First Report of Grapevine Rupestris Vein Feathering Virus in Grapevine in Australia

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Grapevine rupestris vein feathering virus (GRV-FV; tentative genus *Marafivirus*; family *Tymoviridae*) was first detected from a Greek grapevine (*Vitis vinifera*) with asteroid mosaic-like symptoms (El Beaino et al. 2001; Ghanem-Sabanadzovic et al. 2003) and was also infected with grapevine fleck virus. GRV-FV has been detected in the United States, South Africa, Canada, Spain, China, New Zealand, Brazil, Germany, Korea, Slovakia, Hungary, and Pakistan (Cho et al. 2018; Mahmood et al. 2019). Transmission vectors are currently unknown. In 2018, nine grapevine samples were collected between May and July in South Australia (SA) and Western Australia (WA) and were analyzed by high-throughput sequencing (HTS) to characterize grapevine viruses in Australian vineyards. Total RNA or double-stranded RNA was extracted from grapevine canes using an RNeasy 96 QIAcube HT kit (Qiagen) with MacKenzie buffer (MacKenzie et al. 1997) or using CF-11 (Balijja et al. 2008). Libraries were prepared using the NEBNext Ultra II RNA library Prep Kit (NEB) or TruSeq Stranded mRNA Prep kit (Illumina) with Ribo-Zero gold plant kit for ribosomal depletion (Illumina, San Diego, CA). Libraries were sequenced using Illumina MiSeq (SA) or HiSeq (WA) technology with 2 × 300 (SA) or 2 × 100 (WA) paired-end reads, which

were trimmed using Trim Galore! (0.4.0) or BBmap (38.20), respectively. De novo assembly, using the SPAdes (version 3.12.0) genome assembler with default settings, resulted in 12 near-full-length GRV-FV genomes (6,713 to 6,737 nt), eight sequences from the WA samples and four from the SA samples. WA samples 171 and 178 and SA sample BV each had two distinct GRV-FV molecular variants. Variants 171-1 and 171-2 (GenBank accessions MT084811 and MT084812) from sample 171 shared 83.39% nucleotide (nt) identity. Variants 178-1 and 178-2 (MT084813 and MT084814) from sample 178 shared 83.54% nt identity. Variants BV6799 and BV8822 (MN974274 and MN974275) from sample BV shared 82.85% nt identity. Only one GRV-FV sequence was obtained from all other samples. The genome of SA isolate LC1 (MN974273) was confirmed by RT-PCR amplification and Sanger sequencing of overlapping genome regions. Tissue from the infected LC1 isolate has been deposited into the Victorian plant pathogen reference collection (VPRI accession no. 43698). When the genomes of all Australian isolates were compared, they had 78.94 to 94.37% nt identity with each other. The SA isolates LC1, BV8822, BV6799, and SEL-L (MN974276) and the WA isolates 172 (MT084807), 179 (MT084808), 180 (MT084809), and 182 (MT084810) were most closely related to the Swiss isolate CHASS (KY513702; 82.87 to 85.46% nt identity). The WA isolates 171-1, 171-2, 178-1, and 178-2 were most closely related to the New Zealand isolate Ch8021 (MF000325; 83.21 to 93.87%). Grapevine leafroll-associated virus 1 (GLRaV-1), GLRaV-3, GLRaV-4 (strain 6 and 9), grapevine virus A, grapevine rupestris stem pitting associated virus, grapevine yellow speckle viroid 1, and hop stunt viroid were also identified in the sequencing data. This is the first report of GRV-FV in Australia. All WA samples were collected during dormancy, and symptoms were not observed. Sample LC1 from SA had Shiraz disease, the other SA samples were asymptomatic, and none had asteroid mosaic-like symptoms. Further research is required to determine its distribution and association with disease in Australia.

References:

- Balijja, A., et al. 2008. J. Virol. Methods 152:32.
- Cho, L., et al. 2018. Plant Dis. 102:1471.
- El Beaino, T., et al. 2001. Vitis 40:65.
- Ghanem-Sabanadzovic, N. A., et al. 2003. Virus Genes 27:11.
- MacKenzie, D. J., et al. 1997. Plant Dis. 81:222.
- Mahmood, M., et al. 2019. J. Plant Pathol. 101:1261.

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