

Genome Assembly of Bell Pepper *Endornavirus* from Small RNA

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The family *Endornaviridae* infects diverse hosts, including plants, fungi, and oomycetes. Here we report for the first time the assembly of bell pepper endornavirus by next-generation sequencing of viral small RNA. Such a population of small RNA indicates the activation of the viral immunity silencing machinery by this cryptic virus, which probably encodes a novel silencing suppressor.

The family *Endornaviridae* infects diverse hosts, including plants, fungi, and oomycetes (1). Endornaviruses consist of a large double-stranded RNA (dsRNA) element with a nick in the coding strand. Endornaviruses possess unique properties, including no evidence of encapsidation and a single long open reading frame (ORF). The ORF encodes a putative polyprotein with methyltransferase, helicase, glycosyltransferase, and RNA-dependent RNA polymerase domains (5). Recently, the complete genomes of two strains of bell pepper endornavirus (BPEV) of genus *Endornavirus*, family *Endornaviridae*, were sequenced using viral dsRNA as a template for reverse transcription, followed by PCR amplification and 5' and 3' rapid amplification of cDNA ends (RACE) (3, 4, 5). Here we report for the first time a complete genome assembly of BPEV from small RNA purified from pepper leaves.

Total RNA was extracted from 5 g of pepper (*Capsicum annuum* L. cv. Yatir) leaves in Israel using TRI reagent, and the pellet was dissolved in nuclease-free water. Small RNA (70 µg) was purified from total RNA using the mirVana microRNA (miRNA) isolation kit (Ambion) and stored at -80°C. Small RNA concentrations were determined by the Agilent 2100 bioanalyzer. Purified small RNA was “deep sequenced” by the SOLiD version 3 instrument (Applied Biosystems Foster, CA) according to the manufacturer's protocols. The bioinformatic analysis used the BFAST (1) alignment tool with the reference genome of BPEV cv. Kyosuzu (BPEV-KY) (GenBank accession number AB597230). Base coverage was 100%, the average coverage depth was 258, and the maximum coverage depth was 2,870 (calculated with Tablet [2]). Alignment against the reference genome of BPEV cv. Yolo Wonder (BPEV-YW) (GenBank accession JN019858) gave 52% coverage, with an average coverage of 57 and a maximum coverage depth of 2,869. The complete genome sequence of the Israeli isolate of BPEV (BPEV-Is) is composed of 14,727 nucleotides, with a typical endornavirus genome organization containing a single open reading frame with a predicted molecular mass of 553 kDa. BPEV-Is has 99% nucleotide identity to BPEV-KY and 88% nu-

cleotide identity to BPEV-YW. Plant viral symptoms are commonly the result of suppressor activity; however, our results indicate that BPEV activates the RNA silencing machinery of the plant immune system without inducing viral symptoms and therefore probably also encodes a novel silencing suppressor.

Nucleotide sequence accession number. This genome sequence was deposited under NCBI GenBank accession number JQ951943.

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