

**EFFECTS OF *FUSARIUM* RESISTANCE GENE ON
AGRONOMIC TRAITS OF COTTON**
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Abstract

Fusarium wilt is one of the most important diseases of *Gossypium hirsutum* L. and causes heavy damage in all cotton growing areas of China. Resistance to the disease is controlled by one dominant gene in upland cotton. It is easy to transfer the resistance gene into susceptible cultivars, but whether the resistance gene has deleterious effects on cotton agronomic traits is unknown. In this experiment, five pairs of resistant- susceptible near isolines were used to evaluate the genetic effects of cotton *Fusarium* resistance genes on agronomic traits in heavily infested and non-infested fields. Three genotypes with gene Fw2 or fw2 under J1 or E18 background derived from a backcross introgression program. The other 2 pairs, J1R/J1S, and E18R/E18S were selected in the heavily infested fields for resistance or susceptibility. The resistance identification of 5 pairs of near-isolines indicated the two methods of developing resistant-susceptible near-isolines were effective. Susceptible lines yield less because of fewer and smaller bolls, lower lint percentage and low density. Generally there were no significant differences between each pair of the near-isolines, except that one pair differed significantly in seed index and fiber length. The results indicated that the resistance gene Fw2 has no deleterious impact on agronomic traits (including plant height, number of fruit branches, boll size, seed index, lint index, and lint percentage) and fiber quality (including fiber length, strength, elongation and fineness). It should be determined if the resistance gene in J1R affects 2.5% fiber span length.

Key words: Cotton, *Fusarium* wilt, resistance gene, genetic effects, near-isogenic line.

Introduction

Fusarium wilt, caused by the seedborne and soil-inhabiting fungus, *Fusarium oxysporum* f. sp. *vasinfectum* (Atk.), is one of the most important diseases in upland cotton (*Gossypium hirsutum* L.) and a major cause of economic losses in almost all cotton growing areas of the world. More than one-third of the cotton in China area is infected by *Fusarium* wilt, and annual losses of lint caused by *Fusarium* wilt and *Verticillium* wilt exceed 70,000~90,000 tons (Shen, 1992). The most effective way to control this disease is to plant resistant cultivars, and more than 200 resistant varieties and lines have been developed (Feng et al., 1996a). Genetic research results suggest that in upland cotton, one dominant gene controls resistance to *Fusarium* wilt (Netzer et al., 1985; Feng et al., 1996b), and two different resistance genes have been identified (Feng et al., 1998). It is easy to transfer the resistance gene to varieties susceptible to *Fusarium* wilt or to pyramid these two genes into one variety to provide longer and stronger resistance. But, it is still unknown whether the resistance gene has deleterious effects on cotton agronomic traits or not. The purpose of this paper is to study the genetic effects of *Fusarium* wilt resistance genes on the economic traits of cotton.

Materials and Methods

Breeding of Near Isolines

Five pairs of *Fusarium* resistant – susceptible near-isolines of cotton were generated by two methods. Two susceptible cotton varieties Ejing1 and

Emian18 were planted in an infested field in 1993, and resistant and susceptible individual plants were screened and selfed. All seeds from resistant plants were mixed into a resistant group and seeds from susceptible plants into a susceptible group. Both groups were planted in a heavily infested field and again re-selected in two directions in subsequent seasons. After 5 rounds of selection, two resistant-susceptible near-isolines, J1R/J1S, E18R/E18S were developed. In 1992, Ejing1 was crossed with varieties Zhongmiansuo12 and Sumian 3, respectively, both with resistance gene Fw2. Emian18 was also crossed with Zhongmiansuo12. These crosses were then backcrossed with the two susceptible cultivars as recurrent parents for four generations. Resistant and susceptible plants were screened from the progenies of these three populations and selfed once in 1997. From them, three pairs of resistant –susceptible near isolines, 8301R/8301S, 8302R/8302S and 8303R/8303S, were developed.

Field Experiment

The experiment was conducted on the farm of Huazhong Agricultural University, Wuhan, China. All 5 pairs of near-isolines were planted in both non-infested and inoculated fields with *Fusarium oxysporum* f. sp. *vasinfectum* race 7, the predominant one in China (Shen, 1992). The experimental design was a randomized complete block with two replications. During the growing season, 10 plants were evaluated for plant height, number of fruiting branches, and number of bolls. From each plot 25 bolls were harvested to determine boll weight, lint index, seed index and lint percentage. Fiber quality was measured with high-volume instrumentation (HVI) 900 system.

Statistic Analysis

ANOVA and LSD test were used to determine differences among treatments or between the means of each pair of near-isolines.

Results and Discussion

Evaluation of Resistance and Agronomic Traits

The resistance identification results are shown in Table 1. The percentages of wilted plants in susceptible lines were higher than 85%, ranging from 85.71~92.00%, the disease index ranged from 54.39 to 72.12, and nearly a quarter to more than a half of the seedlings died of the wilt disease. All these lines were subject to the disease. However, the disease index of the 5 resistant cotton lines were less than 5, no plant died of the wilt disease, the percentages of wilted plants were lower than 10%. These results suggested that these lines had a high level of resistance to *Fusarium* wilt (Figure 1~3), however the resistance was not equal to immunity since not all plants escaped the disease.

Susceptible varieties may contain resistance genes in the population, and the relatively low frequencies of resistance genes and resistant genotypes can be increased through continuous selection. In China, many cultivars were developed by systematic selection from susceptible germplasm, especially in the 1950s' to 1970s' (Feng et al., 19996). Such selection provides an effective way to generate resistant-susceptible near-isolines in addition to the introgression methods. While developing these lines, only the characters – resistant or susceptible to disease – were selected consciously, so other characteristics were selected randomly. Therefore, we can treat each pair of lines as near-isolines according to their response to the *Fusarium* wilt disease.

The yield components and some morphological traits might be compensated by larger space, which may lessen the differences among the resistant and susceptible lines. However, differences were still detected among the means of the 5 pairs of near-isolines for 4 characteristics: plant height, numbers of bolls, boll size and lint percentage. The plant height of three resistant lines J1R, E18R and 8302R were 110.5cm, 120.6cm and 114.6cm, significantly higher than those of their counterpart susceptible lines, which were 98.5cm, 98.5cm and 96.6cm (Table 2). The bolls of the

three resistant lines were larger than their susceptible near-isolines (5.3g, 5.2g, 5.4g vs. 4.8g, 4.7g, 4.8g). The resistant lines bore more bolls than those of susceptible lines except for 8301R, which did not differ from 8301S. However, the lint percentage of 8301R (43.6%) was significantly higher than that of 8301S (41.2%). According to the results of this experiment, the yield of susceptible lines in a heavily infected field was decreased due to fewer and smaller bolls and lower lint percentage, as well as a lower density of the plant population. Effects of *Fusarium* wilt on fiber quality were reported previously (Shen, 1992), but no effects were detected in this experiment.

Genetic Effects on Agronomic Traits

Analysis of variance of 12 characteristics indicated that there were differences among the means of the 10 lines in 5 characteristics: number of fruiting branches, lint index, 2.5% span length, fiber uniformity, fiber strength. But differences were only found between the means of some pairs in the seed index and fiber 2.5% span length. The seed index of 8301S was 9.6g, and that of 8301R was 8.5g (Table3), the former being significantly larger. The 2.5% span length of J1S (29.6mm) was significantly longer than that of J1R (27.7mm). But no difference could be detected between the means of these two characteristics in other pairs of near-isolines.

Theoretically, the genetic effects of a gene on other characteristics may be due to two reasons. One is the linkage of the target gene with another unidentified gene, which may affect the performance of agronomic traits. The other one is possible pleiotropic effects.

Either the resistance gene or the background was the same in 8301R and 8302R. No difference was found between the means of seed index in 8302R and 8302S. So the effects are thought to result from linkage drag instead of the effect of resistance gene Fw2. Allelism of the resistance gene in J1R and Fw2 should be tested. If it is the same resistance gene in J1R, the effect on 2.5% fiber span length could also come from the linkage drag. If not, then the resistance gene in J1R might affect 2.5% span length in some genetic backgrounds.

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Table 1. Identification of resistance to *Fusarium* wilt in 5 pairs of near-isolines .

Lines	Wilted Plants		Dead Seedlings		Disease Index
	Percentage (%)	Percentage (%)	Percentage (%)	Percentage (%)	
J1R	8.99	0.00	0.00	4.49	
J1S	92.00	41.33	41.33	67.00	
E18R	5.95	0.00	0.00	2.68	
E18S	85.71	35.06	35.06	59.09	
8301R	7.46	0.00	0.00	4.10	
8301S	86.49	24.32	24.32	54.39	
8302R	8.70	0.00	0.00	4.71	
8302S	86.96	49.28	49.28	68.12	
8303R	8.82	0.00	0.00	4.78	
8303S	87.18	53.85	53.85	72.12	

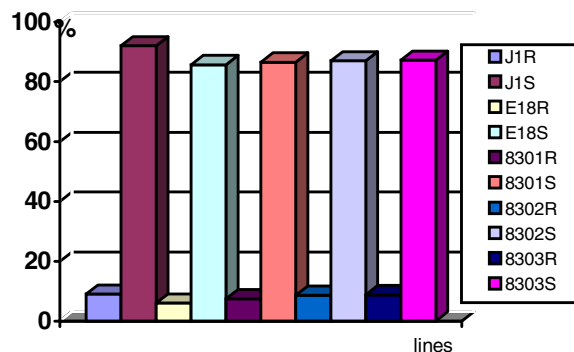


Figure 1. The percentages of wilted plants of 5 pairs of near isolines.

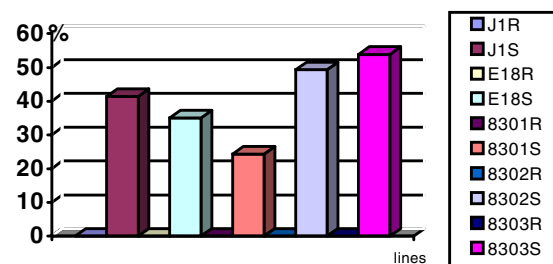


Figure 2. The percentages of dead seedlings of 5 pairs of near-isolines.

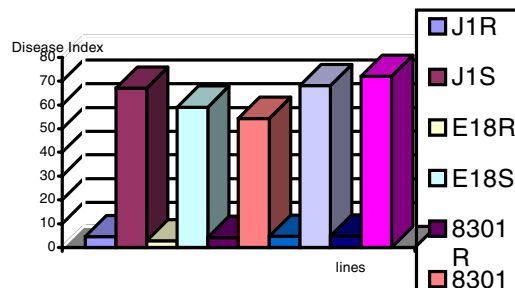


Figure 3. Disease index of 5 pairs of near-isolines.

Table 2. Agronomic traits of 5 pairs of isolines in a heavily infected field

Line	Plant height (mm)	No. of branches	No. of bolls	Boll size (g)	LI (g)	SI (g)
J1R	110.5	16.0	23.1	5.3	7.5	9.4
J1S	98.5	13.4	11.3	4.8	7.4	9.3
E18R	120.6	16.4	16.3	5.2	7.2	9.8
E18S	98.5	13.4	11.0	4.7	7.1	9.2
8301R	110.1	14.9	18.7	5.1	7.5	9.3
8301S	104.8	16.6	14.2	4.9	7.3	9.6
8302R	114.6	17.7	19.4	5.4	7.3	10.0
8302S	96.6	15.3	14.3	4.8	7.1	9.6
8303R	111.7	14.6	19.2	5.0	7.3	9.5
8303S	104.2	15.2	9.3	4.8	6.9	9.2

Line	Lint %	2.5% SL (mm)	UR (%)	T1 g/tex	E1	Mic
J1R	43.0	28.5	47.7	20.7	6.4	5.6
J1S	44.4	27.7	47.4	18.5	5.3	4.7
E18R	43.9	28.8	47.7	21.6	6.5	5.2
E18S	42.8	27.4	49.0	20.6	6.3	5.0
8301R	43.6	27.7	49.0	21.6	6.5	5.0
8301S	41.2	28.6	46.4	20.6	6.3	5.0
8302R	42.6	28.8	46.9	21.6	6.4	4.6
8302S	42.8	27.5	49.1	21.7	6.4	5.0
8303R	42.3	28.0	49.1	22.5	6.6	5.0
8303S	42.7	27.0	49.5	21.3	6.4	5.2

Table 3. Agronomic traits of 5 pairs of isolines in a non-infected field

Line	Plant height (mm)	No. of branches	No. of bolls	Boll size (g)	LI (g)	SI (g)
J1R	103.6	14.8	16.6	5.1	6.6	8.8
J1S	98.9	13.5	16.7	5.4	6.9	8.7
E18R	101.7	13.1	16.5	5.4	6.8	9.7
E18S	101.7	13.4	16.8	5.3	6.9	10.1
8301R	106.3	15.3	17.4	4.9	6.5	8.5
8301S	106.3	15.9	18.0	5.1	7.1	9.6
8302R	107.7	15.1	15.4	5.2	7.0	9.5
8302S	106.3	14.9	15.0	5.0	7.3	9.9
8303R	108.6	14.6	15.1	5.3	6.6	9.6
8303S	103.1	13.9	14.9	5.1	6.7	8.9

Line	Lint %	2.5% SL (mm)	UR (%)	T1 g/tex	E1	Mic
J1R	41.9	27.7	49.9	23.3	7.3	5.4
J1S	41.9	29.6	48.3	22.6	7.0	5.2
E18R	41.8	28.3	49.7	24.9	7.9	5.4
E18S	41.0	27.1	50.3	24.9	7.8	5.3
8301R	42.9	27.2	49.5	21.7	6.9	5.4
8301S	40.7	28.1	48.0	21.4	6.6	5.2
8302R	41.5	28.6	48.1	22.8	6.8	5.2
8302S	41.6	28.0	49.2	23.0	6.9	5.2
8303R	41.9	27.3	49.1	23.4	7.3	5.2
8303S	41.0	26.4	51.4	22.3	7.1	5.5