IDENTIFICATION OF AN ALTERNATE SOURCE OF INOCULUM CAUSING BACTERIAL BLIGHT IN COTTON

Jessica Koczan
David W. Albers
Monsanto Company
Saint Louis, MO
Keylon Gholston
Monsanto Company
Baldwyn, MS

Abstract

A field survey was conducted to help in determining whether different weed species can serve as hosts for overwintering inoculum in a field with a previous history of bacterial blight in cotton.

Introduction

Bacterial blight caused by *Xanthomonas campestris* pv *malvacearum* (Xcm) infects all stages in cotton and can have an impact on yield potential in most cotton growing regions when the environment is favorable for disease development. Symptoms of bacterial blight in cotton usually appear first as water soaking on leaves which develop into dark angular spots that can move into the veins (Figure 1). Monitoring of the Xcm and bacterial blight can help with disease prediction and identification of potential race shifts.

Sources for inoculum can occur from overwintering of contaminated debris in the soil, in which Xcm can be viable up to five months in plant debris, late-season infection by other infected plants in the field, and on seed. When this pathogen is on seed, the acid delinting process reduces pathogen populations.

Xanthomonas is a robust genus with numerous pathogenic and nonpathogenic isolates that are known to infect over 350 plant species. *Xanthomonas* is divided into two major groups, the second including *X. citri*, *X. vasicola*, *X. oryzae*, *X. axonpodis*, and *X. campestris*. Different species have different functional virulence factors, but most produce xanthan which is known to aid in epiphytic lifestyle (i.e. *X. axonopodis* pv *citri*, *X. axonopodis* pv *allii*, *X. axonopodis* pv *phaseoli*, *X. albilineans*, *X. campestris* pv *vesicatoria*). The epiphytic survival of other *Xanthomonas* species on weeds and non-host plants (*X. axonopodis* pv *allii*, *X. axonopodis* pv *manihotis*, *X. axonopodis* pv *phaseoli*, *X. axonopodis* pv *vignicola*, *X. campestris* pv *vitians*). The epiphytic lifestyle allows the pathogen to survive on nonhost plants without displaying any signs or symptoms of the disease.

Figure 1. Bacterial blight caused by *Xanthomonas campestris* pv *malvacearum* on a cotton leaf.

Materials and Methods

A limited field survey was conducted to determine if weed material has the potential to serve as reservoir for Xcm. The field survey included four sites where bacterial blight was confirmed in the fields the previous year. Weeds present in the field and sampled included velvetleaf, marestail, pigweed, ragweed, Johnsongrass (carcass), jimsonweed, and wild sunflower. Weed samples were collected and leaf tissue was shipped overnight to labs for processing.

Weed samples were collected on June 8, 2016. At each location, at least two plant samples were collected, but weed species varied by site. Three leaves of each species were bulked to represent one species sample from each site. Weed species collected by site are provided in Table 1.

Table 1. Weed species collected at each site for *Xanthomonas campestris* pv *malvacearum*.

Site	Weed Species Collected at Site
1	Velvetleaf, marestail, pigweed
2	Johnsongrass refuge, pigweed refuge
3	Pigweed, ragweed, wild sunflower, refuge
4	Jimson weed, velvetleaf, marestail, pigweed

Weeds were processed at a lab within 24 hours of collection. Leaf material was ground and plated. After two days, single colonies were selected (both target and off-target in appearance). In all, 238 samples were isolated for testing. Known Xcm isolates were used as controls, as were known off-target xanthomonads. A published molecular assay was used to identify xanthomonads using the ITS, and pathogenic versus nonpathogenic (group 1 or 2) was determined using BOX-A1R to separate Xcm. Cotton variety DP388 was inoculated with 238 isolates or controls and observed for bacterial blight symptoms.

Results and Discussion

Lab reports concluded that three of the four locations had isolates on weed samples that were positive for bacterial blight (Table 2). All isolates were re-isolated after producing disease symptoms on cotton.

Table 1. Results of isolate screening at four sites.

Site	11/238 isolates screened were positive on DP 388	17/238 isolates screened were positive using PCR
1	0 isolates	0 isolates
2	2 isolates	4 isolates
3	2 isolates	6 isolates
4	7 isolates	7 isolates

Of the four sites examined, three sites had weed species with Xcm present. Not all weed species collected supported epiphytic Xcm in this study. There were seventeen isolates identified using PCR and 11 were confirmed in pathogenicity tests on cotton. All isolates that were positive in the plant screen were also positive using PCR.

Summary

These results indicate the potential that winter weeds and other plant material left in a field after a bacterial blight infestation can serve as a source for inoculum the following season.

Individual results may vary, and performance may vary from location to location and from year to year. This result may not be an indicator of results you may obtain as local growing, soil and weather conditions may vary. Growers should evaluate data from multiple locations and years whenever possible. **ALWAYS READ AND FOLLOW PESTICIDE LABEL DIRECTIONS.** All other trademarks are the property of their respective owners. ©2017 Monsanto Company. 01032016CRB.