POSTER SUMMARY

FIRST REPORT ON MAIZE STREAK VIRUS IN THE SOUTH AFRICAN SUGAR INDUSTRY

McFARLANE SA, VAN ANTWERPEN T, GOVENDER P and BUCHANAN GF

South African Sugarcane Research Institute, Private Bag X02, Mount Edgecombe, 4300, South Africa
Sharon.McFarlane@sugar.org.za Tania.van.Antwerpen@sugar.org.za
Pavithra.Naidoo@sugar.org.za Grant.Buchanan@sugar.org.za

Abstract

Elongated, chlorotic lesions were observed on leaves of a newly released sugarcane cultivar, N44, in KwaZulu-Natal, South Africa, in May 2007. Surveys identified the symptoms in further fields of N44 and in two additional cultivars (N27 and N36) in several other locations in the area, as well as in the KwaZulu-Natal Midlands and Mpumlanga province. The causal organism was identified as maize streak virus (MSV). MSV was also identified in wild grass growing next to the field where the disease was first seen. The virus is related to, but different from, the sugarcane streak virus that infected the variety Uba in KwaZulu-Natal in the 1920s. MSV has been reported to have caused severe stunting in two sugarcane varieties in glasshouse trials conducted in Mauritius, and is spread by the leafhopper *Cicadulina mbila* Naude. MSV could have serious implications for the South African sugar industry. This is believed to be the first report of maize streak virus in sugarcane in South Africa.

Introduction

The Masteroviruses (family Geminiviridae) cause diseases of economically important Graminaeceous crops in Africa, including maize, wheat and sugarcane. Sugarcane streak virus (SSV) is one of three currently described sugarcane-infecting mastrevirus species which caused serious disease in sugarcane in Africa until the introduction of resistant cultivars almost eradicated the disease (Bigarre *et al*., 1999). Recently, sugarcane plants presenting with streak symptoms have been identified in certain sugarcane growing regions of South Africa. Unlike the characteristic fine stippling and streaking of SSV, however, the symptoms currently being reported resemble the broader, elongated chlorotic lesions commonly observed in maize and wild grass species infected with a different mastrevirus, namely maize streak virus (MSV).

Importantly, these symptoms have been reported on a newly released South African sugarcane cultivar, N44 (Figure 1). The lesions were first observed on one plant in the Nqabeni-Hluka area in southern KwaZulu-Natal in February 2006. The plant was eradicated and no further symptoms were evident in the field until May 2007, when the disease reappeared. Surveys identified the symptoms in further fields under N44 and in two additional cultivars, N27 and N36, in southern KwaZulu-Natal. Symptoms have since been observed on N44 in the KwaZulu-Natal midlands and North Coast, and on N36 in Mpumalanga province. Wild grass species adjacent to a field of N44 in the Nqabeni-Hluka area presented with similar streaking symptoms.

Figure 1. Sugarcane cultivar N44 showing elongated chlorotic lesions, symptoms characteristic of maize streak virus (MSV), at the South African Sugarcane Research Institute's research station at Kearsney (Photo: A Walton).

Materials and Methods

DNA was extracted from sugarcane leaves and grasses using the Qiagen DNeasy Plant Mini Kit (Cat. no 69104) according to the manufacturer's instructions. Streak virus sequences were designed by aligning known streak viral sequences obtained from the Genbank (BLAST) database. These included the sugarcane streak virus strains from Natal, Reunion and Egypt, as well as the maize streak virus sequence. Primers were designed and tested for their self-annealing or primer dimer formations as well as their melting points using the OligoCalc software (http://www.basic.northwestern.edu/biotools/oligocalc.html). Primer sequences were then compared to published sequences on the Genbank database to confirm their ability to detect genera from the Geminiviridae. Published primers for MSV (Rybicki and Hughes, 1990) were used for comparison with primer pair G2/G4. PCR was performed according to the protocol described by Rybicki and Hughes (1990) and sequencing was performed according to the manufacturer's instructions (Applied Biosciences). Sequences were compared with sequences on the Genbank database using the BLASTN search tool.

Results

Primer pair G4/G6 was able to detect sugarcane streak virus (Natal), sugarcane streak virus (Egypt), sugarcane streak virus (Mauritius), maize streak virus and wheat dwarf virus. A 1 200 bp fragment was amplified from DNA extracted from variety N44 with apparent maize streak virus symptoms, and from a grass (*Digitaria* spp) that was growing on the edge of the field where the symptoms were found, using primer pair V2/C1 (Rybicki and Hughes, 1990).

A fragment of 900 bp was amplified from the DNA when primer pair G4/G6 was used on the same samples. Both fragments were purified with the Qiagen Gel extraction kit and sequenced. All but one of the sequences failed using primer pair G4/G6. The successful sequence was obtained using primer G4; this sequence showed the highest homology to maize streak virus when it was compared to the published sequences for the different streak viruses. Sequences obtained using primers V2 and C1 confirmed that it was maize streak virus.

Primer pair V2/C1 did not amplify the DNA extracted from sugarcane variety Uba with sugarcane streak symptoms, suggesting that the sugarcane streak virus in Uba differs from other streak strains in sugarcane.

Future work

MSV infections could have serious implications for the South African sugar industry. Besides possible yield losses in infected plants, the virus could be considerably more difficult to control than it is in maize because sugarcane is vegetatively propagated and individual plants remain within fields for years rather than months. In addition, the virus has alternate hosts, and is vector-transmitted. Plans are underway to assess the susceptibility of all commonly grown and newly released South African sugarcane varieties to MSV infection. Those varieties developing symptoms will be included in yield loss trials.

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