First Report of Grapevine Virus L Infecting Grapevine in Southeast France

L. Svanella-Dumas,¹ T. Candresse,¹ M. Lefebvre,¹ J. Lluch,² S. Valiere,² P. Larignon,³ and A. Marais^{1,†}

¹ Univ. Bordeaux, INRAE, UMR BFP, CS 20032, 33882 Villenave d'Ornon, France

² INRAE, US 1426, GeT-PlaGe, Genotoul, 31326 Castanet-Tolosan, France

³ IFV, 30230 Rodilhan, France

Funding: The authors are grateful to Plan National Dépérissement Vignoble (SIREPA 2019-0020652) for the financial support. Plant Dis. 106:1536, 2022; published online as <https://doi.org/10.1094/PDIS-10-21-2310-PDN>. Accepted for publication 29 December 2021.

Grapevine virus L (GVL) is a recently described vitivirus (family *Betaflexiviridae*) with a positive-sense single-stranded RNA genome. It has so far been reported from China, Croatia, New Zealand, the United States, and Tunisia (Alabi et al. 2020; Ben Amar et al. 2020; Debat et al. 2019; Diaz-Lara et al. 2019). It has significant genetic variability (up to 26% nucleotide divergence between isolates) and the existence of four phylogroups has been proposed (Alabi et al. 2020). In a project investigating the possible links between grapevine trunk diseases and the grapevine virome, viral high throughput sequencing (HTS)-based testing was performed on symptomatic and asymptomatic grapevines collected in July 2019 in vineyards of four areas in France (Bourgogne, Charentes, Gard, Gironde) corresponding to five cultivars of *Vitis vinifera* (Cabernet Franc, Cabernet Sauvignon, Chardonnay, Sauvignon, Ugni Blanc). Total RNAs were purified from the powder of 105 trunk wood samples using the Spectrum Plant Total RNA Kit (Sigma-Aldrich, Saint-Quentin-Fallavier, France) and RNA-seq libraries were prepared using Zymo-Seq RiboFree Total RNA Library Prep Kit (Ozyme, Saint Cyr l'Ecole, France). HTS was performed on an S4 lane of Illumina Nova-Seq 6000 using a paired-end read length of 2 × 150 bp. The trimmed sequence reads obtained from Chardonnay plants CH30-75M (99.9 M) and

CH37-19S (114 M) from a vineyard in Gard were analyzed using CLC Genomics Workbench v21 (Qiagen, Courtaboeuf, France) and revealed complex mixed infections. Besides contigs representing a complete GVL genome (average scaffold coverage: 6,197× and 2,970×, respectively), contigs from grapevine rupestris stem pitting virus (1,697×; 1,124×), grapevine virus A (82×; 95×), grapevine pinot gris virus (1,475×; 866×), grapevine leafroll-associated virus 3 (5,122×; 1,042×), hop stunt viroid (13,783×; 29,514×), and grapevine yellow speckle viroid 1 (690×; 1,158×) were also identified. Plant CH37-19S was also coinfecting by grapevine rupestris vein feathering virus (164×). The GVL contigs integrated, respectively, 320,000 and 152,000 reads (corresponding to 0.32 and 0.11% of filtered/trimmed reads, respectively). The GVL genomic sequences from each sample (7,616 nt) have been deposited in GenBank (Accession nos. OK042110 and OK042111, respectively). The two contigs are nearly identical (99.9% nt identity) and share, respectively, 97.5 and 95.9% identity with GVL-KA from the United States (MH643739) and GVL-RS from China (MH248020), the closest isolates in GenBank. To confirm the presence of GVL, the original grapevines were resampled in the field and total RNAs were extracted as described above from cambial scrapings and leaves. Total RNAs were used for RT-PCR tests using primers targeting a 279-bp fragment corresponding to the 3' end of the coat protein gene and part of the nucleic acid binding protein gene (Debat et al. 2019). The Sanger-derived sequences from the amplicons shared 100% nt identities with the corresponding sequences of the HTS assembled genomes, confirming the presence of GVL in both tissues of both grapevine samples. To our knowledge, this represents the first report of the occurrence of GVL in vineyards in France. Given the complex mixed infection present in the two analyzed grapevines, no conclusions can be drawn on the pathogenicity of GVL. Further efforts are needed to better understand GVL distribution and its potential pathogenicity to grapevine.

References:

- Alabi, O. J., et al. 2020. Arch. Virol. 165:1905.
- Ben Amar, A., et al. 2020. Plant Dis. 104:3274.
- Debat, H., et al. 2019. Eur. J. Plant Pathol. 155:319.
- Diaz-Lara, A., et al. 2019. Arch. Virol. 164:2573.

The author(s) declare no conflict of interest.

Keywords: grapevine, pathogen detection, viruses and viroids

[†]Indicates the corresponding author.

A. Marais; armelle.marais-colombel@inrae.fr