live yeast in nature at the food source to mate, and it is essential to provide them with live yeast in studying mating behavior. This fact has been mentioned by Manning and others in the past, but no data have been published heretofore on this point.
(This work was supported by Contract No. AT(30-1)-1775, U.S. Atomic Energy Commission at University of Pittsburgh.)

Lifschytz, E., and R. Falk. The Hebrew University, Jerusalem, Israel. A new system for fine structure analysis of genes in Drosophila.

In recent years a number of systems for high power resolution of recombination and back-mutation have been described for Drosophila. We constructed a system for high power resolution analysis based on the lethal interaction between pn and K-pn and on lethals in the X-chromosome, covered by segments of the X-chromosome translocated to the Y-chromosome. The stages that were involved in the construction of the system will be described elsewhere. Only the final system is given here:

a. $\frac{y^2\ pn^i\ cv\ l^{B57}}{F\ M\ 6\ (1)} \times \frac{pn^j\ l^{3des}}{Y\cdot\ pn^-w^+}$

b. $\frac{y^2\ pn^i\ cv\ l^{B57} + \quad +}{pn^j \quad + l^{3des}};\frac{}{+} \times \frac{v\ g\ l^{B57}\ l^{3des}}{Y\cdot\ ma\text{-}l^+};\frac{ca\ K\text{-}pn}{ca\ K\text{-}pn}$

The system includes two stages:
a. The stage for large scale "automatic" collection of virgin females.
b. The stage for the detection of recombinants in heterozygotes for different pn-alleles or of back-mutations in homozygotes for a single pn-allele.

It is easy to see that all progeny should die, excluding males that are recombinants (or back-mutants) in the pn-locus and females that are recombinants between the lethals or products of non-disjunction in the fathers.

For the "automatic virgin" system the lethals were chosen so that one was proximal enough to be covered by both $w^+\cdot Y$ and by $ma\text{-}l^+\cdot Y$, while the other was somewhat more distal, thus covered only by the $ma\text{-}l^+\cdot Y$-chromosome. We verified that the frequency of non-disjunction was low and that the lethals did not produce "Durchbrenners" even under the uncrowded conditions that prevailed when most larvae died. The lethals were chosen so that there was about 0.5% crossing-over between them, so that there were enough viable progeny per culture (3-10 females) to facilitate the eventual single rare recombinant between pn-alleles. Furthermore, since the frequency of recombination between the lethals was predetermined, the number of females per culture served to estimate the total number of zygotes that had been produced.

In order to minimize the work involved, we found it best to use 20 pairs of flies per mating in 1/4 litre culture bottles (somewhat above the optimum) and to transfer the parents twice to fresh cultures, after they stayed for 4 days in the old ones. Only a sample of the bottles was etherized and from them the mean number of females per culture was determined. In the remaining bottles the presence of males was checked by inspection without etherization. Analyses of 1.2×10^6 zygotes may be carried out routinely by a single technician.

Preliminary analyses resolved the pn-locus into three sites: $pn^1\text{-}pn^2, pn^{59j}\text{-}pn^{AA1}$.

A somewhat modified system in which the recombinants between pn-alleles were the female progeny and the recombinants between the lethals were the male progeny was also constructed. With proper selection of lethals these systems may be utilized also for analyses of other events in the chromosome, such as unequal crossing-over or negative interference.