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Many general genetics courses utilize some form of a *Drosophila* transmission genetics experiment in the laboratory. Such an experiment can take on a number of forms and many provide the student with an unknown mutant stock. The student's exercise is to localize the unknown gene

on its appropriate linkage group. This can be accomplished in several ways. The mutant females may be crossed with males from a multiply marked stock containing a series of dominant genes such as *Cy/Pm;H/Sb* (Strickberger, 1962, p. 53). The cross is then carried to an F_2 generation after selecting F_1 males and performing a back cross to mutant females. Alternatively, two simultaneous but separate crosses may be made where mutant females are mated to males marked with a recessive gene on either of the two major autosomes (King, 1967 p. 429) and carried to the F_2 generation.

In either case, if the crosses are properly executed, the unknown gene may be unequivocally located on its proper chromosome. Such an exercise may precede a mapping exercise, a prediction of the locus and finally a confirming allelism test.

This paper describes a computer program which simulates the localization of the linkage group of an unknown recessive mutant gene by the previously described "two cross" method. Such a program may be utilized as an effective teaching technique in several ways. It may be applied during the initial phases of the actual laboratory experiment to reinforce the students' understanding prior to their data collection or when time is the essence or no laboratory is included in the course, it can effectively replace the laboratory work.

The simulation was written in RSTS (Resource Timesharing System) BASIC-PLUS, an advanced BASIC language used by the PDP-11 family of computers. For convenience of execution, it is divided into four parts: 1) an instructor's program, 2) the F_1 exercise, 3) the F_2 exercise, and 4) a Chi square analysis.

The instructor's program is used to set up an information file for any number of unknown mutants. The file contains an identification number, the linkage group, and a phenotypic description for each unknown.

The F_1 program randomly selects an unknown from this file each time the program is run. The readout provides the user with the identification number, the phenotypic description, and F_1 data for two crosses between the unknown female and a recessive marker male from the II and III linkage group. The 300-500 offspring for each cross are number keyed for all eight possible male and female phenotypes and the data code numbers are printed in rows of varying length which finally assume the shape of a half-pint milk bottle. Since all of the unknowns are recessive, the F_1 results are of one of two types. If the unknown is sex-linked, only wild type females and unknown mutant males result. If the unknown is an autosomal gene, all F_1 offspring for both crosses are wild type. In the former case, the gene has been localized on the X-chromosome.

If the unknown mutant is determined to be autosomal, the user can then call up the F_2 program and input the identification number of his unknown. This program provides the $F_1 \times F_1$ data for both of the original crosses, using the same number coding system for the phenotypes and printing the data in the same bottle shape. These data, when analyzed, provide the necessary information for the determination of the linkage group in question.

Both programs are designed to simulate the normal probability distributions encountered in an actual experiment and therefore give different numbers of offspring and different random variations from the ideal phenotypic ratio each time the program is run. These deviations from the ideal may be analyzed with the separate Chi square program which can provide χ^2 values for any data analysis, including actual laboratory work.

We have found this to be a valuable experience for general genetics students. The entire three programs may be completed in 15 minutes and can be run any number of times by the same student. In addition to simulating the transmission experiment it assures that all students at this educational level will have at least an introduction to the use of the computer.

If you have a sincere interest in applying such a simulation to your genetics teaching, we will be pleased to provide you with the programs as written in BASIC-PLUS for use with our PDP-11/20 timesharing system.

References: King, R.C. 1967, *Genetics*, Oxford, N.Y.; Strickberger, M. 1962, *Experiments with Drosophila*, John Wiley, N.Y.