RACE IDENTIFICATION AND SEVERITY OF BACTERIAL BLIGHT FROM NATURAL INFESTATIONS ACROSS THE COTTON BELT

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Abstract

Bacterial blight of cotton is caused by *Xanthomonas campestris* pv *malvacearum* (*Xcm*), and affects all plant parts resulting in defoliation and thus yield loss. Infected leaves was collected from several regions in the Cotton Belt including North Carolina, Louisiana, Missouri, New Mexico and several locations in Texas. The pathogen was isolated from the diseased tissue and *Xcm* race identified based on disease reactions of a set of ten host differentials. The most virulent race 18 was the predominate race isolated from diseased tissue from all states. However, race 2 was isolated from disease tissue of cotton plants grown in Weslaco from seed that originated from Uzbekistan. The use of resistant cultivars is the most effective method for controlling bacterial blight in cotton.

Introduction

Xanthomonas campestris pv *malvacearum* (Smith) Dye (*Xcm*), the bacterial blight pathogen of cotton, can survive in and on planting seed and on undecomposed plant debris. Thus, the bacterium can be disseminated when such materials are moved about by wind, water, insects or field equipment. Losses of 10 to 30% are often experienced in Asian and African countries. Yield losses could be as high as 50 to 70% in severe epidemics; where extensive leaf, stem, and boll infection occur (Hillocks 1992). Bacterial blight caused an estimated average yield loss of 1.5% annually in the United States from 1952 to 2000, with a range of 0.1% to 2.3%. In areas where bacterial blight occurs, sanitary practices during ginning and processing, using acid-delinted and fungicide treated seed, disposal of residues from the previous crop have minimized the potential loss in yield and fiber quality caused by *Xcm.* Management in areas where sanitation practices can be controlled, and where it is practical to enforce regulations governing these actions such as California can eradicate the pathogen. In most areas of the cotton growing regions it is impossible if not impractical to use only management for control. Consequently, the use of resistant cultivars is considered the most economical and effective means of controlling bacterial blight (El-Zik and Thaxton 1989).

At least 20 major genes for resistance to *Xcm* have been reported (Hillocks 1992; Verma 1986). The majority of genes identified have been described as partially to completely dominant for resistance. Researchers (Bird 1982; Bird 1986; Brinkerhoff 1970; El-Zik and Thaxton 1989; Hunter et. al, 1968; Innes 1974; Knight 1944) have reported on the effectiveness of specific "*B*" genes and gene combinations in conferring resistance, and provided evidence of the effect of the genetic background and modifier genes on enhancing resistance. The MAR program has been successful in transferring genes for resistance into adapted cottons. The MAR germplasm has combinations of the B_2, B_3, B_4, b_6 and B_7 genes for resistance. Based on DNA mapping of the resistant genes, the B_2 and B_3 genes were mapped on chromosome 20 supporting data suggesting linkage between B_2 and B_3 genes (Wright et. al. 1998). The B_{12} gene was mapped on chromosome 14 (Wright et. al. 1998).

For the past five years, over 75% of the cotton acreage in Texas was planted to cultivars susceptible to bacterial blight. For the past several growing seasons, a progressive increase in disease incidence of bacterial blight has been observed in parts of the Cotton Belt. There is a need to identify the current races of the bacterial blight pathogen in the different cotton growing regions, and to determine levels of resistance to specific races in currently grown and new cotton cultivars. The objective of this research was to identify and ascertain the status of predominate race(s) of the bacterial blight pathogen currently in cotton fields across the Cotton Belt.

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Materials and Methods

Infected leaves of susceptible cotton plants were collected from cotton growing fields in Louisiana, Missouri, New Mexico, North Carolina, and Texas. Leaf tissue also was collected from susceptible cotton cultivars grown in Weslaco that originated from Uzbekistan. Diseased leaf tissue was surfaced sterilized with 70% ethanol, rinsed in sterile water and placed in five mls of sterile water and macerated (Thaxton and El-Zik 1993). The disease tissue and water was agitated for several minutes to make a bacterial suspension. The bacterial suspension was then streaked over the surface of Potato Carrot-Dextrose Agar (PCDA). After three days, individual colonies were transferred and maintained on PCDA at the College Station multi-adversity resistance (MAR) laboratory at 22°C and transferred every 14 days.

Race identification of *Xcm* isolates is based on disease reaction on a set of upland (*Gossypium hirsutum*) host differential strains (Bird 1986; Hunter et. al. 1968). The host differentials are Acala 44, Stoneville 2BS9, Stoneville 20, Mebane, 1-10B, 20-3, 101-102B, Gregg, Empire B-4 and DP-P4. Inoculum was prepared from 5-day old cultures by placing a small amount of the bacterial growth inside a small glass vial and diluting it with sterile water to produce an inoculum density of approximately 1.0×10^6 cfu/m. The host differential strains were planted in the greenhouse and cotyledons of the ten host differentials were inoculated using the toothpick method with a separate scratch for each isolate. In addition, known control races 1, 2 and 18 of the pathogen were inoculated onto each seedling. Each scratch was graded 10 days after inoculation based on a grading system of 1 to 10 [1 representing immunity progressing to 10 for severe susceptibility (Bird 1982; Hunter et. al. 1968; Thaxton and El-Zik 1993)], and designated as being susceptible or resistant on a host differential. A disease grade of 1 represented immunity, 2 to 3 resistance, while a grade of 4 to 10 represented degrees of susceptibility. Based on disease reactions on the ten host differentials, a race number (1-19) was identified for each isolate.

Results and Discussion

Isolates were obtained from the disease tissue at the different locations. Grades resulting from the inoculation of the isolates on the host differentials are shown in Table 1. Disease grades of isolates from tissues ranged 1.0 (resistant reaction) to 8 (susceptible reaction). With the exception of Weslaco, all isolates had a positive or resistant reaction on all host differentials except 101-102B. The isolate from Weslaco was positive on Acala 44, Stoneville 2BS9, Stoneville 20 and Gregg and gave a negative reaction on the other host differentials.

Based on disease reactions and comparing the isolates to the host differential reaction table, the isolates from North Carolina, Missouri, New Mexico and three locations in Texas were identified as race 18 (Table 2). The isolate from the Uzbekistan cultivar was identified as race 2. The control races 1, 2 and 18 confirmed their designated race. Since Xcm is a seed-borne disease, the bacteria was endemic to the seed from Uzbekistan when it was planted. We reported in 1992 that the predominate race in Texas cotton fields also was race 18 (Thaxton et al. 1992).

Race 18 is the most virulent race of *Xcm*. New cultivars with high levels of resistance to pathogens are essential for the survival and future progress of the cotton growers and industry in the United States. The results of this research will be useful in determining the major races and virulence of the

bacterial blight pathogen in the Cotton Belt and help in predicting the possibility of an epidemic or severe outbreak of bacterial blight resulting in loss in yield and fiber quality.

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Table 1. Pathogenic reaction grades of isolates on ten host differentials.

	Host Differential									
Isolate Location	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
North Carolina	6	7	6	7	6	6	1	7	7	7
Missouri	6	6	5	7	6	5	1	7	7	7
Corpus Christi	6	6	6	7	6	6	1	8	7	7
Brazos Valley	6	6	6	6	6	6	1	7	7	6
Hillsboro	6	5	5	7	6	6	1	6	7	7
Missouri	8	7	6	6	6	6	1	6	7	7
New Mexico – 1	8	7	6	6	6	6	1	6	7	6
New Mexico – 2	6	7	6	6	6	6	1	6	7	6
Weslaco (Usbekistan)	6	6	6	1	1	1	1	6	-	-

1, Acala-44; 2, Stoneville 2B-S9; 3, Stoneville 20; 4, Mebane; 5, 1-10B; 6, 20-3; 7, 101-102B; 8, Gregg; 9, Empire B-4; 10, DP-P4.

Table 2. Race identification of isolates of *Xanthomonas campestris* pv *malvacearum*.

Isolate Location	**Race Number**
North Carolina	18
Louisiana	18
Texas	
Brazos Valley	18
Hillsboro	18
Weslaco – Russian	18
Missouri	18
New Mexico – 1	18
New Mexico – 2	18
Race 1 – ck	1
Race 2 – ck	2
Race 18 – ck	18