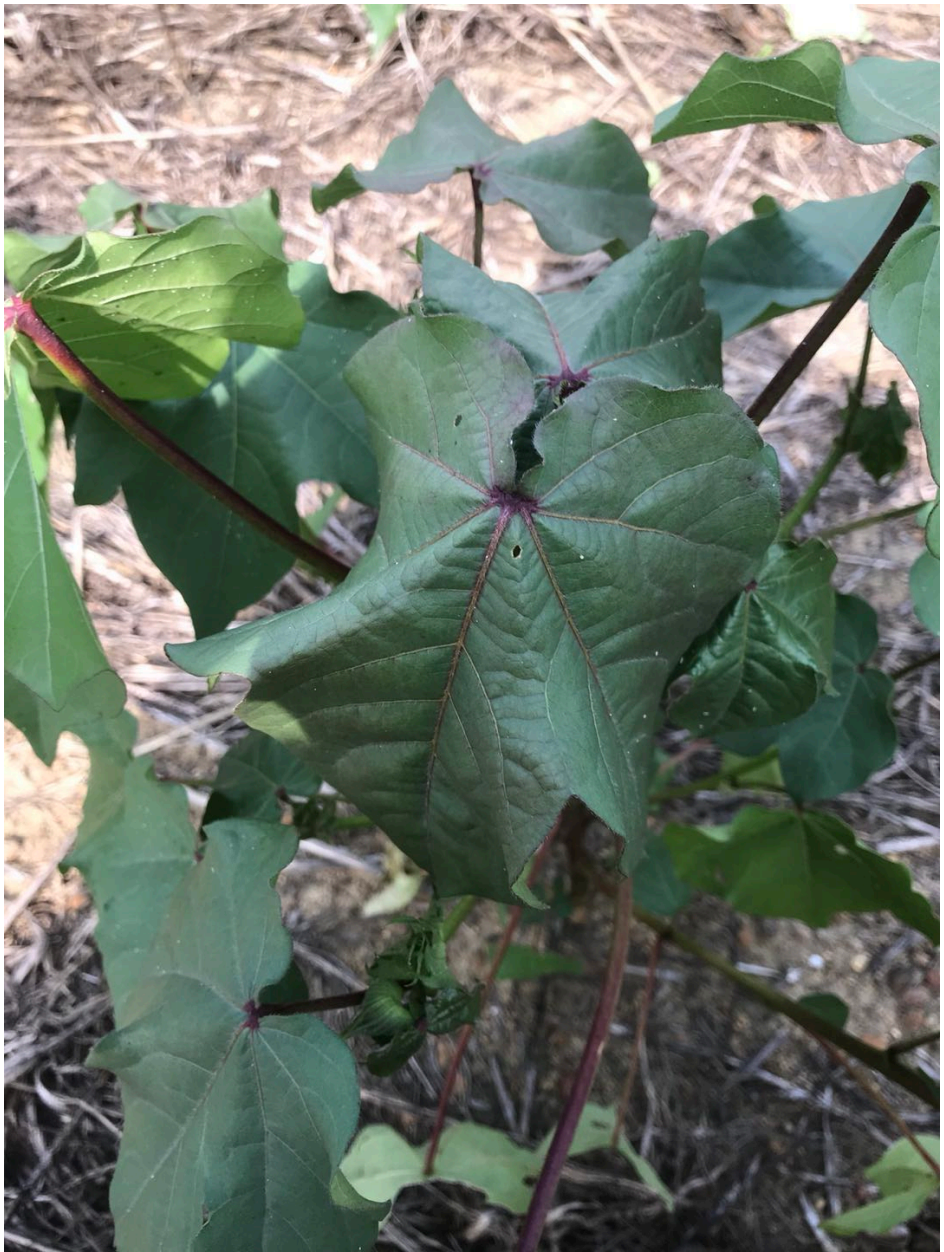
Host Plant Resistance to Cotton Blue Disease



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Beltwide Cotton Conference
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Cotton blue disease in Brazil

Sources of resistance to blue disease

Table 4 Cotton varieties used to clone DC20027 marker fragments associated with *Cbd*

#	Variety[a]	Country of origin	CBD resistance	DC20027 marker fragment	
				Size (bp)[b]	Linked to *Cbd* allele
1	*G. raimondii*	D genome	Unknown	182	NA
2	Delta Opal	Australia	R	182	NA
3	DP388	USA	S	182	NA
4	PM183	USA	S	198	r
5	DP388	USA	S	200	r
6	DP90	USA	S	200	r
7	DP5305	USA	S	200	r
8	IAC21	Brazil	S	200	r
9	SG747	USA	S	200	r
10	Delta Opal	Australia	R	202	R
11	Sicala 32	Australia	R	202	R
12	Reba 50	Central Africa Republic	R	202	R
13	Pora	Argentina	R	202	R
14	CD401	Brazil	R	202	R
15	Guazuncho	Argentina	R	202	R
16	Albar AF884	Zimbabwe	R	202	R
17	*G. arboreum*	A genome	R	202	R
18	*G. herbaceum*	A genome	R	202	R

[a] *G. arboreum* and *G. herbaceum* are diploid A genome specie, *G. raimondii* is a diploid D genome species. All others are Upland cotton (*G. hirsutum*) varieties

[b] 182 bp fragment is from Dt subgenome

Fang et al 2010

Breeding strategy – typical CBD

Resistance to CBD is conferred by a single gene located on Chromosome 10 linked to the SSR markers DC20027 and BNL3646

- Use marker-assisted backcrossing to transfer the resistance gene *Cdb* from BRS268 to elite germplasm
- Perform two to five backcrosses to recover the recurrent genetic background
- In each backcross, the progenies will be genotyped with the molecular markers to ensure that the resistance gene is present

Complete genome sequences of two new virus isolates associated with cotton blue disease resistance breaking in Brazil

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Abstract Since 2006, Brazilian cotton (*Gossypium hirsutum*) crops planted with cultivars that are resistant to cotton blue disease have developed a new disease termed "atypical" cotton blue disease or atypical vein mosaic disease. Here, we describe the complete genomes of two virus isolates associated with this disease. The new virus isolates, called CLRDV-Acr3 and CLRDV-IMA2, were found to have a high degree of nucleotide and amino acid sequence similarity to previously described isolates of cotton leafroll dwarf virus, the causal agent of cotton blue disease. However, their P0 proteins were 86.1 % identical. These results show that this new disease is caused by a new CLRDV genotype that seems to have acquired the ability to overcome cotton blue disease resistance.

Cotton blue disease (CBD) is an important disease affecting cotton crops in Asia, South America and Africa [1]. In Brazil, it is present in almost all cotton crop areas, leading to cotton productivity losses of up to 80 %. Symptoms include leaf rolling, intense green foliage, and severe to moderate stunting. The disease is transmitted by *Aphis gossypii* (Glover) and is caused by cotton leafroll dwarf virus (CLRDV; family *Luteoviridae,* genus *Polerovirus*)

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ORIGINAL ARTICLE

Cotton blue disease in central-west Brazil: Occurrence, vector (*Aphis gossypii*) control levels and cultivar reaction

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Abstract Cotton blue disease (CBD) is the viral disease which poses the greatest threat to cotton in Brazil. One efficient way of controlling this disease is by using resistant cultivars. However, the recent emergence of an atypical form of CBD (ACBD), caused by a new virus genotype capable of overcoming these resistant cultivars, is causing concern. Thus, the aims of this study were to evaluate the distribution of ACBD in the states of Mato Grosso (MT) and Goiás (GO), to determine the relationship between vector infestation level, disease incidence and yield, and to check the reaction of cotton cultivars to two viral isolates. In both cotton production areas, 1128 plots were surveyed and 6.5% showed plants with the virus, 97.3% and 2.7% with ACBD and CBD, respectively. In cultivars susceptible to ACBD, a positive linear relationship between changes in the levels of aphid infestation and incidence of viral infection was indentified, and a negative linear relationship between infestation level and yield. The maximum acceptable level of aphids up to 80 days after sowing for susceptible cultivars was approximately 15%. Although 83% of the cultivars were shown to be resistant to CBD, only 19.2% were resistant to ACBD. There was also a number of cultivars with considerable resistance to both isolates.

Keywords Atypical cotton blue disease · Genotype resistance · CLRDV · Cotton leafroll dwarf virus · Vein mosaic virus

Table 3 Cotton cultivar reactions to blue disease (CBD) and atypical cotton blue disease (ACBD) under greenhouse conditions in 2014

Cultivar	CBD[a]	ACBD	Cultivar	CBD	ACBD
BRS 368RF	1.0a	1.5a	IMA 5675BT2RF	1.0a	3.3b
DP 555BGRR	2.3b	2.0b	TMG 11WS	1.0a	3.3b
FM 944GL	1.0a	3.8b	TMG 41WS	1.0a	3.3b
FM 951LL	1.0a	1.3a	TMG 42WS	1.0a	1.8a
FM 966LL	5.0d	3.0b	TMG 81WS	1.0a	3.3b
FM 975WS	1.0a	2.5b	TMG 82WS	1.0a	2.8b
FM 982GL	3.8c	3.0b	Delta Opal	1.0a	1.0a
IAC 26RMD	1.3a	3.0b	FMT701	1.0a	4.5b
C.V. (%)	4.9	11			
r[b]	0.1n.s.				

[a] Scale from 1 to 5 with an increasing incidence of the disease. 1, plants without symptoms of the disease; 2, one plant per plot with symptoms of the disease; 3, two plants per plot with symptoms of the disease; 4, three plants with symptoms of the disease; 5, four (all) plants per plot with symptoms of the disease. Means followed by the same letter in the column within each virus do not differ significantly from each other according to the Scott and Knott test, at 5% probability

[b] Correlation between the results of CBD vs. ACBD

Galbieri et al 2017

Table 4 Cotton cultivar reactions to blue disease (CBD) and atypical cotton blue disease (ACBD) under greenhouse conditions in 2015

Cultivar	CBD[a]	ACBD	Cultivar	CBD	ACBD
BRS 368RF	1.0a	1.0a	FM 975WS	1.0a	3.8d
BRS 369RF	1.0a	2.0b	FM 980GLT	1.0a	2.3b
BRS 371RF	2.0b	4.0d	FM 982GL	2.0b	4.0d
BRS 372	1.3a	3.0c	IAC 26RMD	1.3a	4.0d
IMA 2106GL	1.0a	3.5c	IMA 5675B2RF	1.0a	4.3d
DP 1227B2RF	1.3a	2.5b	TMG 11WS	1.0a	1.8b
DP 1228B2RF	2.8c	4.8d	TMG 41WS	1.0a	1.8b
DP 1240B2RF	1.0a	3.0c	TMG 42WS	1.0a	1.5a
IMA 8405GLT	1.0a	2.6b	TMG 43WS	1.0a	1.5a
FM 913GLT	1.0a	1.3a	TMG 81WS	1.0a	2.3b
FM 940GLT	1.0a	1.8b	TMG 82WS	1.0a	2.5b
FM 944GL	1.0a	4.5d	Delta Opal	1.0a	1.0a
FM 966LL	3.8d	3.3c	FMT 701	1.0a	4.5d
C.V. (%)	6.3	8.7			
r[b]	0.4n.s.				

[a] Scale from 1 to 5 with an increasing incidence of the disease. 1, plants without symptoms of the disease; 2, one plant per plot with symptoms of the disease; 3, two plants per plot with symptoms of the disease; 4, three plants with symptoms of the disease; 5, four (all) plants per plot with symptoms of the disease. Means followed by the same letter in the column within each virus do not differ significantly from each other according to the Scott and Knott test, at 5% probability

[b] Correlation between the results of CBD vs. ACBD

Galbieri et al 2017

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Tiragem
2000 exemplares

Sintomas em algodoeiro causados por *Meloidogyne incognita* em condições de casa de vegetação. Raízes de genótipo resistente ao nematoide (à esquerda) e suscetível (à direita). (Foto: Rafael Galbieri)

Reação de cultivares de algodoeiro
a doenças e nematoides, safra 2017/18

Rafael Galbieri[1], Edivaldo Cia[2], Jean L. Belot[1], Alberto S. Boldt[1], Julio Isao Kondo[2], Patrícia A. Vilela[1]

1. Introdução

Resistência genética é uma das formas mais eficientes e de fácil implementação no controle de doenças de plantas. Há tempos é explorada dentro dos programas de melhoramento genético do algodoeiro em atividade no Brasil. Há considerável variação no nível de resistência a doenças nas cultivares disponíveis para o plantio no país.

O trabalho tem como objetivo caracterizar essas cultivares frente a diferentes patógenos de ocorrência no algodoeiro, no sentido de fornecer informações aos produtores para promover controle genético de doenças garantindo melhor sustentabilidade da cultura nas condições de clima tropical.

2. Metodologia

Foram conduzidos 18 ensaios específicos para avaliações de doenças e nematoides, distribuídos em diferentes regiões de produção de algodão no Brasil. As áreas foram selecionadas em função do histórico de ocorrência dos patógenos em locais onde tradicionalmente desenvolvem-se trabalhos com doenças sob alta pressão de inóculo (*Quadro 1*).

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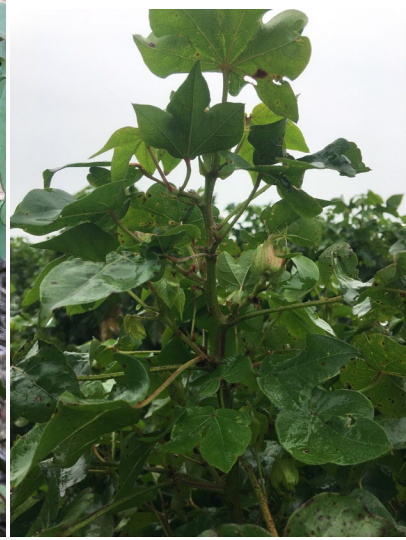
Tabela 1. Reação de cultivares de algodoeiro a doenças e nematoides no cerrado, safra 2017/18.

Cultivares	Fungos				Bactéria	Nematoides			Viroses	
	Ramularia *		Ramulose	Murcha Fusarium	Mancha angular	*Meloidogyne***		Reniformes	Doença Azul	Virose Atípica
	Isolado 1	Isolado 2				Resistência	Tolerância	Tolerância		
BRS 430B2RF	S	S	MS	S	R	S	I	I	R	MR
BRS 432B2RF	S	MS	MS	MS	R	S	MT	MI	R	MR
BRS 433FL B2RF	S	S	MS	MR	R	S	MI	MI	MR	MR
DP 1536B2RF	S	S	MS	MS	R	S	MI	I	R	MS
DP 1552RF	MS	S	MS	MR	MS	S	MT	MT	R	MS
DP 1746B2RF	S	S	MS	S	R	S	MI	MT	R	MS
FM 906GLT	S	MS	MS	S	R	S	I	I	R	MS
FM 940GLT	S	MS	MS	MS	R	S	I	I	R	MS
FM 944GL	S	S	MS	MS	R	S	MI	MT	R	MS
FM 954GLT	S	S	MS	S	R	S	MI	I	R	MS
FM 975WS	S	S	MS	MS	R	S	MI	MI	R	MS
IAC RDM	MR	MS	MS	R	R	MR	T	MT	R	MS
IMA 2106GL	S	S	MR	MS	R	S	MT	MI	R	MS
IMA 5801B2RF	R	R	MS	MR	MS	R	T	MI	R	MS
IMA 6501B2RF	S	S	MS	MR	R	S	MT	MT	R	MS
IMA 7501WS	MR	MS	MR	MS	R	S	MT	MT	R	MS
IMA 8405GLT	MS	S	MS	S	R	S	MI	MI	R	MS
TMG 42WS	R	MS	MS	S	R	S	I	MI	R	MR
TMG 44B2RF	MR	S	MS	S	R	S	I	I	R	MR
TMG 45B2RF	MR	S	MS	S	R	S	MI	MI	R	MR
TMG 47B2RF	R	S	S	S	R	S	I	I	R	MR
TMG 81WS	S	S	MS	S	R	S	MT	MT	R	S

Breeding strategy – Atypical CBD

- Develop field and greenhouse screening protocols in Alabama and Georgia
- Screen cultivars/germplasm for resistance
- Screen breeding/genetic populations segregating for resistance



Breeding strategy – Atypical CBD

Resistance to ACBD is available but DNA marker linked to the resistant gene(s) has not been identified.

- Develop genetic populations segregating for resistance to ACBD.
- Screen populations to determine the segregation of resistance
- Genotype populations with DNA markers to determine the location of R gene and identify markers associated with resistance

Molecular mapping of bunchy top disease resistance in *Gossypium hirsutum* L.

Marc H. Ellis · Warwick N. Stiller · Tanya Phongkham · Walter A. Tate · Vanessa J. Gillespie · Washington J. Gapare · Qian-Hao Zhu · Danny J. Llewellyn · Iain W. Wilson

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