Williamson, R.L. City of Hope Medical Center, Duarte, California. A notation for genetic mosaics.

A notation which allows a genetically mosaic fly to be symbolized is long overdue. This can be accomplished simply by separating the geno- types by double oblique strokes. Thus, for in- stance, y w/o//y w/+ + is a gynandromorph whose male side carries yellow body and white eyes and whose female side is heterozygous for these mutations. y w/o;4/o//y w/+ +;4/4 is a more complex mosaic involving loss of the fourth chro- mosome on the male side. X-irradiation of a y w/+ + fly during development might cause the formation of a y w/y w//+ +/+ +//y w/+ + individual by somatic recombination.

This notation is simple, immediately understandable and can be found on any typewriter. It has been used previously in the abstracts listed below.

References: Williamson, R.L. and W.D. Kaplan 1976, Genetics 83:s82; Kaplan, W.D., W.E. Trout and C. Parseghian 1978, XIV Int. Cong. of Genetics, Moscow, Contrib. Papers I:552; Trout, W.E., P. Wong and R. Williamson 1978, XIV Ing. Cong. of Genetics, Moscow, Contrib. Papers I:566.

TEACHING NOTES

Bryant, S.H. Western Illinois Univer- sity. Salivary preparations from D. pseudoobscura.

I have found that the use of D. pseudoobscura rather than D. melanogaster is much easier for salivary preparations. The larvae are much larger, and so are the salivary glands. Stu- dents also have a much easier time extracting the glands from D. pseudoobscura than they do from D. melanogaster. While not as many interesting chromosome aberrations are available in D. pseudoobscura, one excellent balanced lethal stock is available which has a very nice sin- gle inversion loop in chromosome 2. This stock is Λ/Ba: Delta/Bare^{Inv}.

Klug, W.S., G.Nicholls and T.W. Kottke, Trenton State College, Trenton, New Jersey. Drosophila transmission genetics computer package.

General genetics courses often include the per- formance of some Drosophila genetics laboratory experiment. Strickberger (1962) and King (1967) discuss the manner in which the appropriate crosses are executed in order to identify an unknown mutation in this organism. Klug and Weller (1972) earlier reported the development of a Drosophila transmission genetics experi- ment simulation program for student use. Written in BASIC-PLUS for the Resource Time Sharing System of the PDP-11 family of computers, this program was intended to complement the actual student laboratory exercise rather than replace it. A new, expanded version of this program has now been written for use with an IBM CALL-OS timesharing system. Two additional programs have been written so that a complete computer based learning package for Drosophila transmis- sion genetics now exists.

The computer simulation package consists of three separate yet interrelated programs. ILUVFLYS, the first computer program that the student uses, serves two functions. During the first encounter with ILUVFLYS the student is randomly assigned one of 25 unknown recessive mu- tations. Homozygous mutant females are independently crossed with male flies with a marker gene on either the second or third chromosome respectively. Two generations are carried out for each cross and the student is supplied with number-coded phenotypes of the offspring. From the phenotype ratios of the offspring the student should be able to determine on which chromo- some the unknown trait is found. The number of offspring supplied for each generation is be- tween 150 and 250, randomly assigned by the computer at the time of the run.

Once the student has counted the number of flies in each phenotype class the ILUVFLYS program may be recalled for a statistical analysis of the data. This second portion of ILUV- FLYS computes the observed class ratios, the chi square statistic for the observed and expec- ted ratios, and provides the probability value that the observed deviation has occurred on the basis of chance.

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 computer 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.

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
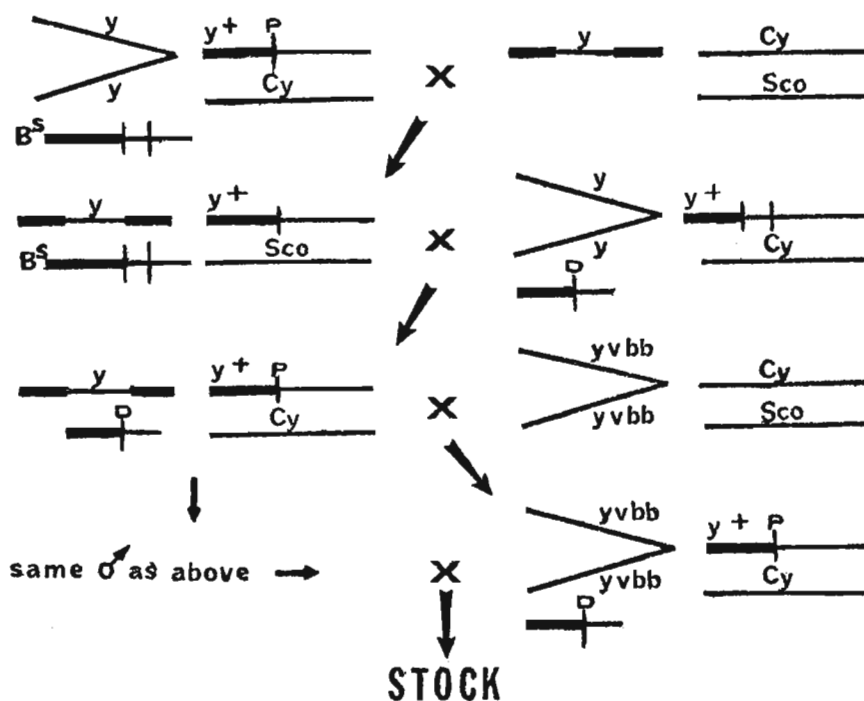

Fig. 1. P = proximal breakpoint; D = distal breakpoint; wide bars = Y chromosome material; attached X chromosomes are C(1) RM; ♂♂ used in generation 1 are $Y^S X \cdot Y^L$, In (1) EN, y/In (2LR) SM1/Sco.