

There appeared to be some association between the segregation of the borer resistance gene and that of the virescent and glossy genes. Some information on the genetic linkage value or cross-over percentage between these loci can be obtained from the glossy-virescent class of the  $F_2$ . If all susceptible plants in this class are assumed to have resulted from the union of two cross-over gametes, the cross-over frequency can be estimated as the square root of the percent of the total glossy-virescent  $F_2$  plants which rated 7 to 9. The cross-over estimate obtained in this case was 37 percent. Likewise, of 121 susceptible plants 14 plants or 11.6 percent were either glossy, virescent, or both. These also can be considered the result of the union of two cross-over gametes and can be used to estimate the percent crossing over. In this case the estimate obtained was 34 percent.

The data for the M14 x  $gl_7 v_{17}$  cross are presented in Table 2. In the  $F_2$  population 105 of 401 plants rated 7 to 9 for corn borer leaf feeding, and an additional 15 plants rated 6. Unless a rather high proportion of the plants rating 6 were assumed homozygous for susceptibility, the ratings did not deviate significantly from what would be expected from segregation at a single locus. In the backcross to M14 165 of 322 plants rated 7 to 9 approximating very closely the 50 percent expected from segregation of a single gene pair.

Linkage of the borer resistance gene with the  $gl_7 v_{17}$  genes was indicated again in this cross. Of the 102  $F_2$  plants which were both glossy and virescent, 10 rated 7 to 9 for borer leaf feeding. Likewise, 11 of the 105 susceptible  $F_2$  plants were either glossy or both glossy and virescent. Using the same assumptions and calculations as explained for the other cross, estimates obtained for the cross-over percentage were 31 and 32.

The data from both crosses could be interpreted similarly. Resistance appeared dominant in both cases and appeared to be conditioned by a single pair of genes. This gene pair was linked with the  $gl_7$  and  $v_{17}$  genes of chromosome 3 with cross-over values estimated at from 31 to 37 percent.