

A COMPUTER PROGRAM TO CALCULATE EXPECTED FREQUENCIES AND TO ESTIMATE PER CENT RECOMBINATION IN A DIHYBRID F_2 WITH LINKAGE IN THE COUPLING PHASE AND VARIOUS TYPES OF LETHAL INHERITANCE.—A Scatran program, designated BT635A, has been written for the IBM 7094 computer of The Ohio State University. This program allows the user to select any one of 9 modes of inheritance (8 of which involve lethal genes, but all of which involve two loci, with two alleles at each locus), an initial value (PS) of the recombination frequency between the two loci, and a decrement value (D) by which amount the initial recombination frequency is to be reduced successively until one of the following conditions obtains:

1. Further reduction would result in a negative recombination frequency, or
2. Nine reductions have been accomplished. (Subsequent reduction of the recombination frequency may be accomplished by additional data cards, providing the recombination frequency does not become negative.)

The program computes the expected genotypic and phenotypic frequencies for the F_2 generation of a dihybrid cross in the coupling phase (AB/ab x AB/ab), for the specified type of inheritance, and for the specified recombination values as determined by the values of PS and D.

The types of inheritance which may be selected are:

1. No lethal genotypes.
2. AA lethal—Semidominant lethal.
3. bb lethal—Recessive lethal.
4. AA and bb lethal.
5. AA and BB lethal.
6. aa and bb lethal.
7. *a* as a unisexual gamete(ophytic) lethal.
8. *a* as a unisexual gamete(ophytic) lethal and bb is lethal also.
9. *a* as a unisexual gamete(ophytic) lethal and BB is lethal also.

Input is in the form of punched cards; output is in the form of printed paper. The program contains a data-checking routine in which the values on each data card are inspected to see that the input parameters are within the proper ranges. If the data-checking routine detects an error on any data card, an appropriate error diagnostic is printed and processing of the input variables on that card is deleted. However, the detection of one or more data composition errors does not prevent processing of any data cards whose input parameters are within the proper ranges.

By appropriately setting the values of PS and D, one may obtain one of the following matrices as output.

1. A 9-by-10 frequency matrix, where the columns correspond to values of the recombination frequency, the rows correspond to the genotypic classes, and the elements of the matrix are expected frequencies. In addition, a 10-element row vector for each of 5 phenotypic classes will be produced, wherein the elements are expected frequencies of the phenotypic classes.
2. A 2-by-10 frequency matrix, where the first column contains elements that are the expected frequencies for the initial recombination value and the second column contains elements that are the expected frequencies for no recombination between the loci.
3. A column vector of expected genotypic frequencies corresponding to the initial recombination value.

Thus the program allows the expected frequencies to be computed for a wide range of situations, from a recombination frequency of 0.50 (independent assortment) with no lethals to a recombination frequency as low as 0.00000001 with a as a unisexual gamete(ophytic) lethal.

BT635A contains the option of receiving, as part of the printed output, up to twelve separate graphic print-outs of an X-Y coordinate system, where the ordinate represents the recombination value and the abscissa represents the frequency of recovery of a given phenotypic or genotypic class in the F_2 . The twelve graphic print-outs which may be obtained are the recombination frequency on any one, or all, of the four phenotypic classes and/or the 9 genotypic classes. There are only twelve genotypic classes instead of thirteen because the aabb genotypic class is regarded as the fourth phenotypic class.

The graphic print-outs provide an estimate of the recombination frequency in the following manner. One simply locates the observed phenotypic frequency on the abscissa, projects it parallel to the ordinate until the plot is intersected, then projects from this intersection, parallel to the abscissa, to the ordinate axis. The value where the second projected line crosses the ordinate is an estimate of the recombination frequency between the two loci. The program is ideally suited for use as a teaching device in an intermediate-level course in genetics, in which the students are interested in becoming professional biologists with a wider background in genetics than that which may be obtained from only an introductory course in heredity. By using the program, the student gains an insight into the simultaneous effects of lethal inheritance and linkage on the frequencies with which various genotypic and phenotypic classes occur, effects which the student might otherwise fail to study because of the rather laborious computations that are required when the two-locus genetic model includes lethality of certain gene groups and dependent assortment of the loci at meiosis.

The basic idea was conceived and developed by the junior author and has been used by him in teaching Plant Genetics each Autumn quarter since 1950. The senior author has developed and tested the computer program. Free computer time was supplied by the Computer Center of The Ohio State University. Copies of the program materials and a more detailed description and documentation of the program are available upon request from the authors.—RUSSELL V. SKAVARIL, *Department of Zoology and Entomology*, and ELTON F. PADDOCK, *Department of Botany, The Ohio State University, Columbus, Ohio*.
