

GENETIC VARIATION OF BERMUDA GRASS SOUTHERN MOSAIC VIRUS ISOLATES BASED ON SEQUENCE OF 3' REGION OF GENOME*

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Abstract

Bermuda grass southern mosaic virus (BgSMV) is a widespread potyvirus inducing mosaic on Bermuda grass in warm regions of southern Iran. In this study, various geographical isolates of the virus were compared phylogenetically. Bermuda grass samples showing mosaic symptom were collected from Jiroft, Bushehr, Borazjan, Ramhormoz, Andimeshk, Shushtar, Behbahan and Darab. Viral RNA was extracted and reverse transcription polymerase chain reaction (RT-PCR) was conducted using specific primers for amplification of the 3' region (CP- UTR) of the viral genome. PCR- products were cloned and sequenced. The sequences of CP- UTR region of BgSMV isolates were compared with each other and with available sequences of cereal potyviruses in the GenBank. Phylogenetic analyses showed that all sequences were grouped into six clades of BgSMV, *Maize dwarf mosaic virus* (MDMV), *Sugarcane mosaic virus* (SCMV), *Johnson grass mosaic virus* (JGMV), *Sorghum mosaic virus* (SrMV), Iranian Johnson grass mosaic virus (IJMV) and *Zea mosaic virus* (ZeMV). IJMV and ZeMV were grouped in the same clade. Among potyviruses, BgSMV was close to MDMV. However it had an additional 90- nucleotide stretch in frame (30 amino acids) in the 5' region of the coat protein compared with MDMV. This difference was consistent in all BgSMV isolates. The mean of the nucleotide similarity in CP- UTR region among BgSMV isolates was 98.1% which indicates low level of genetic diversity in intra- population of BgSMV. Despite the high nucleotide sequence similarity between BgSMV and MDMV, differences between the two viruses in host range and serology, and presence of additional 90 nt in the 5' region of CP gene, make BgSMV a distinct potyvirus species close to MDMV.

Keywords: Potyviruses, Phylogenetic analysis, MDMV, BgSMV, CP-UTR.

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