WHEAT-BUNT FIELD TRIALS, II

GEORGE A. BAKER AND FRED N. BRIGGS

UNIVERSITY OF CALIFORNIA, DAVIS

1. Introduction

In the study of inheritance of resistance to bunt, *Tilletia tritici*, in wheat it is necessary to grow F_3 progenies from F_2 plants in order to determine the genotype of the latter. This is necessary because all susceptible plants in a population usually do not show evidence of the disease under prevailing conditions. Such susceptible plants merely escape infection and do not differ genetically from those which exhibit bunt. Some trials are further complicated by the fact that some heterozygous and occasionally some homozygous-resistant plants become diseased.

Briggs [2], [3], [4][1] has shown that there is little difficulty in distinguishing the three genotypes (homozygous-susceptible, heterozygous, and homozygous-resistant) in crosses when the parents differ by a single dominant factor for resistance to bunt if F_3 rows of 50 plants each are grown. Even with 50 plants per row, however, there are usually a few rows which cannot be positively classified. The proportion of infected plants in both heterozygous and homozygous-susceptible rows of 50 plants usually exhibit a range of about 0.50. When parents differ by two or more factors for resistance, as reported by Briggs [2], the overlapping of the proportions of infected plants in rows of 50 belonging to the different genotypes makes it difficult, if not impossible, to recognize the rows belonging to the various genotypes. Thus, genetical analysis under these conditions may be very unsatisfactory.

For these reasons it is important to consider the question of whether the variability in bunt infection among rows of a given genotype can be accounted for on the basis of sampling error, and whether this variability would decrease according to random-sampling expectations as the number of plants per row increased. A decrease in variability ensures that the limits of the three genotypes are more certainly defined when a single-factor difference exists. If the decrease in variability is sufficient, a greater number of genotypes can be recognized when more factors are involved. An alternative approach to analyzing the more complicated crosses on the basis of classifying rows with respect to genotype would be to set up a theoretical distribution, using the necessary factors with the proper mean effects and variabilities, to fit the observed distribution of proportions of infected plants. In order to set up such a theoretical distribution, it is necessary properly to evaluate the expected variability of proportions of infected plants of each genotype for rows of a given length or number of plants.

Salmon [6] has shown that the theoretical binomial sampling error will not account for the variation in bunt infection among wheat varieties. He found it necessary to increase this error by a factor a, which varied for different environmental conditions and levels of infection.

---

[1] Boldface numbers in brackets refer to references at the end of the paper (see p. 491).