Complementarity of genes for resistance to greenbug

\[ \text{[Schizaphis graminum (Rondani)], biotype E, in sorghum [Sorghum bicolor (L.) Moench]} \]

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Summary. Gene complementarity among various sources of resistance to greenbug biotype E was assessed. Analysis of the F$_2$ generation of crosses between susceptible and resistant parents (mating 1) and among sources of resistance (mating 2) suggested that resistance in sorghum to greenbug biotype E was complexly inherited and, to some extent, dependent on the nature of both the resistant and susceptible parents. Positive transgressive segregation in the F$_2$ generations of both matings was found to be due to effective plus factors, contributed by both parents in a cross, which complemented each other. The number of plus factors ranged from one to two in the susceptible parents and from two to five in the resistant parents of mating 1, and from one to five in the parents of mating 2. The consistently significant reciprocal effects shown by Sarvasi and PI264453 indicated that these sources had major factors for resistance in their cytoplasm, which were expressed in all their crosses. The results from this study indicated that the sources of resistance complemented each other to give increased number of F$_2$ segregates with increased resistance. Thus, it should be possible to increase and diversify resistance of sorghum to greenbug biotype E by accumulating different, effective plus factors from various sources through recurrent selection.

Key words: Transgressive segregation – Epistasis – Frequency distribution – Castle-Wright formula – Number of effective factors

Introduction

One of the major economic pests of sorghum in the USA is the greenbug \[ \text{[Schizaphis graminum (Rondani)]}. \] This aphid has been a destructive pest of sorghum \[ \text{[Sorghum bicolor (L.) Moench.]} \] since 1968 when biotype C developed (Harvey and Hackerott 1969; Hackerott and Harvey 1971; Teetes and Johnson 1973). Since then, sorghum breeders have attempted to genetically manipulate exotic resistant germ plasm to develop agronomically acceptable, insect-resistant, high-yielding hybrids. Resistant hybrids have several advantages. They are economical for the producer; they are specific to the target species; they leave no harmful residue in foods or in the environment; and they are compatible with biological, chemical, and other control methods.

By 1980, at least 90% of the sorghum acreage in the US was planted to resistant hybrids. Then, biotype E developed and overcame the majority of the known sources of resistance within sorghum germ plasm (Porter et al. 1982). Greenbug resistance of sorghum had been reported by many researchers to be simply inherited and incompletely dominant (Boozaya-Angoon 1983; Hackerott et al. 1983; Teetes 1975; Weibel et al. 1972). Recently (Dixon et al. 1990), 12 new exotic sources of resistance to greenbug biotype E, including the four sources previously resistant to biotype C, have been identified. To effectively utilize these new sources in a breeding program and diversify the resistance when transferred into elite materials, it is essential to compare the genetics of resistance among various sources. By combining genes that relate to different sources and/or mechanisms, we may identify epistatic interactions such that higher levels of resistance can be developed to protect sorghum from a future biotype change. The specific objectives of this study were: (1) to determine if genes for resistance to
greenbug biotype E combine complementarily in crosses, and (2) to investigate if whole plant resistance is influenced by reciprocal effects.

Materials and methods

Genetic material

Seven sources of resistance [IS2388, Sarvasi, PI264453, PI220248, PI229828, N50735, and N43172] and three inbred lines (Redlan, Wheatland, and Tx2536) of sorghum susceptible to greenbug biotype E were used as parents in this study. All possible crosses, including reciprocals, were made between the susceptible lines and the sources of resistance (mating 1) and among the sources of resistance (mating 2). The parents and F2 generations from the matings were evaluated for plant resistance to greenbug biotype E in a greenhouse, using the flat screening technique (Starks and Burton 1977). The greenhouse was kept at an average temperature of about 30°C and a photoperiod regime of 14 h.

Design and management of experiments

The sorghum entries were grown in a randomized complete block with six replications in galvanized metal flats (35.6 x 50.8 x 9.53 cm) with a soil mixture. Each flat had ten equidistant rows of about 25 plants per row; five rows were assigned to the test entries and were alternated with rows of a susceptible check, Rex 16-6. All entries were uniformly infested with five greenbugs per plant at the two-leaf stage (about 9 days after planting). Greenbug biotype E of various ages, cultured on a susceptible commercial hybrid (NC + 630-X), was used. The greenbugs were allowed to feed, develop, and reproduce until the susceptible check rows were dying; this typically took between 11 and 14 days. Then, whole plant resistance was measured by visually rating individual plants on a scale from 1 to 9, representing the percentage of damage incurred: 1 = 0 - 10; 2 = 11 - 20; 3 = 21 - 30; 4 = 31 - 40; 5 = 41 - 50; 6 = 51 - 60; 7 = 61 - 70; 8 = 71 - 80; and 9 = 81 to death of the plant.

Statistical analysis

A positive transgressive segregate was defined as an F2 progeny rated at least one damage class lower than the average damage class of the better parent. The average damage score of a parent or a cross was defined as the summation of the product of the frequency count and the value of the damage class, divided by the total number of plants evaluated. The frequency distribution of the F2 generation was used to determine the relative percentage of transgressive segregates. The number of independently segregating, effective factor pairs was estimated by using the Castle-Wright formula (Castle 1922; Wright 1968). Lawrence and Frey (1976) argued that the range of F2 segregates was a more appropriate estimate of (P1 - P2) when the parents did not represent the genotypic extremes for the segregating loci. Therefore, the range between the extreme F2 segregates (R) was used, instead of the parental range. In this study, the variance of each F2 from a cross contained some nonadditive genetic variance and, hence, the formula used (Lawrence and Frey 1976) to estimate the minimum number of effective factors (n) is represented as:

\[ \hat{n} = \frac{R^2}{8 \sigma_p^2}, \]

where \( R \) = range of the F2 segregates in the cross and \( \sigma_p^2 \) is the genetic variance. Thus, the number of factors affecting a trait contributed by each parent in a cross was estimated.

The number of favorable factors in the poorer parents was calculated as:

\[ \hat{n} = \frac{(X_b^0 - X_{pl}) + (X_{p2} - X_w)}{2} \times \frac{N}{R}, \]

where \( n \) = number of plus (favorable) factors contributed by the poor parent, \( X_b \) = score of the best segregate of the cross, \( X_{pl} \) = score of the better parent of the cross, \( X_{p2} \) = score of the poor parent of the cross, and \( X_w \) = score of the poorest F2 segregate of the cross. The number of favorable factors in the better parent was obtained by subtraction, and because the number of factors estimated was the minimum, the number was approximated to the next largest integer.

The ANOVA statistics (\( df = R - 1 \)) of the Cochran-Mantel-Haenzel Chi-square were used to determine significant differences in the distribution of F2 scores among the various sources of resistance, and to test for reciprocal differences in the F2 distribution of the crosses.

Results and discussion

The resistant parents used in this study did not represent the genotypic extremes, but showed intermediate levels of resistance to greenbug biotype E (Dixon et al. 1990). The range was between 4.5 for both PI229828 and N43172 and 6.2 for Sarvasi (Table 1). If a score of 1 to 6 is considered resistant, then Sarvasi would be classified as susceptible. The susceptible lines Redlan, Wheatland, and Tx2536, as expected, were in the susceptible range. The range of the sources of resistance was only 1.7, yet with a few exceptions, the segregating F2 generations resulting from resistant-by-susceptible crosses (mating 1) and from resistant-by-resistant crosses (mating 2) showed no tendency to fall into distinct classes (Tables 1 and 2).

Transgressive segregation was observed in F2 progenies of both mating 1 (Table 3) and mating 2 (Table 4). Only positive transgressive segregates (at least one damage score lower than the better parent) are shown. Crosses involving Sarvasi, the poorest of the resistant sources, had the highest frequency of transgressive segregates for both the resistant-by-susceptible and the resistant-by-resistant crosses. A high frequency of positive transgressive segregates was found in crosses of Redlan with N50735 and PI220248. The frequency of transgressive segregates was generally higher in the F2 progenies of crosses between the susceptible and resistant parents, when the resistant parents were used as females. There were a number of reciprocal differences in the frequency of transgressive segregates in mating 2 (Table 4). The crosses among resistant parents generally had a higher frequency of positive transgressive segregates than the crosses between susceptible and resistant parents.

The presence of transgressive segregation in this study constituted further evidence for multiple-factor control for resistance, which involved different alleles in different parents and was cumulative for degree of resistance. The Castle-Wright formula was used to estimate the mini-