Host Plant Resistance to Cotton Blue Disease

Jenny Koebernick
Auburn University

Peng Chee
University of Georgia

Beltwide Cotton Conference
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Cotton blue disease in Brazil
Table 4 Cotton varieties used to clone DC20027 marker fragments associated with *Cbd*

<table>
<thead>
<tr>
<th>#</th>
<th>Variety</th>
<th>Country of origin</th>
<th>CBD resistance</th>
<th>DC20027 marker fragment</th>
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<td>Reba 50</td>
<td>Central Africa Republic</td>
<td>R</td>
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<td>Argentina</td>
<td>R</td>
<td>202</td>
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<td>14</td>
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<td>Brazil</td>
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<td>202</td>
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<tr>
<td>15</td>
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<td>Argentina</td>
<td>R</td>
<td>202</td>
</tr>
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<td>16</td>
<td>Albar AF884</td>
<td>Zimbabwe</td>
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<td>202</td>
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<td>17</td>
<td><em>G. arboreum</em></td>
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<td>202</td>
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<tr>
<td>18</td>
<td><em>G. herbaceum</em></td>
<td>A genome</td>
<td>R</td>
<td>202</td>
</tr>
</tbody>
</table>

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

*b* 182 bp fragment is from Dt subgenome.

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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 $C_{db}$ 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

Anna Karoline Fausto da Silva · Elisson Romanel · Tatiane da F. Silva · Yamá Castilhos · Carlos G. Schrago · Rafael Galbieri · Jean-Louis Be'lot · Maite F. S. Vaslin

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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)

Arch Virol
DOI 10.1007/s00705-015-2380-8
Cotton blue disease in central-west Brazil: Occurrence, vector (*Aphis gossypii*) control levels and cultivar reaction

Rafael Galbieri¹,² · Alberto S. Boldt¹ · Leonardo B. Scoz¹ · Sandra M. Rodrigues³ · Diego O. Rabel⁴ · Jean L. Belot¹ · Maíte Vaslin⁵ · Tatiane da Franca Silva⁵,⁶ · Leimi Kobayasti⁷ · Luiz Gonzaga Chitarra³

Received: 10 January 2017 / Accepted: 30 May 2017 © Sociedade Brasileira de Fitopatologia 2017

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 identified, 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

<table>
<thead>
<tr>
<th>Cultivar</th>
<th>CBD</th>
<th>ACBD</th>
<th>Cultivar</th>
<th>CBD</th>
<th>ACBD</th>
</tr>
</thead>
<tbody>
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<td>BRS 368RF</td>
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<td>1.5a</td>
<td>IMA 5675BT2RF</td>
<td>1.0a</td>
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<td>2.0b</td>
<td>TMG 11WS</td>
<td>1.0a</td>
<td>3.3b</td>
</tr>
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<td>1.0a</td>
<td>3.8b</td>
<td>TMG 41WS</td>
<td>1.0a</td>
<td>3.3b</td>
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<td>TMG 42WS</td>
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<td>1.8a</td>
</tr>
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<td>TMG 81WS</td>
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<td>3.3b</td>
</tr>
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<td>Delta Opal</td>
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<td>1.0a</td>
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<td>C.V. (%)</td>
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</table>

\(^a\) 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
<table>
<thead>
<tr>
<th>Cultivar</th>
<th>CBD</th>
<th>ACBD</th>
<th>Cultivar</th>
<th>CBD</th>
<th>ACBD</th>
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<tr>
<td>BRS 368RF</td>
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\(^a\) 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.
Reação de cultivares de algodoeiro a doenças e nematoides, safra 2017/18

Rafael Galbiati*1, Edvaldo Cia1, Jean L. Beto2, Alberto S. Boldrini2, Julio Issa Kondo3, Patricia A. Vilela1

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 ampla escala. Há considerável variação no nível de resistência a doenças nas cultivares disponíveis para plantio no país.

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 da histórica ocorrência dos patógenos em locais onde tradicionalmente desenvolvem-se trabalhos com doenças sob alta pressão de inoculo (Quadro 1).

<table>
<thead>
<tr>
<th>Cultivares</th>
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<td>MS</td>
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Sintomas em algodoeiro causados por Meloidogyne incognita em condições de casa de vegetação. Plantas de genótipos resistentes ao nematode (a esquerda) e suscetíveis (a direita) (Fotos: Rafael Galbiati)
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

Euphytica

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