



# First report of Australian grapevine viroid infecting grapevines in Korea

Jae-Yun Heo<sup>1</sup> · Do-Hoon Lee<sup>1</sup> · Chang-Ho Lee<sup>1,2</sup>

Received: 19 May 2022 / Accepted: 3 August 2022 / Published online: 11 August 2022  
© The Author(s) under exclusive licence to Società Italiana di Patologia Vegetale (S.I.Pa.V.) 2022

**Keywords** AGVd · Grape · RT-PCR · Viroid

Grapevine, one of the major fruit crops in Korea, ranks fourth among fruit crops in the cultivation area (Kim et al. 2021). Five distinct viroids, Australian grapevine viroid (AGVd), citrus exocortis viroid (CEVd), grapevine yellow speckle viroid 1 (GYSVd-1), grapevine yellow speckle viroid 2 (GYSVd-2), and hop stunt viroid (HSVd), have been detected in grapevines globally. AGVd belongs to the genus *Apscaviroid* of the family *Pospiviroidae* and infects grapevines in Australia, China, Greece, India, Iran, Italy, Thailand, the United States, Tunisia, and Turkey. However, AGVd has not yet been reported in Korea. In October 2020, leaves from 15 plants showing symptom of viroid infection were collected from grape cultivar Shine Muscat. Nine samples were obtained from three vineyards located in Yeongwol, and the remaining six samples were harvested from two vineyards located in Gangneung, South Korea. From each leaf sample, total RNA was extracted, reverse transcription–polymerase chain reaction (RT-PCR) was performed using the specific primer pair AGVd-mF and AGVd-mR (Hajizadeh et al. 2012). Two samples, one collected from Gangneung and the other from Yeongwol, yielded the expected 195 base pair (bp) fragment, testing positive for AGVd. To verify the occurrence of AGVd in Korea, a second RT-PCR was performed using another AGVd-specific primer pair, AGVd-P7 (5'-ACCTGCAGGGAAGCTAGCTGGGTC-3') and AGVd-P8 (5'-CCCTGCAGGTTTCGCCAGCAAGCGC-3') (Jiang et al. 2009).

Fragments of the expected size (369 bp) were also detected from the two samples. PCR amplicons were then purified and subjected to Sanger sequencing in both directions. The resulting sequences were assembled using BioEdit v7.2.5 and deposited to GenBank under accession numbers ON049349 and ON049350. Similarity searches using BLAST demonstrated that the sequences of AGVd isolated from Yeongwol (ON049349) and Gangneung (ON049350) shared 100% nucleotide identity with the isolate AGVd\_mahalat from Iran (KF876038) and the isolate AGVd\_Ths from Chile (KF0072710), respectively. The genomes between the two Korean AGVd isolates shared 98.6% identity. The variability observed between these two isolates collected from different regions suggests that the infection route of AGVd can differ. To the best of our knowledge, this is the first report of AGVd infecting grapevines in Korea, highlighting the global spread of AGVd.

**Acknowledgements** This work was supported by the National Research Foundation of Korea (No. 2020R1F1A1073922).

## References

- Hajizadeh M, Navarro B, Bashir NS, Torchetti EM, Di Serio F (2012) Development and validation of a multiplex RT-PCR method for simultaneous detecting five grapevine viroids. *J Virol Methods* 179:62–69
- Jiang D, Peng S, Wu Z, Cheng Z, Li S (2009) Genetic diversity and phylogenetic analysis of Australian Grapevine Viroid (AGVd) isolated from different grapevines in China. *Virus Genes* 38:178–183
- Kim SH, Jeong SH, Heo JY (2021) Incidence of 14 grapevine viruses in Korean vineyards. *Not Bot Horti Agrobot Cluj Napoca* 49:12490

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

✉ Chang-Ho Lee  
chlee.gwnu@gmail.com

Jae-Yun Heo  
jyheo@gwnu.ac.kr

Do-Hoon Lee  
dhlee.gwnu@gmail.com

<sup>1</sup> Department of Plant Science, Gangneung-Wonju National University, Gangneung 25457, Republic of Korea

<sup>2</sup> Yeongwol-Gun Agricultural Technology Center, Yeongwol 26231, Republic of Korea