



Complete Genome Sequence of a Divergent Isolate of Cherry Virus A from *Prunus avium* in China

Yunxiao Xu,^a Rui Gao,^a Shifang Li,^a  Meiguang Lu^a

^aState Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China

ABSTRACT Here, we report the complete genome sequence of a divergent cherry virus A (CVA) isolate (ChYT56) from *Prunus avium* in China. The genome nucleotide sequence has low identity (80.7%) with a CVA from *P. avium* (GenBank accession number [FN691959](#)) and high identity (97%) with a CVA from *P. armeniaca* (GenBank accession number [LC125634](#)).

Cherry virus A (CVA) is a member of the genus *Capillovirus*, family *Betaflexiviridae*, which was first described in Germany from sweet cherry (*Prunus avium*) (1). CVA has been detected in *Prunus* hosts, such as cherry (2), apricot, peach (3), mume, and plum (4, 5). The virus is widely distributed in more than 10 countries, including Germany (1), Canada (3), India (6), and other countries (7). Previously, we reported the complete nucleotide sequences of three Chinese isolates (ChTA11, ChTA12, and ChYT52) of CVA from cherry (7, 8). The sequences of isolates ChTA11 and ChTA12 are closely related and cluster in phylogroup I with a cherry isolate (GenBank accession number [X82547](#)). The majority of noncherry isolates cluster in phylogroup III, while isolate ChYT52, as a consequence of a recombination event that occurred between CVA isolates from cherry and noncherry hosts, clusters in phylogroup II (7, 8). However, the genetic diversity analyses among the CVA sequences derived from 31 samples in 3 genomic regions that correspond to the coat protein (CP), the RNA-dependent RNA polymerase (RdRp), and the movement protein (MP) showed that the ChYT56 cherry tree is the only sample for which only a single haplotype was detected for all 3 genes (7, 8).

The complete genome sequence was determined for a CVA isolate from a ChYT56 sweet cherry tree in Shandong Province, China. Total RNA was extracted from this ChYT56 tree isolate, and reverse transcription-PCR (RT-PCR) was performed as described by Gao et al. (7). Four pairs of PCR primers (7) and one pair of primers, F (5'-TTCCCTGACAAATCCAAAGG-3') and R (5'-CAGTTTGGCCAAGGATGACT-3'), which direct the amplification of overlapping fragments that span the entire CVA genome, were used. The 3' and 5'-terminal regions were amplified using an oligo(dT) primer and a 5'-full rapid amplification of cDNA ends (RACE) kit with tobacco acid pyrophosphatase (TAP; TaKaRa, Beijing, China). All amplification products were cloned and sequenced (using the ABI Prism 3730XL DNA analyzer). The resulting overlapping sequences were then assembled (using DNAMAN 6.0) into the complete genome sequence of the CVA isolate, named ChYT56.

The complete genome of isolate ChYT56 consists of 7,433 nucleotides, encodes 2 open reading frames (ORFs), and has a GC content of 39.45%. ORF1 (nucleotide positions 107 to 7135) encodes the RdRp and CP proteins, and the overlapping ORF2 (nucleotide positions 5452 to 6843) encodes the MP. The genome nucleotide sequence had low identity (80.7%) with a CVA from *P. avium* (GenBank accession number [FN691959](#)) and high identity (97%) with a CVA from *P. armeniaca* (GenBank accession number [LC125634](#)). Phylogenetic analysis of the ChYT56 genome with CVA genomes present in GenBank resulted in the same clusters as those shown by Gao et al. (7), and

Received 11 September 2018 Accepted 1 October 2018 Published 25 October 2018

Citation Xu Y, Gao R, Li S, Lu M. 2018. Complete genome sequence of a divergent isolate of cherry virus A from *Prunus avium* in China. *Microbiol Resour Announc* 7:e01218-18. <https://doi.org/10.1128/MRA.01218-18>.

Editor Irene L. G. Newton, Indiana University Bloomington

Copyright © 2018 Xu et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](#).

Address correspondence to Meiguang Lu, mglu@ippcaas.cn.

isolate ChYT56 clusters into phylogroup III, the cluster containing the majority of noncherry isolates. It has been suggested that ChYT56 is a highly divergent isolate from *P. avium*. We also found that the sequences from a few isolates from *P. avium* obtained using next-generation sequencing (9) clustered into phylogroup III, while ChYT56 is the only isolate sequence divided into phylogroup III from *P. avium* that was amplified by conventional RT-PCR.

Data availability. The complete genome sequence of ChYT56 has been deposited in GenBank under the accession number [MH806869](https://www.ncbi.nlm.nih.gov/nuclseq/MH806869).

ACKNOWLEDGMENTS

This work was supported by the National Natural Science Foundation of China (grant number 31471752) and Key Inter-Governmental Projects of the National Key Research and Development Program (grant number 2017YFE0110900).

REFERENCES

- Jelkmann W. 1995. Cherry virus A: cDNA cloning of dsRNA, nucleotide sequence analysis and serology reveal a new plant capillovirus in sweet cherry. *J Gen Virol* 76:2015–2024. <https://doi.org/10.1099/0022-1317-76-8-2015>.
- Mandic B, Matic S, Al Rwahnih M, Jelkmann W, Myrta A. 2007. Viruses of sweet and sour cherry in Serbia. *J Plant Pathol* 89:103–108.
- James D, Jelkmann W. 1998. Detection of cherry virus A in Canada and Germany, p 299–303. *In* 17th International Symposium on Virus and Virus-Like Diseases of Temperate Fruit Crops: Fruit Tree Diseases. International Society for Horticultural Science, Leuven, Belgium. <https://doi.org/10.17660/ActaHortic.1998.472.35>.
- Šafařová D, Navrátil M, Paprštejn F, Candresse T, Marais A. 2013. Cherry virus A infecting cherries and plums in the Czech Republic—short communication. *Hort Sci (Praha)* 40:37–39. <https://doi.org/10.17221/141/2012-HORTSCI>.
- Marais A, Faure C, Svanelle-Dumas L, Candresse T. 2008. First report of cherry virus A in *Prunus mume* in China. *Plant Dis* 92:1589–1589. <https://doi.org/10.1094/PDIS-92-11-1589A>.
- Noorani MS, Awasthi P, Singh RM, Ram R, Sharma MP, Singh SR, Ahmed N, Hallan V, Zaidi AA. 2010. Complete nucleotide sequence of cherry virus A (CVA) infecting sweet cherry in India. *Arch Virol* 155:2079–2082. <https://doi.org/10.1007/s00705-010-0826-6>.
- Gao R, Xu YX, Candresse T, He Z, Li SF, Ma YX, Lu MG. 2017. Further insight to genetic variation and haplotype diversity of cherry virus A from China. *PLoS One* 12:e0186273. <https://doi.org/10.1371/journal.pone.0186273>.
- Gao R, Li SF, Lu MG. 2016. Complete nucleotide sequences of two isolates of cherry virus A from sweet cherry in China. *J Integr Agric* 15:1667–1671. [https://doi.org/10.1016/S2095-3119\(16\)61343-6](https://doi.org/10.1016/S2095-3119(16)61343-6).
- Kesanakurti P, Belton M, Saeed H, Rast H, Boyes I, Rott M. 2017. Comparative analysis of cherry virus A genome sequences assembled from deep sequencing data. *Arch Virol* 162:2821–2828. <https://doi.org/10.1007/s00705-017-3394-1>.