Complete genome sequence of *Bean pod mottle virus* identified from common bean (*Phaseolus vulgaris*)

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*Bean pod mottle virus* (BPMV) in the genus *Comovirus* is a plant virus infecting common bean. We obtained genomes of two BPMV isolates referred as Tigerskin-A and Tigerskin-B consisting of two RNA segments from common bean plants displaying viral disease symptoms by RNA-sequencing. RNA1 encodes a single polyprotein containing five mature proteins while RNA2 encodes a single polyprotein containing a movement protein and two coat proteins. The two BPMV isolates showed high sequence similarity (99.65% to 99.70%) to two isolates, IA-Di1 and Iowa-Desmodium illinoense 1, from the *Desmodium illinoense* in USA belonging to a flowering plant in the bean family.

**Keywords:** *Bean pod mottle virus*, common bean, genome, virus

*Bean pod mottle virus* (BPMV) consists of two RNA segments, RNA1 and RNA2 (Di *et al.*, 1999). The hosts of BPMV are legumes such as common bean (*Phaseolus vulgaris*), soybean (*Glycine max* L.), and clovers. BPMV is transmitted by leaf-feeding beetles, sap, and seeds (Redinbaugh *et al.*, 2010). Infection of BPMV results in severe damage on the seed quality and production (Giesler *et al.*, 2002). The plants infected by BPMV show yellow mottling or distorted leaves. Moreover, the BPMV infected bean plants produce mottled or discolored seeds.

We observed severe viral disease symptoms from several common bean plants growing in the field located in Hoengseong, Korea. To identify viruses causing yellow mottling and distorted leaf disease, we collected leaf tissues showing strong disease symptoms from two individual common bean plants. The harvested leaves were used for total RNA extraction using RNeasy Plant Mini kit (Qiagen) according to manufacturer’s instruction. Two mRNA libraries were generated using the TruSeq RNA Library Preparation Kit v2 (Illumina). The generated mRNA libraries were paired-end sequenced with a NovaSeq6000 system (Macrogen). The obtained raw sequence reads were
subjected to de novo transcriptome assembly using Trinity program (version 2.10.0) with default parameters (Haas et al., 2013). The assembled transcriptomes were subjected to BLASTX search against with E-value 1e-10 as a cutoff against the NCBI’s non-redundant (NR) protein database. Based on BLASTX results, virus-associated contigs were identified. The identified virus-associated contigs were further subjected to open reading frame (ORF) prediction using ORFfinder program (https://www.ncbi.nlm.nih.gov/orffinder/). The phylogenetic trees were constructed using available complete genomes of BPMV using the MEGA7 program (Kumar et al., 2016).

From the two different libraries, we obtained complete genomes of two BPMV isolates referred as Tigerskin-A and Tigerskin-B consisting of two RNA segments. The sizes of two RNA1 segments were 5,926 (Tigerskin-A) and 5,953 (Tigerskin-B) nucleotides (nt) in length while the sizes of two RNA2 segments were 3,654 (Tigerskin-A) and 3,665 (Tigerskin-B) nt in length. The nucleotide identities for the two RNA1 segments was 99.66% while the two RNA2 segments were identical. RNA1 of BPMV isolate Tigerskin-A (GenBank accession MW019503) encodes a single polyprotein of 1,851 amino acids containing five mature proteins for replication such as a protease cofactor, a putative helicase, a viral protein genome-linked (VPg), a protease, and a putative RNA-dependent RNA polymerase (RdRp) (Fig. 1A). RNA2 of BPMV isolate Tigerskin-A (GenBank accession MW019504) encodes a single polyprotein of 1,019 aa containing movement protein, large coat protein, and small coat protein (Fig. 1B).

BLASTN results revealed that the two RNA1 segments of two isolates showed sequence similarity to RNA1 of BPMV isolate 1A-Di1 (GenBank GU562879.1) with 100% coverage and 99.70% nt identity while the two RNA2 segments of two isolates showed sequence similarity to RNA2 of BPMV Iowa-Desmodium illinoense 1 (GenBank GQ996949.1) with 100% coverage and 99.65% nt identity. To reveal phylogenetic relationship of identified BPMV isolates, two phylogenetic trees were constructed using the MEGA7 program with Maximum likelihood method and 1,000 bootstrap replicates.

Fig. 1. Genomic features and phylogenetic relationship of BPMV isolates Tigerskin-A and Tigerskin-B. Genomic features of BPMV isolate Tigerskin-A consists of RNA1 (A) and RNA2 (B). Each RNA segment encodes a polyprotein, which is processed into five proteins (RNA1) and two proteins (RNA2). Phylogenetic relationship of BPMV isolates Tigerskin-A and Tigerskin-B with other BPMV isolates using RNA1 (C) and RNA2 (D) sequences. The phylogenetic tree was constructed using the MEGA7 program with Maximum likelihood method and 1,000 bootstrap replicates.
constructed using complete nucleotide sequences of RNA1 and RNA2 segments, respectively. We collected all available complete genome sequences for BPMV RNA1 (10 genomes) and RNA2 (8 genomes). Except the two BPMV isolates from this study, all available complete genome sequences of BPMV were derived from USA. The phylogenetic tree for BPMV RNA1 showed two groups of BPMV isolates (Fig. 1C). Two isolates Tigerskin-A and Tigerskin-B belong to the group A with five isolates from USA. Three isolates with identical name as Iowa-Desmodium illinoense were phylogenetically different from each other. Similarly, the phylogenetic tree for BPMV RNA2 identified two groups of BPMV isolates (Fig. 1D). Two BPMV isolates in this study belong to the group A with six isolates from USA while two isolates, IL-Cb1 and G-7 belong to the group B. Two phylogenetic trees revealed that the two isolates, Tigerskin-A and Tigerskin-B, were closely related with other two isolates, IA-Di1 and Iowa-Desmodium illinoense 1 identified from the Desmodium illinoense which is a flowering plant in the bean family (Fabaceae). Based on BLASTN results and phylogenetic analyses, the two BPMV isolates in this study were closely related with other BPMV isolates derived from USA.

Taken together, we report the complete genomes of two BPMV isolates causing yellowing mottling, and distortion symptoms in common bean plants in Korea using RNA-sequencing.

Nucleotide sequence accession number

The complete genome sequences of Bean pod mottle virus isolates Tigerskin-A and Tigerskin-B have been deposited in GenBank under the accession numbers, MW019502, MW019503, MW019504, and MW019506.

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Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References


