A PEDIGREE ANALYSIS OF COTTON CULTIVARS AFFECTED BY BRONZE WILT K. M. El-Zik and P. M. Thaxton Texas Agricultural Experiment Station Texas A&M University College Station, TX J. B. Creech Delta Research and Extension Center Mississippi Agricultural and Forestry Experiment Station Stoneville, MS

Abstract

Since 1995 bronze wilt has been observed in several cotton cultivars in the USA with some germplasm and cultivars more severe than others. Plant age, fruit set and load, earliness in fruiting and maturity, and high yield potential effect symptom severity. Differences in resistance to bronze wilt are affected by cultivar, environment (temperature, light intensity, and photoperiod), soil type and fertility, nitrogen content of fertilize and fertilizer rate of phosphorous and potassium, production practices and abiotic stresses (high temperature and water stress). Cultivars from several seed companies were reported to be susceptible to bronze wilt. Some researchers have linked susceptibility to bronze wilt to the presence of Tamcot SP37 and bacterial blight (B) resistance genes in the genetic background of susceptible cultivars. Our pedigree analysis of Upland and Pima cultivars released between 1970 and 1990 and other recent cultivars indicates that not all cultivars susceptible to bronze wilt were developed by crossing to Tamcot SP37; examples are Pima's and several upland cultivars. Also, not all cultivars resistant to bacterial blight or carry the $B_2B_3B_7$ gene combination are susceptible to bronze wilt; examples are Tamcot Sphinx, Tamcot Luxor, Sure-Grow 747, and Stoneville 239. Many commercial cultivars in Texas are direct selection from Tamcot SP37, in others SP37 is a parent. Rarely did these cultivars show symptoms of bronze wilt; examples are All-Tex, Cascot, G&P, Holland, Lockett, Pioneer/Lankart cultivars. What traits or genes other than bacterial blight resistance genes are associated with bronze wilt? Could it be due to cold tolerance, earliness, high fruit production and boll retention, high yield potential, or other traits? A common dominator among the bronze wilt susceptible cultivars is their earliness and high yield potential. Bronze wilt could not logically be attributed to Tamcot SP37 being in their parentage or to bacterial blight (B) resistance genes. DNA molecular techniques should be useful in establishing relationships and evidence of reticulation, and cause of the disorder.

Introduction

Bronze wilt was observed in several cotton cultivars in the USA since 1995 and in Brazil, Argentina, and Bolivia with some germplasm and cultivars being more severe than others. The exact cause of the disorder has yet to be ascertained. However, it has been suggested that probable cause of bronze wilt is high concentrations of certain strains of *Agrobacterium* spp., a soil and seed bacterium, that cause damage to the secondary roots (Bell 1998, 1999, 2000b). Differences in resistance to bronze wilt are affected by cultivar, environment (temperature, light intensity, and photoperiod), soil type and fertility, relative nitrogen content of fertilizer and fertilizer ratio of phosphorous and potassium, production practices and abiotic stresses (high temperature and water stress). Plant age, fruit set and load, earliness in fruiting and maturity, and high yield potential also effect symptom severity.

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Environmental Variables

Prolonged exposure to day temperatures above 95°F (35°C) enhances foliar bronze wilt symptoms, and necrosis and browning of fine roots (Bell 1999, 2000a). Necrosis of fine roots reduces the ability of the plant to actively take up water and certain nutrients, such as potassium and iron. Light intensity and photoperiod appear to affect the relative resistance to bronze wilt, implicating photosynthesis in damage caused by bronze wilt. Bell (2000a) reported that as the photoperiod was increased from 16h to 20h, there was greater damage to the roots of susceptible cultivars (Paymaster 1220 and Stoneville 373) but not to the roots of the resistant cultivars (Sure-Grow 125 and Tamcot Sphinx). Water availability to the plant is very critical, bronze wilt is more severe under drought conditions and heat stress.

Nutritional Factors

Differences in resistance to bronze wilt are influenced by relative nitrogen content of fertilizer and fertilizer rates, soil type and pH. Bronze wilt severity is directly proportional to nitrogen fertilizer rate and inversely related to phosphorus rate (Bell 1998, 2000a, 2000b). Availability and uptake of a balanced fertilizer of nitrogen, phosphorus, potassium, sulfur, iron, and micronutrients are important to reduce bronze wilt severity. Early maturing cotton cultivars are more sensitive to potassium deficiencies than late maturing cultivars (Tupper et. al. 1996).

The Cotton Crop

Plant age, fruit set and load, earliness in fruiting and maturity, and high yield potential have been reported to affect symptom severity, suggesting a relationship with the carbohydrate sink and assimilate allocation.

Bacterial Blight Resistance Genes

Bacterial blight resistance (*B*) genes have been implicated in the bronze wilt syndrome. Bacterial blight of cotton is one of the most studied diseases for the past 50 years. At least 22 major genes in addition to several minor genes conferring resistance to the pathogen have been identified, described, and reviewed (El-Zik and Bird 1970; Innes 1983; Verma 1986; Wallace and El-Zik 1989). Horizontal resistance is conferred by a combination of the *B* genes (El-Zik and Thaxton 1995). The MAR Tamcot cultivars carry the $B_2B_3B_7$ gene combination, in addition to the b_6 gene in Tamcot CD3H and germplasm with CD3H in its parentage (El-Zik and Thaxton 1989, 1995). Nineteen races of the bacterial blight pathogen *Xanthomonas campestris* pv. *malvacearum (Xcm)* are currently recognized in the USA based on their reaction to 10 host differentials. In addition virulent isolates of the pathogen have appeared in Africa and may cause epidemics.

What is the original source of these genes in Upland cotton?

- B_2 a strong dominant gene from the African cultivar Uganda 31.
- B_3 a partially dominant gene from Schroeder 1306 (an offtype of *Gossypium hirsutum* var. *punctatum*).
- B_7 a gene from Stoneville 20 (dominance of this gene depends on the genetic background and race of the pathogen).
- $B_{\rm Dm}$ a polygene complex found in Deltapine.
- $B_{\rm Sm}$ a polygene complex found in Stoneville 2B and in Empire.

In analyzing pedigrees of recent cultivars, from 1970 to 1990, we found that some of the early USA cotton cultivars also carry bacterial blight resistance genes. These cultivars were released in the 1920's to 1950's, and they have been used in almost every commercial and public cotton breeding program in the U.S. Mebane has the B_2 gene, Northern Star B_N , Stoneville 2B B_{Sm} ,

Stormproof 1 B_s , Empire B_{Sm} , Stoneville 20 B_7B_{Sm} , Empire WR $B_2B_3B_{Sm}$, and Auburn 56-5714 the B_2B_3 gene combination.

Recent molecular research has identified chromosomal locations for several *B* genes (B_2 , B_3 , B_2b_6 in the Empire background, and B_{12} in S295 from Africa), and linkage groups for QTLs. B_2 is on chromosome 20 near the DNA marker G121, and B_3 on chromosome 20 near the DNA marker PGH510a (Wright et. al. 1998). B_3 is more than 50 cM away from B_2 , supporting data suggesting linkage between B_2 and B_3 . B_{12} is on chromosome 14, near the DNA marker pAR043. The B_2 , B_3 and B_{12} genes were mapped on D-subgenome and b_6 on A-subgenome chromosomes.

Pedigrees of Selected Cotton Cultivars

Pedigrees of cotton cultivars (both *G. hirsutum* and *G. barbadense*) released between 1970 and 1990 (Calhoun et. al. 1994), coefficients of parentage among 260 cultivars (Bowman et. al. 1995), and genetic base of upland cotton cultivars (Bowman et. al. 1996) have been reported. Since the inception of the MAR program in the mid-1960's the program has released more than 362 elite cotton breeding lines and 13 Tamcot cultivars. The Tamcot cultivars and their pedigrees are presented in Table 1. Commercial seed companies have selected and released 33 cultivars from the MAR germplasm, in addition to cultivars resulting from crosses with MAR elite lines and Tamcot cultivars as parents. These commercial cultivars are presented in Table 2 and include All-Tex (2), Cascot (5), Dunn (3), G&P (7) - four cultivars are selections from Tamcot SP37, Holland (3), HY007, Lankart/Pioneer (2), Lockett (2), Paymaster 145, Rogers, Simwalt, and Stoneville 132 (Calhoun et. al. 1994).

Discussion

What does the pedigrees show regarding bronze wilt? Bronze wilt has been generally observed only in the past 4 to 5 years on most germplasm and cultivars, some have few plants, in others it is more severe. Environment, nutrition, and stage of crop development have a major role on symptom expression and severity.

Some cotton cultivars are more susceptible to bronze wilt than others. Cultivars from several seed companies were reported to be susceptible (Bell 1999, 2000a; Creech 1999; Creech and Fieber 2000). Susceptibility to bronze wilt has been linked by some researchers to the presence of Tamcot SP37 and (*B*) bacterial blight resistance genes in the genetic background of cultivars susceptible to bronze wilt.

The pedigree of TAMCOT SP37 is [K4808-5 (1&2) D//Blightmaster/39-11-20/3/K4808-5 (1&2) A/Paymaster 54-M-105-3]. It has the $B_2B_3B_7$ genes for resistance to the bacterial blight pathogen. K4808 was derived by transferring the B_2B_3 genes for bacterial blight from R. L. Knight's BAR 4/16 Sakel (*G. barbadense*) strain to an "Empire WR" background. "Blightmaster" is a storm resistant cultivar, having the B_7 gene for bacterial blight resistance that was developed at the Texas Agric. Exp. Stn., Lubbock, Texas. 39-11-20 was a glandless genetic stock, having the gl_1gl_2 genes, from the Cotton Research Center, Shafter, California. PayM54-M-105-3 was a Paymaster 54 breeding stock, which was obtained from the ACCO Seed Company, Aiken, Texas.

Our pedigree analysis indicates that not all cultivars resistant to bacterial blight or carry the $B_2B_3B_7$ gene combination are susceptible to bronze wilt. Examples are Tamcot Sphinx, Tamcot Luxor, Sure-Grow 747, and Stoneville 239. Also, not all cultivars susceptible to bronze wilt were developed by crossing to Tamcot SP37, which was released in 1971 – 30 years ago and bronze wilt appeared only in the last five years. Examples are Pima's and several upland cultivars (Bell 2000a). These cultivars are also susceptible to bacterial blight. The Paymaster PM H1560 series (PM 1560 BG and PM 1560 BG/RR) is an example of a recent cultivar showing

bronze wilt symptoms and does not have Tamcot SP37 in its background. The H1560 is from the Louisiana State University Program, tested as LA830909, and developed from the cross LA434-1031-C/DES119. LA434-1031-C originated from the Cross Bayou 7769/Deltapine 16.

Many commercial cultivars in Texas are direct selection from Tamcot SP37, in others SP37 is a parent (Table 2). Rarely did these cultivars show symptoms of bronze wilt; examples are All-Tex, Cascot, G&P, Holland, Lockett, Lankart/Pioneer cultivars. What traits or genes other than bacterial blight resistance (*B*) genes are associated with bronze wilt? Could it be due to cold tolerance, earliness, high fruit production and boll retention, high yield potential, or other traits?

Conclusion

A common dominator among the bronze wilt susceptible cultivars is their earliness and high yield potential. Bronze wilt could not logically be attributed to using Tamcot SP37 in crosses or to bacterial blight (*B*) resistance genes. We believe that DNA molecular techniques should be useful in establishing relationships and evidence of reticulation, and cause of the disorder.

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Table 1. Pedigrees of Tamcot cotton cultivars.

| Tamcot SP37 | K4808-5 (1&2)D//Blightmaster/39-11- |
|----------------|--|
| | 20/3/K4808-5 (1&2)A/Paymaster 54-M-105-3 |
| Tamcot SP21 | K4808-5 (1&2)D//Blightmaster/39-11- |
| | 20/3/K4808-5 (1&2)A/Paymaster 54-M-105-3 |
| Tamcot SP23 | K4808-5 (1&2)D//Blightmaster/39-11- |
| | 20/3/K4808-5 (1&2)A/Paymaster 54-M-105-3 |
| Tamcot SP37H | 66N, B.V.65/52q, B.V.65 |
| Tamcot SP21S | SP21F/SP33F//SP21V/SP37V |
| Tamcot CAMD-E | MDR.SP7-67/17M2//SP46-67/17M2 |
| Tamcot CAB-CS | CAMD-21-S-78/BCUS-8-76 |
| Tamcot CD3H | Tamcot SP37H/CDPS-1-77 |
| Tamcot GCNH | CAMD-21S-5-80/GN-8-76 |
| Tamcot HQ95 | Tamcot CD3H/MAR-CABU'CS-2-1-83 |
| Tamcot Sphinx | MAR-CDP37HPIH-1-1-86/Sel. PM 145 |
| Tamcot Luxor | MAR-CABUCAHUGS-1-88/CABUCAG8US-1-88 |
| Tamcot Pyramid | MAR-CD3PIHP45H-2-89/CD3HGCBU8S-1-91 |

Table 2. Pedigrees of selected upland cotton cultivars with MAR germplasm or Tamcot cultivars in their parentage[†].

| Cultivar | Pedigree |
|-----------------------------|---|
| All-Tex E-2 | Tamcot CAMD-E/Paymaster 792 |
| All-Tex Quickie | ORHU-1-78/Tamcot CAMD-E |
| Cascot 2910 | Sel. Cascot BR-1C |
| Cascot B-2 | Sel. TX-Bonham |
| Cascot BR-1 | Sel. TX-Bonham |
| Cascot C-13 | Sel. TX-Bonham |
| Cascot L-7 | Sel. TX-Lewis |
| Dunn 1047 | Tamcot SP-21/Dunn 219 |
| Dunn 120 | Sel. Tamcot SP23 |
| Dunn HS 120 | Dunn 219/Dunn 120 |
| G&P 1005 | Sel. CAMD S75C |
| G&P 1068 | GPX 105-81/Tamcot CD3H//G&P 3774/CA3029 |
| G&P 3755 | Sel. Tamcot SP-37 |
| G&P 3774 | Sel. Tamcot SP-37 |
| G&P 5479 | Sel. Tamcot SP-37 |
| G&P 74+ | Sel. G&P 3774 |
| G&P 785 | Tamcot CAB-CS/CA3016 |
| Holland 1379 | Sel. TX-Bonham |
| Holland 850 | Cascot C-13//Tx-Le6873/Mo 63-277J |
| Holland 4002 | Sel. Holland 5677 (Sel. Bonham) |
| HY 007 | Cascot C-13//Tx-Le6873/Mo63-277J |
| Lankart 511 | Lockett 4789/3/Lockett 4789-A//SP52- |
| | 67/79N.BV65 |
| Lankart PR 75 | Lockett 4789-A/SP11-67//79N.BV65/HI-67 |
| Lockett 77 | Lockett 4789-A/SP12-67//Lockett 4789A/CA563 |
| Lockett BXL | Lockett 4789 (31)/SP19//SP20 |
| Paymaster 145 | Sel. Tamcot SP-21 |
| Rogers 7590 | Quapaw/Lyman G11//2*RDC 10N |
| Simwalt 82 | Tamcot 24/3306 |
| Stoneville 132 | Sel. MC-T8-27-8C [DES56/Tamcot SP37] |
| * After Calhoun et al. 1004 | |

[†] After Calhoun et al. 1994.