943

Detection of *Cotton leafroll dwarf virus* in cotton blue disease-resistant plants Silva, TF1; Corrêa, RL1; Castilho, Y1; Suassuna, ND2; Silvie, P3; Bélot, J-L3; Vaslin, MFS1. [1]Laboratório de Virologia Molecular Vegetal, Deptò. Virologia, IMPPG, UFRJ. [2]Embrapa Algodão, Campina Grande, PB, Brasil. [3]Centre de Coopération Internationale en Recherche Agronomique pour le Développement, CIRAD. E-mail: mvaslin@biologia.ufrj.br. Detecção do *Cotton leafroll dwarf virus* em plantas resistentes à doença azul do algodoeiro.

Cotton blue disease (CBD), a cotton-crop pathology distributed worldwide, is responsible for high productivity losses. The Polerovirus *Cotton leaf roll dwarf virus* (CLRDV), transmitted by the aphid *Aphis gossypii*, is associated with CBD in Brazil. Several CBD-resistant were developed and preferentially used by Brazilian producers. However since 2006, typical CBD symptoms (internodal shortening, leaf rolling, intense green foliage and yellowing veins) and atypical symptoms (including reddish leaves), are being observed in resistant cotton crops. To check if CLRDV is associated with the emergence of CBD in resistant plants, we analyzed 18 CBD symptomatic plants from different resistant cotton varieties. In this work, we report the CLRDV resistance breakdown in resistant plants with CBD symptoms. Comparison in viral coat protein, RNA polymerase and movement protein amino acids sequences shows that resistant break isolates are very closely related to the CLRDV original isolate. However, two amino acids substitutions (Thr140Met and Ile167Thr) were found in all RB isolates analyzed. The shifts in MP sequences of the RB isolates might have played a role in the CLRDV resistance-breakdown phenomenon.

944

Desenvolvimento de teste sorológico para a doença azul do algodoeiro Oliveira, AAQ[1]; Corrêa, RL[1]; Vaslin, MFS[1]. [1]Laboratório de Virologia Molecular Vegetal/ Departamento de Virologia/ IMPPG/ UFRJ, CP 68039, CEP 21941590, Rio de Janeiro, RJ, Brasil. E-mail: maite.vaslin@gmail.com Development of a serological test for cotton blue disease.

Dentre as moléstias que geram grande impacto na cultura do algodão no Brasil pode-se citar a doença azul do algodoeiro (DA). Os principais sintomas são a redução do porte das plantas, o enrolamento e o amarelecimento das nervuras das folhas. A transmissão é feita pelo pulgão *Aphis gossypii* e seu agente etiológico é um vírus nomeado de *Cotton leafroll dwarf virus* (CLRDV). O objetivo deste trabalho foi estabelecer um protocolo para detectar o CLRDV por Western blot e DAS-ELISA utilizando anticorpos policlonais contra a partícula viral purificada. Em Western blot, o anticorpo anti-CLRDV foi capaz de reconhecer a suspensão viral purificada, sugerindo a detecção da proteína *readthrough* (RTP) e da proteína capsidial. Este anticorpo também detectou a RTP em plantas infectadas provenientes de Primavera do Leste (MT). Houve reação positiva com extratos de *A. gossypii* coletado em plantas de algodão com sintomas da doença e também em plantas com a doença "Cotton bunchy top". Não houve reação para o extrato de planta sadia. Foi utilizado o programa Lasergene para predizer as regiões de maior antigenicidade da RTP, totalizando 28 regiões, distribuídas ao longo de toda a proteína. Testes de DAS-ELISA preliminares mostraram resultados positivos utilizando o anticorpo anti-CLRDV e este mesmo conjugado à fosfatase alcalina em plantas infectadas em casa de vegetação e em plantas provenientes de campo.

945

High conservation of Polerovirus minor capsid protein P5 in two distinct disease transmitted by the same aphid in Brazil and Australia Castilho, Ŷ[1]; Silva, TF[1]; Corrêa, RL[1]; Ellis, M[2]; Vaslin, MFS[1]. [1]Laboratório de Virologia Molecular Vegetal, Depto. Virologia, IMPPG, UFRJ, [2]CSIRO Plant Industry, Canberra, Australia. E-mail: maite.vaslin@gmail.br. Alta conservação de seqüência entre a P5 de um polerovírus brasileiro e um australiano.transmitido pelo mesmo afídeo.

Aphid transmission of poleroviruses is highly specific, but the viral determinants governing this specificity are little known. Studies of different virus-vector combination demonstrate that P5 (readthrough protein/RTD) seems to be fundamental in this interaction. It was suggest that the N-terminal (conserved) half of the RTD may be the site of the primary vector specificity determinant for all luteovirids. Here we show that two newly identified luteovirus, the Cotton leafroll dwarf virus (CLRDV), responsible for cotton blue disease in Brazil and the Australian virus associated to a completely distinct disease, the cotton bunchy top, share a very close sequence in this portion of P5. Both viruses are transmitted by the same aphid, *Aphis gossypii*. Cotton bunchy top is a cotton disease witch casual agent was unknown, and seems to be restricted to Australia. Designing primers based on sequence homologies of all *A. gossypii* transmitted virus, we were able to amplify part of cotton bunchy top virus genome. Walking along the virus genome we observed that this virus is quite different in others sequences from CLRDV, although they share a very similar P5 N-terminal sequence.

946

Occurrence of Melon yellowing-associated virus (MYaV) in melon producing areas of Brazilian Northeast Lima, MF[1]; Nagata, T[2]; Neves, FM[3]; Inoue-Nagata, AK[1]; Moita, AC[1]; Sousa, C[4]; Della Vecchia, M[4]; Rangel, MG[4]; Dias, RCS[5]; Dutra, LD[3]; de Ávila, AC[1]. [1]Embrapa Hortaliças, CP 218, 70359-970, Brasília-DF; [2]UnB, CP 153081, 70910-900, Brasília-DF; [3]Univ. Católica de Brasília, 70790-160, Brasília-DF; 4Syngenta Seeds Ltda, CP 71, 62800-000, Aracati-CE; 5Embrapa Semi-Árido, CP 23, 56302-970, Petrolina-PE. E-mail: mflima@cnph.embrapa.br. Ocorrência do Melon yellowing associated virus (MYaV) em áreas produtoras de melão no Nordeste brasileiro.

The Brazilian Northeast is the main melon-producing region of the country, being responsible for more than 90% of the total national production. However, a new disease known as "yellowing of melon plants", has been reported to cause damage on this crop since 1999. The presence of a new viral agent, the Melon yellowing-associated virus (MYaV), is most likely associated with symptom development. The aim of this study was to evaluate the occurrence of the MYaV in melon plants exhibiting suspicious symptoms of the disease in major melon growing fields of Northeast. In November 2007, 374 samples were collected in the States of Rio Grande do Norte (RN; 54) and Ceará (CE; 37) and in the "Submédio São Francisco" (283), in Bahia (BA) and Pernambuco (PE) States. Sample evaluation was performed by DAS-Elisa using polyclonal antibodies developed at the Embrapa Hortaliças for MYaV detection. Extracts prepared from leaves and stems of symptomatic plants were used as antigen. The MYaV was detected in 58.0% of the samples. Virus concentration was higher in stems than in leaves. The incidence of MYaV was higher in samples collected from RN (96.3%) and CE (75.7%) than in those from the "Submédio São Francisco" (PE and BA: 48.4%). These data confirmed the efficiency of the antibodies for MYaV detection and the widespread occurrence of the virus in melon fields of the main melon-producing areas of Brazil. Apoio Financeiro: CNPq.