



Characterization of variation in *Sugarcane bacilliform virus* (SCBV) associated with leaf fleck disease of sugarcane in India

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In India, presence of *Sugarcane bacilliform virus* (SCBV) was found in sugarcane germplasm during 1992 and subsequently it was found in cultivated varieties. Although presence of the virus was reported in the country, information on the viral genome and genomic variation were not available. We characterized Indian SCBV isolates and performed phylogenetic analyses in relation to SCBV and other closely related badnaviruses reported from other parts of the world. The virus isolate SCBV-BO91 from cv. BO 91 representing commercial cultivars and SCBV-BB, SCBV-BT, SCBV-BRU and SCBV-Iscam from *Saccharum officinarum* genotypes were sequenced to complete genome level and the viral genome lengths ranged from 7553 to 7884 nucleotides. The genome size of the isolates SCBV-BRU and SCBV-BO91 were found to be larger than that of the virus species reported in badnaviruses to date. The Indian SCBV isolates shared identities of 69-85% for the complete genomic sequence, indicating wide genetic diversity among them, and share 70-82% identity with *Sugarcane bacilliform Ireng Maleng virus* (SCBIMV) and *Sugarcane bacilliform Morocco Virus* (SCBMV), as well as 43-46% identity with *Banana streak virus* (BSV) and BSV-related SCBV species from Guadeloupe, indicating that the Indian SCBV isolates are distinct from SCBV isolates reported to date. Irrespective of the region compared, SCBV isolates from India, Australia and Morocco clustered together. BSV and BSV-related SCBV sequences from Guadeloupe formed another cluster. PASC and phylogenetic analysis evidenced that in India, the symptoms associated with badnaviruses in sugarcane are caused by at least three species, SCBBbV, SCBBoV and SCBBruV, besides SCBIMV and SCBMV represented by SCBV-BT and SCBV-Iscam, respectively for the first time. However, in this study, the substantial variability observed even within a limited number of isolates further suggests the occurrence of highly diverged virus isolates in the world sugarcane germplasm collections at Kannur, India. Also, SCBV-BO91 being a different genome may represent the virus present cultivated sugarcane varieties of India. The sequence comparison and phylogenetic study with another 16 partially characterized Indian SCBV isolates revealed that the existing genetic variation in the SCBV infecting *S. officinarum* is higher than those occurs in hybrid cultivars.

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