



Complete Genome Sequence of *Nectarine stem pitting-associated virus*, Isolated from *Prunus persica* in Cheongdo County, South Korea

Davaajargal Igori,^{a,b} Dasom Baek,^{a,b} San Yeong Kim,^c Euncheol Seo,^c Su-Heon Lee,^d Rae-Dong Jeong,^e Seung-In Yi,^f Jin-Jong Bong,^g Jae Sun Moon^{a,b}

Biotechnology Program, University of Science and Technology, Daejeon, Republic of Korea^a; Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea^b; Cheongdo Peach Research Institute, Gyeongsangbuk-do Agricultural Research and Extension Services, Cheongdo, Republic of Korea^c; School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea^d; Department of Applied Biology, Chonnam National University, Gwangju, Republic of Korea^e; Korea Seed and Variety Service, Ministry of Agriculture, Food and Rural Affairs, Gimcheon-si, Republic of Korea^f; NEXBIO Co., Ltd., Daejeon, Republic of Korea^g

ABSTRACT We report here the first complete genome sequence of a South Korean isolate of *Nectarine stem pitting-associated virus* (NSPaV) from peach and compare it with previously described complete NSPaV genome sequences. The highest whole-genome nucleotide sequence identity was 95.3% with GenBank accession no. KT273409 (NSPaV) from the United States.

Nectarine stem pitting-associated virus (NSPaV) is a single-stranded positive-sense RNA virus of the genus *Luteovirus* in the family *Luteoviridae*, which was first described in the United States in nectarine (*Prunus persica*) (1, 2). It was recently detected in *Prunus* spp. in China (3), Japan (4), South Korea (5), and Hungary (6). The NSPaV genome has four open reading frames.

Peach (genus *Prunus*, family *Rosaceae*) is an economically important crop that is infected by a number of plant viruses and viroids. Peach tree (*Prunus persica*) leaves with and without symptoms were collected in Cheongdo County, South Korea, in May 2015. Total RNA was isolated from the leaf tissue using a WizPrep Plant RNA minikit (Wizbiosolutions, Seongnam, South Korea). Before library construction, ribosomal RNA (rRNA) was removed from extracted total RNA using a Ribo-Zero rRNA removal kit (Plant Leaf; Epicentre, Madison, WI, USA). A library was constructed from the rRNA-depleted RNA using a TruSeq RNA sample prep kit (Illumina, San Diego, CA, USA) and sequenced using an Illumina HiSeq2500 sequencer. The obtained raw reads were trimmed and then *de novo* assembled from the remaining high-quality reads using Trinity software. BLASTn analysis showed that, among the assembled contigs, one long contig, representing nearly the entire genome (4,874 bp), had the highest nucleotide sequence similarity (95% identity) to NSPaV (GenBank accession no. KT273409) and was designated the NSPaV-SK contig. To confirm the sequence of the NSPaV-SK contig, specific primer sets were designed based on the contig sequence. Complementary DNA (cDNA) was synthesized from isolated total RNA from a peach sample using a random N25 primer with RevertAid reverse transcriptase (RT) (Thermo Scientific, Waltham, MA, USA). RT-PCR was conducted with the synthesized cDNA and specific primer pairs using AccuPower ProFi Taq PCR premix (Bioneer, Daejeon, South Korea). RT-PCR products were cloned into the RBC T&A cloning vector (RBC Bioscience, Taipei, Taiwan) and sequenced by GenoTech (Daejeon, South Korea). To complete the genome sequence of NSPaV-SK, the 5' and 3' termini of the viral RNA were verified using a 5'/3' RACE system

Received 21 July 2017 Accepted 26 July 2017 Published 31 August 2017

Citation Igori D, Baek D, Kim SY, Seo E, Lee S-H, Jeong R-D, Yi S-I, Bong J-J, Moon JS, 2017. Complete genome sequence of *Nectarine stem pitting-associated virus*, isolated from *Prunus persica* in Cheongdo County, South Korea. *Genome Announc* 5:e00908-17. <https://doi.org/10.1128/genomeA.00908-17>.

Copyright © 2017 Igori et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Jae Sun Moon, jsmoon@kribb.re.kr.

