Diseases Caused by Viruses

First Report of Grapevine rupestris vein feathering virus in Wine Grapes in Idaho

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Grapevine rupestris vein feathering virus (GRVFFV) was found associated with chlorotic discolorations of leaf veins in a Greek grapevine cultivar (Abou Ghanem-Sabanadzovic et al. 2003; El Beaino et al. 2001) or with Syrah decline (Al Rwahnih et al. 2009). In the United States, GRVFFV was reported to occur in California (Al Rwahnih et al. 2009) and in Washington State (Chingandu et al. 2021). Wine grape production in Idaho is known to be affected by several viruses, such as grapevine leafroll-associated virus 3 (GLRaV-3; Mekuria et al. 2009; Thompson et al. 2019a), grapevine fleck virus (GFKV; Kanuya et al. 2012), and grapevine red blotch virus (GRBV; Thompson et al. 2019b), but the GRVFFV status was not addressed previously. In 2018, leaf and petiole samples from five declining Chardonnay vines were collected from a single vineyard in Canyon County of Idaho. Ribodepleted total RNA prepared from these samples was subjected to a high-throughput sequencing (HTS) analysis on a MiSeq platform as described previously (Thompson et al. 2019a), yielding between 3,623,716 and 4,467,149 300-bp paired-end reads. Briefly, raw reads were adapter and quality cleaned and mapped against the *Vitis vinifera* L. reference genome. Unmapped paired reads were assembled, producing between 829 and 1,996 contigs over 1,000 nt in length. All five samples were found to contain GLRaV-3 and the two common viroids, hop stunt viroid and grapevine yellow speckle viroid, while four contigs ranging in size from 1,361 to 6,736 nt and exhibiting homology with GRVFFV were found in three out of the five Chardonnay samples

analyzed. Those GRVFFV-specific contigs had 98.5 to 98.7% pairwise identity. A nearly complete genome of GRVFFV-ID was assembled from the HTS data of one sample, and the 3'-terminus of the genome was acquired using the RACE methodology; the 6,736-nt sequence has been deposited in the GenBank database under the accession number MZ027155. BLASTn analysis of this sequence revealed 90.7% identity to the closest match in the GenBank database (MH544699, isolate SK931 from Slovakia). In the fall of 2020, six commercially operating vineyards in Canyon and Nez Perce counties of Idaho, including the original one, were sampled for the total of 26 sampled plants of white and red wine grape cultivars, based on visual symptoms of leaf reddening, leaf rolling, and chlorosis, and tested by reverse transcription (RT)-PCR using newly designed GRVFFV-specific primers, GRVFFV-F1 (5'-GAAGCAACAGTGCCCGTCTC-3') and GRVFFV-R1 (5'-AGGTCGCTT-TACGGACCTTTTCTT-3'). Four plants were found positive for GRVFFV by RT-PCR; these positive samples came from three vineyards in Canyon County from the same wine grape cultivar, Chardonnay. Amplified RT-PCR products were directly sequenced using conventional Sanger methodology and confirmed to represent 662-nt segments of the GRVFFV genome exhibiting 98.6 to 99.1% pairwise identity to the HTS-derived full-length genome of GRVFFV-ID (MZ027155). The four corresponding partial sequences were deposited under the accession numbers MZ020577 to MZ020580. This close identity between the GRVFFV sequences from three different Idaho vineyards, coming from the same cultivar Chardonnay, may suggest a common origin of the GRVFFV infection, possibly the same supplier of the original Chardonnay planting material. The California GRVFFV sequence AY706994 was 80% identical to the GRVFFV-ID, while the recently reported partial sequences of GRVFFV from Washington State (MT782067 to MT782070; Chingandu et al. 2021) were found to be only 82 to 85% identical to the GRVFFV-ID. Presence of GRVFFV might have contributed to the decline of the original Chardonnay vines, although the exact role of GRVFFV in a mixed infection with GLRaV-3 is not clear at the moment. To the best of our knowledge, this is the first report of GRVFFV in wine grapes in Idaho.

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