

A.L.T.Perera

Dept. of Agric.Biology, Faculty of Agriculture  
University of Peradeniya

A complete genetic analysis was undertaken at the Department of Genetics, University of Birmingham, U.K., on a computer simulated population of a crop plant. At the beginning, no information about the population was available, but it was possible to obtain any kind of data from it to carry out any of the genetic designs available to a breeder.

Initially, to study the characteristics of the distribution, several random samples of individuals were taken to test for skewness and kurtosis. By comparing the means of an inbred sample and a biparental progeny sample it was possible to identify the type of mating system.

A genetic analysis of the basic generation by model fitting technique indicated absence of epistasis.

The gene frequency was determined by considering the mean of inbred samples and  $m$  obtained by Cavalli test.

Four genetic designs were used to analyse components of variation viz Biparental Progeny, NCMI, NCMII and TTC. The TTC gave independent estimates of  $D$  &  $H$  which were the most accurate. From the results of these designs it was possible to estimate the number of loci and number of effective factors contributing to the character.