Grapevine leafroll disease (GLD) is the most economically destructive virus disease of wine grapes (Vitis vinifera), severely affecting vine health and fruit yield and quality. It continues to threaten the sustainability of premium wine grape production in Washington State. Grapevine leafroll-associated viruses (GLRaVs) are a group of viruses documented in GLD-affected vines. Among them, Grapevine leafroll-associated virus 3 (GLRaV-3) is the most widespread and insidious in Washington State vineyards (Rayapati et al. 2008; Naidu et al. 2015). GLRaVs have an exceptionally complex genome organization. Studies on the genetic variability of GLRaV-3 across grapevine-growing regions in the United States and abroad have reported the existence of multiple genetic variants. Based on examination of critical virus-encoded genes, ten distinct GLRaV-3 genetic variant groups, named I through X, have been reported thus far (Naidu et al. 2015; Burger et al. 2017; Diaz-Lara et al. 2018; Thompson et al. 2018).

**OBJECTIVE**

The goal of this project was to explore the genetic diversity landscape of GLRaV-3 in Washington State vineyards, gain research-based insight into GLD epidemiology, and ultimately apply that knowledge to area-wide clean plant programs for managing grapevine leafroll disease in vineyards.

**METHODOLOGY**

1. Sample collection from commercial WA vineyards.
2. Sample processing (Rowhani et al. 2000).
3. Reverse Transcription-Polymerase Chain Reaction (RT-PCR) assay with Hsp70h-based primers (Donda et al. 2016).
5. Sequence alignment with globally reported GLRaV-3 sequences and phylogenetic analysis (MEGA7 software package).

**RESULTS**

The partial Hsp70h gene sequences of GLRaV-3 isolates found in Washington vineyards were compared with corresponding virus sequences reported from other grapevine-growing regions worldwide to profile genetic diversity of the virus. Phylogenetic analysis of Hsp70h gene sequences showed that GLRaV-3 isolates from Washington State fell into 5 reported variant groups of GLRaV-3: groups I, II, III, V, and VI, and the majority of GLRaV-3 isolates belonged to variant group I (Fig. 3).

**CONCLUSIONS**

This is the first comprehensive report demonstrating the presence of several distinct genetic variant groups of GLRaV-3 in Washington State vineyards. GLRaV-3 isolates belonging to five reported variant groups were identified in this study. Isolates belonging to variant group I were predominant compared to isolates belonging to other reported GLRaV-3 variant groups. Although majority of the GLRaV-3 isolate sequences aligned with reported variant groups, 4% of the isolates were ‘divergent’ and did not align with the established classification system of GLRaV-3 genetic variants. Occurrence of these distinct variants warrant further research to understand their overall diversity and spread across vineyards in the state. The data from this study will be used in improving the currently used laboratory-based diagnostic methods for detecting all variants of GLRaV-3 in planting materials. Therefore, knowledge of the genetic diversity of GLRaV-3 will provide opportunities to resolve the complex epidemiology of GLD for implementing disease management strategies and improving grapevine planting material supply chain for healthy vineyards.

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