# INHERITANCE OF BIOTYPE E GREENBUG RESISTANCE IN BREAD WHEAT CI 17882 AND ITS RELATIONSHIP WITH WHEAT STREAK MOSAIC VIRUS RESISTANCE\*

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Received 20 September 1985

#### INDEX WORDS

Triticum speltoides, Aegilops speltoides, Triticum aestivum, wheat, Schizaphis graminum, greenbug, wheat streak mosaic virus, insect biotypes, host plant resistance.

### SUMMARY

Genetic studies were conducted to determine the inheritance of biotype E greenbug resistance in CI 17882 (CI 15092/T. speltoides//Fletcher/3/4\* Centurk), a wheat germplasm line previously released as resistant to wheat streak mosaic virus (WSMV). In addition, the association of greenbug and WSMV resistance in CI 17882 was examined. Results indicated that biotype E greenbug resistance in CI 17882 is conditioned by a single dominant gene that is not linked with the WSMV resistance gene.

## INTRODUCTION

The greenbug, Schizaphis graminum (Rondani) is a serious pest of wheat, Triticum aestivum L. em. Thell. The periodic occurrence of new virulent greenbug biotypes has made the development of greenbug-resistant wheat cultivars difficult. 'Dickinson No. 485' (CI 3707), has a recessive gene that confers resistance to biotype A (Curtis et al., 1960), but not to biotypes B (Wood, 1961), C (Harvey & Hackerott, 1969), and E (Porter et al., 1982). 'Amigo' (CI 17609) a wheat germplasm line released by Sebesta & Wood (1978) has a single dominant gene located on wheat chromosome 1A (Hollenhorst & Joppa, 1983) derived from 'Insave F.A.' rye (Secale cereale L.) that provides resistance to biotypes A, B, and C. The latest greenbug variant was discovered in 1980 and designated as biotype E. Resistance to biotype E, derived from T. tauschii (Coss.) Schmal., has been identified in amphiploids of T. turgidum/T. tauschii ('Largo', CI 17895) (Joppa et al., 1980) and T. durum/T. tauschii (CI 17959) (Martin et al., 1982). Greenbug resistance in 'Largo' is inherited as a single dominant gene (Joppa et al., 1980) located on chromosome 7D (Hollenhorst & Joppa, 1983).

<sup>\*</sup> Cooperative research of the USDA, Agricultural Research Service and the Oklahoma Agricultural Experiment Station. Journal article 4845 of the Oklahoma Agric. Exp. Stn., Oklahoma State Univ., Stillwater, OK 74078.

Resistance to biotype E was identified in wheat germplasm lines CI 17882, 17884, and 17885 (Tyler et al., 1985) that previously had been released by Wells et al. (1982) as resistant to wheat streak mosaic virus (WSMV). The lines are from the cross CI 15092/T. speltoides//'Fletcher' (CI 139851/3/5\* 'Centurk' (CI 15075). The T. speltoides (Tausch) Gren. ex Richter parent was determined to be the donor of the greenbug resistance. The WSMV-resistant parent, CI 15092, is a 42-chromosome wheat line that has a disomic substitution from Agropyron intermedium (Host.) Beauv.

The research reported here was conducted to determine the inheritance of greenbug resistance in CI 17882 and to investigate the association of WSMV and greenbug resistance.

## MATERIALS AND METHODS

Inheritance of greenbug resistance. CI 17882 was crossed with the greenbug-susceptible cultivars, TAM 105 (CI 17826) and Newton (CI 17715). CI 17882 plants used in crosses were confirmed to be homozygous for biotype E greenbug resistance by progeny testing. Reactions of plants from F1, F2, F3, and backcross generations of both crosses to biotype E infestations provided phenotypic ratios which were used to estimate the mode of inheritance of greenbug resistance. Data from the F2, F3, and backcross generations were tested by the chi-square goodness of fit test. Checks included in the tests were biotype C resistant 'Amigo', biotype E resistant 'Largo', the susceptible parents 'TAM 105' and 'Newton', and the resistant parent CI 17882.

Plants were evaluated for greenbug resistance using methods similar to those described by STARKS & BURTON (1977). The F1, F2, F3, and backcross seeds and seeds of checks were planted in rows in uncaged greenhouse flats containing a 3:1:1 soil, peat moss, sand mix. When the seedlings were in the one-leaf stage (ca. 4 to 8 cm in height) they were infested with biotype E greenbugs at the rate of 10 to 15 greenbugs per plant. Reinfestations were made as needed to maintain proper greenbug numbers. Greenbugs used were from greenhouse cultures that are checked periodically to confirm biotype identity. About two weeks after infestation susceptible plants were chlorotic and stunted. Most of the susceptible plants eventually died. Resistant plants maintained their green color and showed little or no damage. Only resistant F2 plants were saved to derive F3 lines. Greenbug tests were conducted in the fall in a greenhouse with no suplemental lighting, and with temperatures ranging from 18 to 25°C.

Association of WSMV and greenbug resistance. To examine the association of WSMV resistance and greenbug resistance in CI 17882, 16 F3 lines from each cross from the greenbug inheritance study were evaluated for WSMV resistance. The 32 F3 lines were derived from greenbug resistant F2 plants that had not been evaluated for WSMV resistance. A standard linkage test that requires evaluation of testcross or F2 plants for both traits was not done because it is not feasible to test a seedling for its reaction to greenbugs and WSMV. Both test procedures severely weaken susceptible seedlings, and even the resistant seedlings become stressed which may result in invalid susceptible readings in the second test. Reactions of F3 lines were used to identify the genotypes of F2 plants for both traits. A chi-square test for independent inheritance of two genes was done.

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Progenies from the crosses 'TAM 105'/CI 17882 and 'Newton'/CI 17882 were evaluated for WSMV resistance. The parents, F1, and F2 plants, and the 32 F3 lines from those crosses were included in the test. There were 25 seeds per row planted in flats containing sterilized soil. A susceptible parent and the resistant parent, and seven rows of progenies from the genetic populations were planted in each flat. The test was conducted in the fall in a greenhouse under the conditions described previously.

Plants were inoculated with WSMV at the 2 to 3 leaf stage. Inoculum was prepared from infected plants grown in a greenhouse. Equal weights of water and fresh leaf tissue from infected plants were placed in a blender and the leaf tissue was ground. The mixture was then strained and a fine abrasive was added to the liquid. A commercial paint gun attached to an air compressor was used to spray the plants with inoculum.

WSMV symptoms on susceptible plants were first noticed about one week after inoculation. Symptoms appeared as yellowish-green chlorotic streaks on newly developed leaves. Plants within each F3 line were scored as resistant or susceptible.

#### RESULTS AND DISCUSSION

Inheritance of greenbug resistance. Reactions of parent, F1, F2, check, backcross plants and F3 lines from the crosses 'TAM 105'/CI 17882 and 'Newton'/CI 17882 are shown in Table 1. All plants of the susceptible parents, 'TAM 105' and 'Newton', were susceptible and all CI 17882 plants were resistant. The resistant reactions of all 'Largo' plants and susceptible reactions of all 'Amigo' plants confirmed that the test greenbugs were biotype E. Resistant reactions of all F1 plants from both crosses indicated complete dominance of greenbug resistance in CI 17882. Complete dominance was also indicated by the backcross data where the ratio of resistant to susceptible plants from the crosses 'Newton'/2/'Newton'/CI 17882 and 'TAM 105'/2/'TAM 105'/CI 17882 gave a close fit to a 1:1 ratio.

Table 1. Reaction of parent, F1, F2, and backcross plants and F3 lines from the wheat crosses 'TAM 105'/CI 17882 and 'Newton'/CI 17882 to biotype E greenbug infestation.

Cultivar, line or cross	Generation	Res. +	Seg.	Sus.	Ratio to be tested	$\chi^2$	P
Amigo		0		83			
Largo		96		0			
TAM 105		0		108			
Newton		0		123			
CI 17882		166		0			
TAM 105/CI 17882	Fl	42		0			
·	F2	459		137	3:1	1.28	0.20-0.30
	F3	31	49		1:2	1.05	0.30-0.50
	Backcross	16		18	1:1	0.11	0.70-0.90
Newton/CI 17882	F1	34		0			
	F2	421		133	3:1	0.29	0.50-0.70
	F3	29	48		1:2	0.64	0.30-0.50
	Backcross	19		22	1:1	0.22	0.50-0.70

<sup>&</sup>lt;sup>+</sup> Res. = resistant, Seg. = segregating, Sus. = susceptible.

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Table 2. Reaction of parent, F1, and F2 plants and F3 lines from the wheat crosses 'TAM 105'/CI 17882 and 'Newton'/CI 17882 to wheat streak mosaic virus infection.

Cultivar, line or cross	Generation	Res. +	Seg.	Sus.	Ratio to be tested	$\chi^2$	P
TAM 105		0		45			
Newton		0		67			
CI 17882		107		0			
TAM 105/CI 17882							
Newton/CI 17882							
Crosses pooled*	F1	14		4			
•	F2	33(19+14)	•)	9(4+5)	3:1	0.28	0.50 - 0.70
	F3	5(1+4)	22(12+10)	5(3+2)	1:2:1	4.50	0.10-0.20

<sup>&</sup>lt;sup>+</sup> Res. = resistant, Seg. = segregating, Sus. = susceptible.

The numbers of resistant and susceptible F2 plants for both crosses suggested a 3 resistant: 1 susceptible ratio, which indicates that greenbug resistance in CI 17882 is conferred by a single dominant gene. Segregation of F3 lines from resistant F2 plants in both crosses suggested a 1 resistant: 2 segregating ratio, which also indicates a single dominant gene.

Results of this genetic study show that greenbug resistance in CI 17882, derived from *T. speltoides*, is simply inherited. Resistance is also simply inherited in those cases documented: in the hexaploid wheat DS 28A, Insave F.A. rye, and *T. tauschii*. Single gene traits are easily handled in breeding programs, and transfer of greenbug resistance in CI 17882 to adapted wheat genotypes should be possible. Since major genes conferring greenbug resistance have been identified in relatives of common wheat, and since genetic-cytogenetic techniques allow interspecific and in some cases intergeneric crosses, it is important to continue research on wheat relatives in an attempt to identify new sources of greenbug resistance. This research is especially important because of the frequent occurrence of new greenbug biotypes.

Association of WSMV and greenbug resistance. After performing a heterogeneity chisquare test (Table 2, footnote), information from both crosses was pooled. Reactions of parent, F1, F2 plants, and F3 lines to WSMV infection are shown in Table 2. All CI 17882 plants showed resistant reactions, whereas all 'TAM 105' and 'Newton' plants were susceptible. Reactions of F1 plants indicated that WSMV resistance in CI 17882 is incompletely dominant. Reactions of F2 plants to WSMV infection strongly suggest a 3 resistant: 1 susceptible ratio, which indicates that CI 17882 has a single dominant gene for resistance to WSMV. These results are consistent with those of WANG & LIANG (1977). They reported that WSMV resistance in CI 15092, the donor of WSMV resistance in CI 17882, is conditioned by a major dominant gene derived from A. intermedium and that full expression of resistance requires a complementary dominant gene located on a wheat chromosome. In our study, no attempt was made to distinguish different levels of resistance within the resistance class. The plants were

<sup>\*</sup> Numbers in parenthesis are the number of plants from each cross, 'TAM 105'/CI 17882 and 'Newton'/CI 17882, respectively. Heterogeneity chi-square values and corresponding P values for pooling F2 and F3 data are  $0.44 \, (P = 0.50-0.70)$  and  $1.50 \, (P = 0.30-0.50)$ , respectively.

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Table 3. Distribution of F2 genotypes from the wheat crosses 'TAM 105'/CI 17882 and 'Newton'/CI 17882 for reaction to biotype E greenbugs and wheat streak mosaic virus.

Genotype <sup>+</sup>	Number of F2 plants		$\chi^2$	P	
	observed	expected*			
GgWw	13	10.66			
GĞWW	2	2.66			
GGWw	9	5.33			
GGww	3	2.66			
GgWW ·	3	5.33			
Ggww	2	5.33			
-8	_		6.34	0.20-0.30	

<sup>&</sup>lt;sup>+</sup> G and g indicate alleles conferring greenbug resistance and susceptibility, respectively. W and w indicate alleles conferring WSMV resistance and susceptibility, respectively.

classified as either resistant or susceptible.

Of the 32 F3 lines tested with WSMV, 14 were resistant and 18 segregated for reaction to biotype E greenbug (Table 3). Of those lines, 5 were resistant, 22 segregated, and 5 were susceptible for reaction to WSMV (Table 2) approaching a 1:2:1 pattern (P = 0.10-0.20). A 1:2:1 segregation pattern of F3 lines is expected for a trait controlled by a single gene if the F3 lines are derived from F2 plants selected at random. The implication is that selection of greenbug resistant F2 plants was essentially random selection for WSMV resistance, therefore, suggesting that the two genes assort independently. The observed numbers of F2 plants of each genotype, and the expected numbers if the genes are not linked are shown in Table 3. The expected values are based on a 1:2:1 expectation for WSMV reaction and a 1:2 expectation for greenbug reaction. The chi-square value of 6.34 with five degrees of freedom (P = 0.20-0.30) is not in disagreement with independent inheritance of the two genes.

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<sup>\*</sup> Expected numbers if the genes are inherited independently, based on 1:2:1 and 1:2 patterns for WSMV and greenbug reaction, respectively, giving a 4:1:2:1:2:2 expected pattern. F2 plant genotypes were confirmed by F3 progenies.

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