DETECTION OF SUGARCANE STREAK MOSAIC VIRUS
IN SUGARCANE FROM SEVERAL ASIAN COUNTRIES

By

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Abstract

FIVE sugarcane leaf samples exhibiting mosaic symptoms and that originated from
Bangladesh, India, Sri Lanka, Thailand, and Vietnam reacted negatively in RT-PCR assays
with Sugarcane mosaic virus (SCMV), Sorghum mosaic virus (SrMV) and potyvirus specific
primers. Mosaic symptoms were reproduced after mechanical inoculation of sugarcane, maize
and sorghum plants with diseased leaf extracts, but symptoms were not as severe as those
carried by SCMV and SrMV. Electron microscopy of partially purified virions from
inoculated plants showed flexuous filaments characteristic of the Potyviridae family. The five
sugarcane leaf samples reacted, however, in RT-PCR assays with two primer pairs designed
to detect Sugarcane streak mosaic virus (SCSMV), the causal agent of sugarcane
streak mosaic, an unclassified member of the Potyviridae family. SCSMV was detected by RT-PCR
in 34 leaf samples from 30 cultivars exhibiting mosaic symptoms and that originated from
Bangladesh, India, Pakistan, Sri Lanka, Thailand, and Vietnam. The amplicon (0.5 kb) from
the coat protein coding region of five virus isolates showed 97% to 99% identity with
SCSMV from Pakistan (GenBank accession number U75456) and 93 to 95% with SCSMV-
AP from India (GenBank accession number Y17738). Our results suggest that: i) SCSMV is
the major cause of mosaic symptoms in sugarcane in several Asian countries; ii) streak
mosaic is widespread in Asia; and iii) the disease is caused by at least two different strains of
SCSMV in India. Additionally, sugarcane leaves exhibiting mosaic symptoms can be
simultaneously infected by SCSMV and SCMV.

Introduction

Historically, the causal agent of sugarcane mosaic was attributed to a single potyvirus called
sugarcane mosaic virus or SCMV with numerous strains, or possibly to a complex of potyviruses (Koike
and Gillaspie, 1989; Shukla et al., 1994). Differentiation of the strains was based on symptom expression
on differential hosts and serological properties.

These sugarcane infecting potyviruses were recently included in a SCMV subgroup consisting of
four related but distinct species of potyviruses (McKern et al., 1991; Shukla et al., 1989, 1992 and 1994):
Sugarcane mosaic virus (SCMV), Sorghum mosaic virus (SrMV), Maize dwarf mosaic virus (MDMV) and
Johnsongrass mosaic virus (JGMV). Zea mosaic virus (ZeMV), a novel potyvirus isolated from maize in
Israel, may also be included in this subgroup (Seifers et al., 2000). Among these viruses, only SCMV and
SrMV are known to infect sugarcane under natural conditions and are considered as the causal agents of
sugarcane mosaic (Grisham, 2000).

The newly determined SCMV species included strains A, B, D, E, SC, Isis and Brisbane from
sugarcane, BC from blue couch grass [Digitaria scalarum (Schweinf.) Chiov.], Bundaberg from wild
sorghum, Sabi from sabi grass [Urochloa mosambicensis (Hack.) Dandy] and several strains from maize
including MDB (formerly MDMV-B) (Shukla et al., 1992 and 1994). Strains from sugarcane and maize
belong, however, to two different monophyletic groups based on the sequence of the coat protein coding region (Alegria et al., 2003). SrMV comprised strains SCH, SCI and SCM from sugarcane. Sugarcane mosaic has been reported in more than 70 countries (Grisham, 2000) and, because the reported strains were only from the USA and Australia, the number of existing SCMV strains is expected to be much greater. Moreover, numerous isolates or strains have not yet been investigated such as SCMV-C, F, G, K and L from the USA (Shukla et al., 1994) and SCMV-N from India (Kondaiah and Nayudu, 1985).

Based on indicator plants, Gillaspie et al. (1978) named an apparent potyvirus isolated in the USA from quarantined sugarcane showing mosaic symptoms and imported from Pakistan, SCMV-F. Molecular cloning, sequencing and phylogenetic analyses later revealed that this virus was different from SCMV, and it was renamed *Sugarcane streak mosaic virus* or SCSMV (Hall et al., 1998). Another virus isolate of SCSMV causing mosaic of commercial sugarcane was recently identified in India (Hema et al., 1999a). It showed 93.6% sequence identity in the coat protein coding region with the isolate from Pakistan, and was named SCSMV-Andhra Pradesh isolate (SCSMV-AP).

These results indicated that at least two different virus species, SCMV and SCSMV, cause mosaic symptoms in sugarcane in Asia. The objective of this study was to identify the causal agent of mosaic symptoms in sugarcane leaf samples from Bangladesh, India, Pakistan, Sri Lanka, Thailand, and Vietnam. SCSMV appeared to be the major cause of sugarcane mosaic symptoms in these Asian countries, and the disease caused by this pathogen was renamed streak mosaic.

**Material and methods**

**Virus isolates**

Sugarcane leaves infected with SCMV CAM6/1 originated from Cameroon (Alegria et al., 2003). Sorghum and sugarcane leaves infected with SrMV-SCM from Louisiana and named SrMV USA501/1 and SrMV USA51/1, respectively, were obtained from the collection maintained in the USA, by M. Grisham (USDA Sugarcane Research Unit, Houma, Louisiana). Symptomatic sugarcane leaves infected with unknown field isolates were sampled in Bangladesh (BSRI), India (SBI-ICAR and SRS Kunrakhat), Pakistan (SSRRI), Sri Lanka (SRS Uda Walawe), Thailand (DOA Bangkok), and Vietnam (QNCS), and stored in Montpellier at minus 80°C (Tables 1 and 2). Studies were conducted with the original fresh samples, with stored samples or with material collected from artificial hosts (maize, sorghum, sugarcane) inoculated with leaf extracts prepared from stored leaves (see below).

**Partial purification of virus isolates and observation by electron microscopy**

Virus-infected leaf material was collected from sugarcane and sorghum plants inoculated as described below. Partially-purified leaf extracts were prepared from one gram of leaves according to the protocol described by Lockhart et al. (1992). Preparations were used for observation by electron microscopy using standard leaf-dip protocols.

**RNA extraction and RT-PCR**

Total RNA was extracted and purified from sugarcane and sorghum leaves showing mosaic symptoms with the RNeasy® Plant Mini Kit (Qiagen) using the manufacturer’s protocol. Total RNA was eluted in a final volume of 40 μL of diethylpyrocarbonate-treated (DEPC) water and stored at minus 20°C. RT-PCR assays to detect SCMV and SrMV with primer pairs SCMV F4-SCMV R3 and SrMV F3-SrMV R3, respectively, were performed as described by Alegria et al. (2003). RT-PCR assays to amplify fragments specific to potyviruses of *Poaceae* with primer pair oligo1n-oligo2n were performed according to Marie-Jeanne et al. (2000). The 25 μL RT-PCR reaction to detect SCSMV was conducted with the Qiagen One Step RT-PCR kit using the manufacturer’s protocol with 10 pmoles of each primer (forward primer ST2 and reverse primers P1 or ST5), 1 μL of eluted RNA and 10 units of ribonuclease inhibitor. The RT-PCR program was 50°C for 30 min, 95°C for 15 min, 30 cycles at 94°C for 1 min, 50°C for 1 min and 72°C for 1 min with a final 72°C extension for 5 min. A 10 μL aliquot of each amplified product was analysed by electrophoresis through a 1% agarose gel. The size of the fragment amplified from leaves infected with SCSMV is ca. 500 bp with primer pair ST2-P1 and ca. 400 bp with primer pair ST2-ST5.

**Purification of RT-PCR products, cloning and sequencing**

RT-PCR products obtained with primers ST2-P1 were purified with Wizard® DNA Clean-Up System (Promega) and cloned using the pGEM® -T Easy Vector System (Promega). Inserts were sequenced from both directions by Genome Express SA (Grenoble, France) using the Applied Biosystems 3700 sequencer and the BigDye Terminators premix according to Applied Biosystems protocol. The
sequencing primers were pUC/M13 Forward and pUC/M13 Reverse. One clone was sequenced for each of five virus isolates. Sequences were compared with the GenBank data base by the BLAST program on the NCBI site (http://www.ncbi.nlm.nih.gov/BLAST/).

**Mechanical inoculation of plants**

The host plants tested included sugarcane (*Saccharum interspecific hybrids*) cultivars B46364, FR96029 and FR96047, sorghum (*Sorghum bicolor*) cultivar Tx412 and maize (*Zea mays*) cultivar Golden Cross Bantam. Sugarcane plants were germinated from cuttings and other plants were grown from true seed. All plants were grown in a mixture of compost, peat and volcanic rock (1/1/1) in 0.9 litre pots in a growth chamber (12 hour photoperiod, 28°C) or an aphid-free greenhouse. Two- to three-week-old seedlings (2–3 leaf stage) of sorghum and maize, and four-week-old (2–3 leaf stage) sugarcane plants were used for mechanical inoculation. Plants were inoculated by depositing ca. one mL of inoculum and a small amount of 400-mesh carborundum abrasive on the top visible unrolled leaf, and rubbing the leaf between thumb and forefinger. The inoculum of infectious leaf extract was prepared by grinding infected leaves in 0.05 M pH 7.2 phosphate buffer (4 mL/g leaf tissue) and 0.01 M sodium sulfite in a mortar with a pestle, and filtering through cheesecloth. Ten plants of each host were inoculated by virus isolate.

**Results**

Sugarcane, maize and sorghum were inoculated with SCMV CAM611 from Cameroon, SrMV USA51/1 from Louisiana and six unknown field isolates from Asia (Table 1): VNM14 from Vietnam, LKA116 from Sri Lanka, BGD131 from Bangladesh, THA151 from Thailand, PAK155 from Pakistan and IND159 from India. SCMV CAM611 produced severe mosaic symptoms on sugarcane, sorghum and maize one to two weeks after inoculation, and symptoms remained severe for several weeks. The same result was obtained after inoculation of the three host plants with isolate PAK155. SrMV isolate USA51/1 produced mild mosaic symptoms on sugarcane and maize but severe symptoms on sorghum. Unknown isolates VNM14, LKA116, BGD131 and IND159 produced light to mild mosaic symptoms on sugarcane, maize and sorghum (Table 1). Isolate THA151 produced only light mosaic symptoms on all three hosts. Plants inoculated with VNM14, LKA116, BGD131, THA151 and IND159 showed mosaic symptoms which appeared only after two to three weeks. Additionally, infection by these isolates produced transient symptoms in numerous plants.

**Table 1**—Pathogenicity and molecular characteristics of *Sugarcane mosaic virus*, *Sorghum mosaic virus*, and six unknown sugarcane mosaic virus isolates from Asia.

<table>
<thead>
<tr>
<th>Diagnostic test</th>
<th>Mosaic virus isolate</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>SCMV CAM6/1</td>
</tr>
<tr>
<td><strong>Pathogenicity in sugarcane</strong></td>
<td>S*</td>
</tr>
<tr>
<td><strong>Pathogenicity in maize</strong></td>
<td>S</td>
</tr>
<tr>
<td><strong>Pathogenicity in sorghum</strong></td>
<td>S</td>
</tr>
<tr>
<td><strong>RT-PCR with primers</strong></td>
<td></td>
</tr>
<tr>
<td>SCMV F4-R3</td>
<td>4</td>
</tr>
<tr>
<td>SrMV F3-R3</td>
<td>-</td>
</tr>
<tr>
<td><strong>RT-PCR with potyvirus primers oligo1n and oligo2n</strong></td>
<td>+</td>
</tr>
<tr>
<td><strong>RT-PCR with primers</strong></td>
<td></td>
</tr>
<tr>
<td>SCMV ST2-P1</td>
<td>-</td>
</tr>
<tr>
<td>SCMV ST2-ST5</td>
<td>-</td>
</tr>
</tbody>
</table>

* L = light mosaic symptoms, M = mild mosaic symptoms, S = severe mosaic symptoms.

b + = positive reaction, – = negative reaction, +/- = variable reaction in replicated assays.
Electron microscopy of partially purified virions from plants inoculated with SCMV CAM6/1 and the six unknown field isolates showed non-enveloped flexuous filaments characteristic of the Potyviridae family. The amount and size of observed particles varied, however, according to the virus isolate. The particles of CAM6/1 and PAK155 were abundant and measured about 750 nm in length and 15 nm in width. The particles of VNM14, LKA116, BGD131, THA151 and IND159 were much less abundant and showed various sizes up to 810 nm in length.

A 0.9 kb SCMV fragment was amplified by RT-PCR with the SCMV F4 and SCMV R3 primers from total RNA extracted from leaves infected by SCMV CAM6/1 and PAK155 (Table 1). A positive RT-PCR reaction was also obtained for these isolates and SrMV USA50/1 with primers oligo1In and oligo2In designed for detection of Poaceae potyviruses. A 0.9 kb SrMV fragment was amplified with SrMV F3 and SCMV R3 primers only from leaves infected by SrMV USA50/1. None of the expected fragments was amplified with the three primer pairs from leaves infected by VNM14, LKA116, BGD131, THA151 and IND159. A ca. 0.5 kb fragment was amplified from these five leaf samples, but also from leaves infected by PAK155, using primers SCSMV-ST2 and SCSMV-P1. However, this amplification product was not consistently obtained with isolate PAK155 when the assay was repeated. A ca. 0.4 kb fragment was amplified from leaves infected by VNM14, LKA116, BGD131, THA151 and IND159, but not from leaves infected by PAK155, using primers SCSMV-ST2 and SCSMV-P1. RT-PCR reaction was negative with both SCMV primer pairs and leaves infected by SCMV CAM6/1 and SrMV USA50/1.

Thirty-four leaf samples from sugarcane or sorghum showing mosaic symptoms were then analysed by RT-PCR assays. These samples were taken from original diseased material stored at minus 80°C or from plants inoculated in this study. They represented 30 sugarcane cultivars exhibiting mosaic symptoms and that originated from Bangladesh (9 samples), India (15), Pakistan (3), Sri Lanka (3), Thailand (2), and Vietnam (2).

The 34 leaf samples, and leaves infected by SCMV CAM6/1 and SrMV USA50/1, were tested by RT-PCR with primer pairs SCMV F4-SCMV R3, SCSMV ST2-P1 and SCSMV ST2-ST5. Different patterns of reaction were obtained, and the 34 unknown field samples were differentiated into two groups (Table 2). Group I contained 30 isolates from five different countries that tested negative with the SCMV specific primers, but positive with the SCSMV specific primers. The four isolates from Pakistan and India belonging to group II reacted positive with the SCMV and the SCSMV specific primers.

### Table 2—Detection of Sugarcane mosaic virus and Sugarcane streak mosaic virus in sugarcane leaves from Asia showing mosaic symptoms.

<table>
<thead>
<tr>
<th>Samples</th>
<th>Origin of samples (number of samples)</th>
<th>RT-PCR assay with primers for</th>
<th>Diagnostic result</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>SCMV&lt;sup&gt;a&lt;/sup&gt;</td>
<td>SCSMV&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Group I</td>
<td>Bangladesh (9) &lt;br&gt;India (14) &lt;br&gt;Sri Lanka (3) &lt;br&gt;Thailand (2) &lt;br&gt;Vietnam (2)</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Group II</td>
<td>Pakistan (3) &lt;br&gt;India (1)</td>
<td>+ or +/-</td>
<td>+ or +/-</td>
</tr>
<tr>
<td>SCMV control</td>
<td>Cameroon (1)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>SrMV control</td>
<td>Louisiana/USA (1)</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

<sup>a</sup> primers SCMV-F4 and SCMV-R3; + = positive reaction, − = negative reaction, +/- = variable result in replicated assays.

<sup>b</sup> primers SCSMV-ST2 and SCSMV-P1, and SCSMV-ST2 and SCSMV-ST5; + = positive reaction with at least one SCSMV-primer pair, − = negative reaction with both primer pairs, +/- = variable result in replicated assays.

The 0.5 kb DNA fragment amplified with SCSMV primers ST2-P1 was cloned and sequenced for five isolates (VNM13 from Vietnam, LKA116 from Sri Lanka, BGD131 from Bangladesh, IND159 and IND167 from India).
The sequence of each isolate was compared to sequences in the GenBank data base and the nucleotide identity for the five isolates ranged from 97% to 99% with SCSMV from Pakistan (GenBank accession number U75456) and from 93% to 95% with SCSMV-AP from India (GenBank accession number Y17738).

Discussion and conclusion

Pathogenicity and molecular investigations with six virus isolates from sugarcane leaves showing mosaic symptoms showed that at least five of them did not belong to SCMV or SrMV. Mosaic symptoms caused by these isolates on sugarcane, maize and sorghum were not as severe as those caused by SCMV or SrMV. Except sample PAK155, no other unknown leaf sample reacted in RT-PCR tests with SCMV and Potyvirus specific primers. Electron microscopy of partially purified virions from inoculated plants showed, however, flexuous filaments characteristic of the Potyviridae family. All six leaf samples reacted with at least one set of SCSMV primers. Based on these results, it was concluded that the six leaf samples from Asia were infected by SCSMV, and that one sample from Pakistan (PAK155) was infected by both SCMV and SCSMV. Serological assays performed with SCMV and SCSMV antibodies confirmed this conclusion (data not shown).

SCMV-F was named Sugarcane streak mosaic virus or SCSMV for the first time in 1998 by Hall et al. who studied a virus isolate from Pakistan with a host range unlike that of other known potyviruses. This name was based on the close phylogenetic relationship of the Pakistani virus with Wheat streak mosaic virus (WSMV) and Brome streak mosaic virus (BrSMV), but not based on symptoms caused by this virus in sugarcane.

A close observation of symptoms caused by SCSMV isolates in this study indicated, however, that numerous small spots or streaks parallel to the veins were present on the foliage of several host plants (data not shown). When these streaks were numerous on the leaf blade, they coalesced and formed a pattern of mosaic similar to the one described for sugarcane streak caused by Sugarcane streak virus (SSV) (Rott and Peterschmitt, 2000).

Because symptoms caused by SCSMV are very close to symptoms caused by SCMV and SSV, the new name streak mosaic was approved by the ISSP (International Society for Plant Pathology) disease name subcommittee (http://www.isspweb.org/names_common.asp) and the ISSCT pathology section (http://issct.intnet.mu/pathreport.htm) for the disease caused by SCSMV. Streak mosaic should therefore be used from now on to describe or report mosaic symptoms caused by SCSMV.

SCSMV induces pinwheel and laminated aggregate type of inclusions that are a characteristic feature of members of the family Potyviridae (Hema et al., 2002). However, phylogenetic analyses revealed that SCSMV is not a potyvirus like SCMV, and that it is different from all virus species described so far. SCSMV may therefore represent an undescribed new genus within the Potyviridae (Hema et al., 2002; Rabenstein et al., 2002).

When still considered SCMV-F, SCSMV was found in different sugarcane growing areas in Asia (Bangladesh, India, Pakistan, Sri Lanka, and Thailand) and the USA (Kolke and Gillaspie, 1989). Additionally, a new strain of SCSMV showing only 94% sequence identity in the coat protein coding region with the Pakistani isolate described by Hall and associates (1998) was recently described in India (Hema et al., 1999a, 1999b and 2002).

Our study confirms the occurrence of SCSMV in several Asian countries and reports for the first time the presence of SCSMV in Vietnam. Because SCSMV was detected in all 34 sugarcane leaf samples from Asia, this virus species and streak mosaic appear to be widespread in sugarcane cultivars in several Asian countries.

A more exhaustive study will be necessary to determine the distribution of SCMV and SCSMV in Asia, but also in other parts of the world. Mixed SCSMV-SCMV infections were detected in this study in samples from India and Pakistan, and an isolate of SCMV from the north-eastern region of India was recently molecularly characterised (Gaur et al., 2003).

The partial coat protein sequence of five SCSMV isolates (including two from India) was much closer to the Pakistani SCSMV isolate (renamed SCSMV-PAK by Hema et al., 2002), than to SCSMV-AP from India. Therefore, at least two different strains of SCMV appear to exist in India. A study published recently by Hema et al. (2003) also suggested the existence of different strains of SCSMV in India. Further investigations are needed to precisely characterise the genetic diversity and the population structure of the causal agent of sugarcane streak mosaic.
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DETECTION DU SUGARCANE STREAK MOSAIC VIRUS DANS DES CANNES À SUCRE ORIGINAUTES DE PLUSIEURS PAYS ASIATIQUES

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Résumé

CINQ échantillons foliaires présentant des symptômes de mosaïque et originaux du Bangladesh, d’Inde, du Sri Lanka, de Thaïlande et du Vietnam n’ont pas réagi en RT-PCR avec des amorces spécifiques du Sugarcane mosaic virus (SCMV), du Sorghum mosaic virus (SrMV) et des potyvirus. Des symptômes de mosaïque ont été reproduits après inoculation mécanique de plants de canne à sucre, de maïs et de sorgho avec des extraits de feuilles malades, mais ces symptômes n’étaient pas aussi sévères que ceux provoqués par le SCMV et le SrMV. Des particules virales caractéristiques de la famille des Potyviridae ont été observées par microscopie électronique dans des extraits foliaires partiellement purifiés à partir de plantes inoculées. Les cinq échantillons foliaires ont par ailleurs réagi en RT-PCR avec deux paires d’amorces dessinées pour détecter le Sugarcane streak mosaic virus (SCSMV), agent causal de la mosaïque en tirets, un membre non classé de la famille des Potyviridae. Le SCSMV a été détecté par RT-PCR dans 34 échantillons foliaires montrant des symptômes de mosaïque et originaires du Bangladesh, d’Inde, du Pakistan, du Sri Lanka, de Thaïlande et du Vietnam. Le produit d’amplification (0,5 kb) de la région codante de la protéine de capsid de cinq isolats viraux présente 97 à 99% d’identité en acides nucléiques avec le SCMV du Pakistan (numéro d’accès GenBank U75456) et 93 à 95% avec la souche SCSMV-AP originaire d’Inde (numéro d’accès GenBank Y17738). Nos résultats suggèrent que i/ le SCSMV est la cause majeure des symptômes de mosaïque sur canne à sucre dans plusieurs pays d’Asie, ii/ la mosaïque en tirets est largement répandue en Asie et iii/ la maladie est causée par au moins deux souches différentes de SCSMV en Inde. De plus, des feuilles de canne à sucre présentant des symptômes de mosaïque peuvent être infectées simultanément par le SCSMV et le SCMV.
DETECCIÓN DEL VIRUS DEL MOSAICO RAYADO DE LA CAÑA DE AZÚCAR EN VARIOS PAÍSES ASIÁTICOS

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PALABRAS CLAVES: Potyviridae, RT-PCR, SCMV, SCSMV.

Resumen

CINCO muestras de hojas con síntomas de mosaico de la caña de azúcar provenientes Bangladesh, India, Sri Lanka, Tailandia, y Vietnam reaccionaron negativamente en un análisis de RT-PCR con el Virus del mosaico de la caña de azúcar (SCMV), el Virus del mosaico del sorgo (SrMV) y cebadores específicos de potivirus. Posteriormente los síntomas de mosaico se reprodujeron a partir de la inoculación mecánica de plantas de caña de azúcar, maíz y sorgo, empleando extractos con hojas infectadas, sin embargo los síntomas no fueron tan severos como aquellos causados por SCMV y SrMV. Mediante microscopía electrónica de viriones parcialmente purificados a partir de plantas inoculadas se observaron filamentos flexuosos característicos de la familia de Potyviridae. Las cinco muestras de hojas de caña de azúcar reaccionaron positivamente, en análisis de RT-PCR con dos pares de cebadores diseñados para detectar el Virus del mosaico de rayado de la caña de azúcar (SCSMV), agente causal del mosaico rayado de la caña de azúcar, miembro sin clasificar de la familia de Potyviridae. El SCSMV fue detectado por RT-PCR en 34 muestras de hoja a partir de 30 cultivares que exhibían síntomas de mosaico y originarios de Bangladesh, India, Pakistán, Sri Lanka, Tailandia, y Vietnam. El amplicon (0.5 KB) de la región de codificación de la cápside proteica de cinco aislamientos del virus mostró una similitud de 97 al 99% con SCSMV de Pakistán (número de accesión U75456 del GenBank) y de 93 al 95% con SCSMV-AP de la India (número de accesión Y17738 del GenBank). Nuestros resultados sugieren que i/ SCSMV es la causa principal de los síntomas de mosaico en caña de azúcar en varios países asiáticos, ii/ el mosaico rayado se encuentra ampliamente distribuido en Asia y iii/ la enfermedad es causada por lo menos por dos razas diferentes del SCSMV en la India. Además, las hojas de la caña de azúcar que muestran síntomas de mosaico pueden estar infectadas simultáneamente por SCSMV y SCVM.