REACTION OF COTTON CULTIVARS AND BREEDING LINES TO TARGET SPOT IN ALABAMA

K.L. Bowen
A. K. Hagan
K. Burch
Auburn University
Auburn, AL
H. B. Miller
Brewton Agricultural Research Unit
Brewton, AL
Don Moore
Prattville Agricultural Research Unit
Prattville, AL
Larry Wells
Wiregrass Research and Extension Center
Headland, AL

Abstract

Target spot of cotton, caused by *Corynespora cassiicola*, has emerged as a problematic disease over the past decade. This problem was first noticed by crop consultants in 2005 in the state of Georgia and was eventually confirmed as being caused by *C. cassiicola* (Fulmer et al., 2012). This fungus is a fairly common pathogen of plants, causing economic losses on crops such as cowpea and tomato (Sumabat et al., 2018) but had not previously been associated with cotton. However, in recent years, losses in yield in cotton due to target spot have been documented as exceeding 28% of the crop in Baldwin Co., Alabama (Bowen et al., 2018) in some years; losses can exceed $14 million in South Alabama alone.

Since *C. cassiicola* is a common pathogen of tomato in Florida, its occurrence on cotton in the U.S. was not due to an invasive introduction. It is possible that *C. cassiicola* has been a minor pathogen of cotton for some time, but has only emerged as problematic because of shifts in components of the disease triangle (environment, host and pathogen). For example, increased adoption of increased conservation tillage by cotton growers and increased instances of mild winters may have allowed greater survival of *C. cassiicola*, leading to more disease over time. Increased occurrences of warm or wet summers could have allowed greater and more rapid reproduction of the pathogen during crop growth leading to the emergence of target spot problems. Cotton cultivars are consistently being developed and released for production; a predominance of cultivars with susceptibility to *C. cassiicola* could have occurred over several years. In addition, there is evidence that *C. cassiicola* isolates from cotton are genetically distinct from isolates from other plants (Sumabat et al., 2018). Thus, a shift in the genotype of the fungus could've resulted in the change to virulence on cotton.

Plant resistance to a pathogen is an efficient way to manage plant disease; thus, regular screening of breeding lines and commercial cultivars should include disease assessments. Three OVT (Official Variety Tests) full season flex trials were monitored for target spot development in 2018; these were located at the Wiregrass Research and Extension Center (WGREC; 31.354, -85.325), Field Crops Unit (FCU; 32.424, -85.888) and Prattville Agricultural Research Unit (PARU; 32.426, -86.446). Forty commercial and advanced breeding lines were screened in these full season flex OVT trials. At WGREC, target spot defoliation ranged from 8% to 81% across lines (Table 1). Target spot defoliation stayed low at FCU and lines did not differentiate from one another. At PARU, the range of defoliation due to target spot was limited across lines (31 to 71%), yet statistical distinctions could be made. In general, those lines with the lowest disease at WGREC also had lower disease at PARU. Because of Hurricane Michael, yield data were obtained only for PARU. Among the best yielding lines were Deltapine 1646 B2XF and PhytoGen PHY3B07W3FE; these two lines also had the lowest defoliation at WGREC. However, Bayer BX1974GLTP also yielded well and was among the lines with the higher levels of target spot. These results suggest that tolerance exists in these genotypes.

Trials were conducted at the Brewton Agricultural Research Unit (BARU) and Prattville Agricultural Research Unit (PARU) to assess cotton cultivar reaction as influenced by an umbrella fungicide program to target spot. The experimental design was a factorial arranged in a split plot with the nine cultivars as whole plots and a 8 fl oz/A Priaxor + 1.5 pt/A Bravo Ultrex umbrella fungicide program as the split plot treatment. At BARU, Stoneville 6182 GLT suffered higher target spot-incited defoliation than the remaining cultivars with the least defoliation recorded for

Stoneville 5115 GLT, which was matched by all remaining cultivars except PhytoGen 450 W3FR and Stoneville 4946 GLB2. A significant cultivar × fungicide interaction indicated that cultivar response to the fungicide program differed. At PARU, the umbrella fungicide program gave effective disease control but a significant cultivar × fungicide program interaction was noted. Overall, the high defoliation levels on Stoneville 5020 GLT and PhytoGen 490 W3RF were matched by PhytoGen 340 W3RF, PhytoGen 450 W3RF, and Deltapine 1646 B2XF. In contrast, similarly low defoliation levels for Deltapine 1538 B2XF and Deltapine 1553 B2XF were noted for Stoneville 5115 GLT and Stoneville 4949 GLT.

Table 1. Breeding lines and commercial cultivars (out of 40 total) lowest and highest amounts of defoliation due to target spot; ranked by disease reaction at WGREC.

	WGREC		FCU	PARU		Lint (lbs/A, PARU)	
Deltapine 1646 B2XF	8.2	N	7.7	47.9	d-i	2708.8	a
PhytoGen PHY3B07W3FE	9.6	mn	13.2	40.2	f-j	2676.2	ab
Deltapine MON17R829B3XF	10.0	mn	12.7	42.8	d-j	2412.6	bcdefgh
Bayer ST 5517GLTP	10.8	lmn	6.7	31.4	j	2105.7	jklm
Bayer ST 5471GLTP	11.2	lmn	18.0	31.2	j	2210.8	ghijklm
PhytoGen PHY4A64W3FE	12.0	klmn	7.6	45.3	d-j	2216	ghijklm
Croplan 9608 B3XF	17.1	g-n	6.0	48.0	defg	2485	abcdefg
Bayer ST5818 GLT	17.4	g-n	20.0	37.9	hij	2046.2	klm
PhytoGen PHY 444 WRF	20.0	f-n	7.8	40.5	fghij	2261.6	fghijkl
PHY 320 W3FE	30.8	c-l	5.7	52.9	b-g	2107.9	jklm
Bayer BX1975GLTP	34.7	cdefg	10.4	71.7	a	2121.4	ijklm
PhytoGen PHY 430 W3FE	41.2	cde	16.3	38.2	ghij	2179.4	hijklm
Bayer BX1973GLTP	42.0	cd	22.2	65.5	ab	2600.7	abc
PhytoGen PX 333 WRF	44.4	bc	12.1	50.5	cdefg	2181.1	hijklm
Bayer BX1974GLTP	63.6	ab	9.9	67.6	ab	2515.6	abcdef
Bayer ST 6182GLT	67.1	a	20.8	53.1	bcdef	2287	defghijk
Bayer ST 5020GLT	81.0	a	13.9	53.2	bcdef	1990.4	lm

Letters following means in each column, when different, indicate significant differences according to Fisher's Least Significant Difference ($P < 0.05$).