The second program in this series is a statistical analysis program called GENCHI. Basically, this program performs the same functions as the second portion of ILUVFLYS except that it is oriented toward the analysis of the student's actual laboratory data rather than compu ter generated data.

To reinforce the students' understanding of basic transmission genetics utilized in ILUVFLYS an informal quiz program called FLYQUIZ forms the third program in the package. In this program the student is asked a series of multiple choice questions which must be answered correctly before the computer will proceed to the next question. The questions are arranged in order of increasing difficulty and include the topics of segregation, independent assortment, sex-linkage and linkage.

All three of the programs in this package are written in the CALL-OS version of FORTRAN IV. ILUVFLYS is 565 lines long (17069 bytes), requires four seconds of CPU time, and usually requires about 10 minutes of student time to run. GENCHI is 280 lines long (8259 bytes), needs two seconds of CPU time, and can be run in about four minutes by the average student. FLYQUIZ has 306 lines in the program (13272 bytes), requires two seconds of CPU time, and requires approximately 15 minutes for the typical student to run. For users with appropriate access, these programs are presently available in the CALL-OS ***library of New Jersey's Educational Computer Network. For individuals without access to this network, but with a sincere interest in utilizing one or more of the above programs, we will be pleased to supply program listings, sample runs and/or punched paper program tapes.

References: King, R.C. 1967, Genetics, Oxford, New York; Klug, W.S. and D. Weller 1972, DIS 49:134; Strickberger, M. 1962, Experiments with Drosophila, John Wiley, New York.

Pye, Q., D. Knipple and R. MacIntyre.
Cornell University, Ithaca, New York.

Construction of segmental deficiency stocks from Y-autosome translocation stocks.

Many Drosophila workers have used the Y-autosome translocations of Lindsley and Sandler et al. (1972) to localize autosomal structural genes coding for enzymes based upon the gene-dosage-dependent enzyme activity in segmental trisomics and monosomics. Once a structural gene is localized, x-ray induced deficiencies spanning the locus can be generated in order to screen for all null activity mutants.

We have obviated the induction of deficiencies with x-rays by constructing strains carrying segmental deficiencies generated from crosses between different T(Y:A) stocks. A basic cross scheme which can be used to construct a strain with a segmental deficiency is shown in Fig. 1.

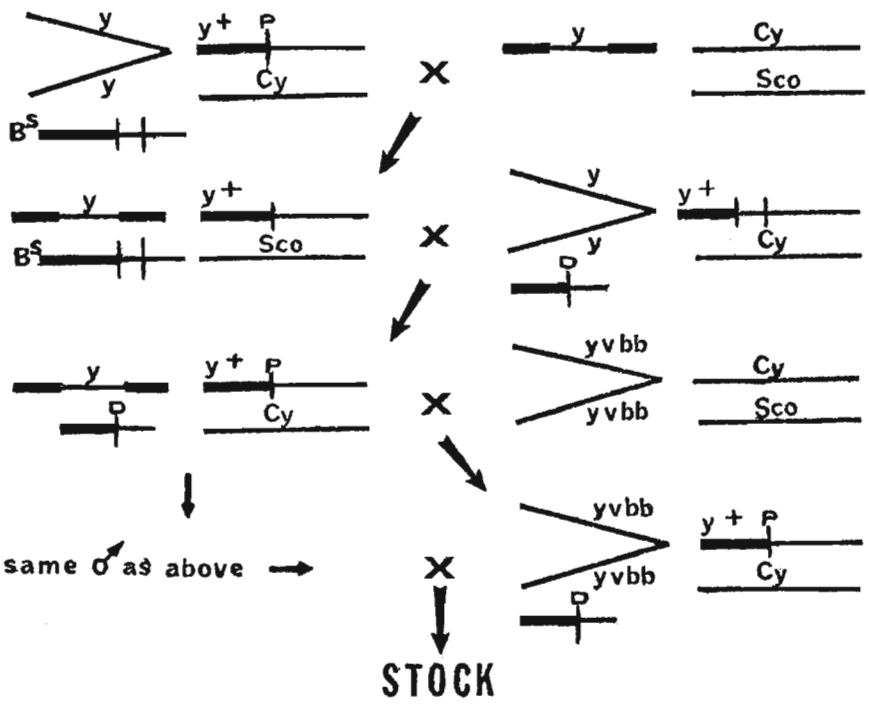

Fig. 1. P = proximal breakpoint; D = distal breakpoint; wide bars = Y chromosome material; attached X chromosomes are C(1) RM; ♂♂ used in generation 1 are $Y^{S}X.Y^{L}$, In (1) EN, y/In (2LR) SM1/Sco.

Deficiency stocks constructed in this manner may exhibit the following phenotypes: y, y^{+}, $y^{+}y^{+}$, y B^{S}, B^{S}, depending upon the location of the breakpoints and the markers present in the Y chromosomes of the T(Y:A) stocks used. In some crosses it is not possible to distinguish the deficiency class from other classes on the basis of phenotypes. It is therefore necessary to make

many (20-100 depending on the markers present and the extent of the deficiency to be generated) single male matings in step 3 of the cross scheme. These males are saved and subsequently mated to their daughters (we have informally designated these males "Big Daddies" or "Dirty Old Men"). The use of single males is also required because the frequency of 3:1 disjunction occurring in this cross scheme can be as high as 10% resulting in euploid individuals which can be phenotypically indistinguishable from the deficiency class. These lines can be tested for the presence of the deficiency by their ability to uncover biochemical, recessive lethal or visible loci.

We have constructed overlapping deficiency stocks which cover the entire region from 25E to 26A (B137 to D211). We have used the following designation for these deficiencies: TDf(Y:2) followed by the designations according to Lindsley and Sandler et al. (1972) of the two translocations used to generate the deficiency, e.g. T Df(Y:2) H69 D211.

There are a number of possible explanations for the failure to produce some segmental deficiency stocks: (1) triplications of Y chromosome material may result in male sterility; (2) deficiency females may not be produced due to the absence of a bb^+ locus in the translocated Y chromosome elements (this problem can be circumvented by initially using a bb^+ C(1) RM in the series of crosses); and (3) the extent of autosomal material which can be deleted is dependent upon the regions involved or the presence of haplo- insufficient loci in the region.

Pye, Q. Cornell University, Ithaca, New York. New white-eyed Drosophila "unknown" stocks for genetics laboratory courses.

In his teaching note MacIntyre (DIS 51:158) discussed the utility of some phenotypically identical (orange eye, dark body and incomplete wing veins) but genotypically unique Drosophila "unknown" stocks for genetics laboratory courses. I have constructed a set of "unknown" stocks that are comparable to his, except that they all have white eyes. White eyes are due to three different situations, (1) the interaction of bw, bw^D, or w^{Bwx} with cn, st or v, (2) the epistatic interaction of w with ca, bw, st, bw^D or v, or (3) the allele w. Another difference between the orange and white-eyed stocks is that some of the white unknowns contain two wing vein mutations (e.g. shf^2; ve or ve ri) that interact to produce the wing phenotype.

Sved, J.A. Sydney University, Australia. A computer program which saves on cooking and washing up.

Any genetic mapping experiment that can be attempted in a one-term course is usually restricted to one in which students are given stocks already built up, and asked to carry out a limited crossing program. Such an experiment usually provides more intellectual exercise for the person setting up the program than for the student, since the student has little opportunity to plan crosses, synthesize required stocks, etc. This note describes briefly the use of computer simulation to enable quite complicated "experiments" to be carried out. Most students seem to enjoy the exercise, and hopefully learn a little genetics in the process.

The philosophy of the program is to simulate as closely as possible the problems faced in an actual mapping experiment. Most importantly, the program manipulates genotypes according to Mendelian principles, but displays only phenotypes rather than genotypes to the student. The program generates for each student a different unknown visible mutant, which may lie anywhere in the genome. A set of about 30 markers is provided, mostly recessives but with some dominants and balancers, and the student has to synthesize any stocks required to localize the unknown mutant. It takes 12-15 generations to get to the stage of constructing and carrying out a three-point testcross with markers reasonably close to the mutant. If one generation is run each day, the exercise therefore takes a minimum of 3 weeks. In practice, few students seem to be able to get through in anything like the minimum time. Each student is also provided with a recessive lethal, the mapping of which constitutes a more advanced exercise.

The simulation as described above uses as data the crosses supplied by the students, who have to be taught how to input crosses (instructions are supplied by the program). The program can also be used in a simpler way that is more suitable for larger elementary classes,