophila melanogaster, studies were made of Notch mutants. Since both "point" and
deficiency mutants are known at this locus, reversion rates in point mutant homozygotes and
point/deficiency heterozygotes could be compared. The point mutant tested was N^{40} and the
deficiency was N^8 . Welshons' (Genetics 47:743, 1962) selector system was used to kill
almost all Notch offspring in the following crosses:

1 + $w^a N^{40} rb/Y w^a N^{40} +; Cy, Dp, bw^v/+ \text{ } \varnothing \times w^a fa^{no} spl/Y; Cy/Pm \text{ } \sigma$
2 $w^a N^{40} rb/+ N^8 +; Cy, Dp, bw^v/+ \text{ } \varnothing \times w^a fa^{no} spl/Y; Cy/Pm \text{ } \sigma$

In one series of experiments, females were radiated with 4000 rads of γ -rays.

15 females and 10 males were mated in quarter pint bottles and 30 bottles per tray.
The flies were transferred through 2 or 3 six day broods. All bottles were checked daily
for offspring from the 10th to the 20th day of the culture. Any possible revertants were
testcrossed to $w^a fa^{no} spl rb$ flies. The number of matings is summarized in the following
table.

Brood Number	Non-irradiated		Irradiated	
	N^{40}/N^{40}	N^{40}/N^8	N^{40}/N^{40}	N^{40}/N^8
1	6 trays	11 trays	12 1/2 trays	7 trays
2	10 trays	11 trays	12 1/2 trays	7 trays
3	2 trays	5 trays	1 tray	--
Total	18 trays	27 trays	26 trays	14 trays
Gametes Sampled	180,000	270,000	108,250	56,700

The number of gametes tested was estimated by crossing test females to Oregon-R males and
counting the number of offspring produced per bottle, the estimate being based on the sum of
half the number of females and all males. No revertants were found in an estimated 450,000
gametes in the non-irradiated and 165,000 gametes in the irradiated series.

While the selector system is relatively efficient, the task of setting up sufficient
numbers of crosses to yield large numbers of test females and males proved too great. Since
it is quite possible that Notch point mutants are of the "shift" type, the system described
should be feasible where facilities and technical help are abundant. (This research was
supported by NRC grant A-1764.)

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Persistence of some recessive lethal genes
in natural populations of *D. melanogaster*.

Many lethal chromosomes (the second
chromosome) were isolated from different
male flies collected simultaneously from
natural populations located at Kofu and
Katsunuma locality in Yamanashi Prefec-
ture in October 1963 and 1964. A total of

16,086 crosses were performed diallelly between the lethal - Curly balanced strains.

The results of allelism tests were divided into three parts; two of them represented

crosses within lethal strains extracted at the same time and the third represented crosses between new and old lethal strains extracted in successive years. The results are given in Table 1.

Table 1. Results of allelism tests between lethal genes isolated from the Kofu and Katsunuma populations in 1963 and 1964.

Year	1963(Middle of Oct.)				1964(late in Oct.)			
Population	Kofu	Katsunuma	Between pops.	Whole loc.	Kofu	Katsunuma	Between pops.	Whole loc.
No. of lethal chr.	61	53	114	114	31	43	74	74
No. of crosses	1830	1378	3233	6441	465	903	1333	2701
No. of allelic c.	60	30	80	170	18	33	55	106
Allelic rate (%)	3.28	2.18	2.47	2.64	3.87	3.65	4.13	3.92
No. of lethal chr.	97				72			
No. of crosses	6984							
No. of allelic crosses	185							
Allelic rate (%)	2.65							

The Kofu and Katsunuma populations are about thirteen kilometers apart from each other, and vineyards occupy the large part of the intervening area. These populations of *D. melanogaster* were very large. The allelic rate between lethals isolated from the different populations was relatively high as compared with those within the populations. The allelic rate between new and old lethals isolated in the successive years was also high. These results could be due to persistence of some common lethal genes distributed in both natural populations.

These common lethal genes were found frequently as shown in Table 2, and most of them were located with a paracentric inversion C or B on a chromosome.

Table 2. Frequent lethal genes isolated from the Kofu and Katsunuma populations and their linked inversion.

Symbol of lethal gene	Frequency of appearance and their linked inversion			
	1963		1964	
1201	13	+ or In(2R)C	6	+ or In(2R)C
1202	8	+ or In(2R)C	6	+ or In(2R)C
1203	6	+	3	+ or In(2R)C
1204*	6	+	7	+ or In(2R)C
1207*	4	+ or In(2L)B	2	+
1208	3	+	1	+

+ standard chromosome (no inversion)

* these lethal genes had been found in 1959.

The frequency of these persistent lethal genes was about 35 per cent of the total number of isolated lethal genes. Two lethals, symbolized 1201 and 1202, were found to be located individually on different chromosomes in 1963 and also in 1964, but these lethal genes were found to be located together on the same chromosome in 1964.

The viability of heterozygotes for these persistent lethal chromosomes and the various kinds of chromosomes (normal, subvital, semi-lethal and lethal) was estimated by using Cy-Pm technique. For the latter, about ten chromosomes were taken randomly from ones of each class. The results are represented in Table 3.

Table 3. Relative viabilities of normal and persistent lethal heterozygotes.

	Mating				Pooled basis	
	N	SV	SL	L'	No. of counted flies	Relative viability
N	N/N	N/SV	N/SL	N/L'	103,035	1.0537 ± 0.00929
L	L/N	L/SV	L/SL	L/L'	161,218	1.0585 ± 0.00748
LL	LL/N	LL/SV	LL/SL	LL/L'	52,625	1.0618 ± 0.01304

The viability of Cy/Pm fly = 1.0000

N:normal SV:subvital SL:semi-lethal L':lethal chromosomes

The viabilities of flies having a single or double lethal chromosome in heterozygous state were slightly higher than that of heterozygotes for a normal chromosome. Although their increases are not significant statistically, it can be said that these persistent lethal chromosomes would not manifest any deleterious effect in combining with various kinds of chromosome. As long as a lethal gene is associated with an epistatic gene complex, including a heterotic inversion, it would be exempted from natural selection.

Ménsua, J. L. University of Barcelona, Spain. Y chromosome effect on inter-ocellar bristles in *D. melanogaster*.

Wolsky (1958) has pointed out the possibility that a polygenic system is involved in the genetic control of inter-ocellar bristles in *D. melanogaster*, as generally happens with many of the quan-

titative characters, and that some genes are situated on the Y chromosome. This last point was deduced by making reciprocal crosses between two *D. melanogaster* strains, with different averages of interocellar bristles, and finding on F₁ an intermediate average among the daughters, whereas the sons had an average more similar to their sires in each cross.

In one experiment carried out with a *D. melanogaster* wild strain from Prat de Llobregat (Barcelona), kept at 17°C in a population-box for 8 months, a clear-cut effect of the Y chromosome on these bristles was found. The experimental procedure was as follows: 80 pairs of flies were crossed at random, 35 eggs of each pair were put in each vial in order to avoid over-crowding. The temperature was set at 17° ± 0.5°C during the experiment. From F₁ 4 males and 4 females of each family were counted, and the offspring-parent regression and the partials regressions daughter-dam, daughter-sire, son-dam and son-sire were calculated, revealing the following results:

Offspring-Parent	b = 0.389 ± 0.079	t = 4.924	P < 0.001
Son-Dam	b = 0.083 ± 0.091	t = 0.912	P ≈ 0.3
Son-Sire	b = 0.307 ± 0.063	t = 4.873	P < 0.001
Daughter-Dam	b = 0.179 ± 0.092	t = 1.945	P ≈ 0.05 *
Daughter-Sire	b = 0.216 ± 0.070	t = 3.085	P ≈ 0.005

* In spite of the fact that the significance level for 0.05 is t = 1.99, we can consider this regression significant.

We can see, on one hand, that the son-dam regression coefficient is not significant, but on the other, the son-sire regression is very significant. Therefore we can conclude that the Y chromosome, which is the only factor received by the sons from the sire, and not from the dam, is the responsible one of these differences between both regressions and that in the Y chromosome where is polygenic activity. But also there is polygenic activity on interocellar bristles on the other chromosomes because the regressions between daughter-dam and daughter-sire are also significant.

In order to see if there was a Y chromosome effect on abdominal and sternopleural bristles, the partial regressions in these bristles were calculated, but no effect at all was found.

References: Wolsky, A., 1958. The formation of interocellar bristles in *D.m.* Proc. Calcutta Zool. Soc., 11:1-7

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