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# First report of grapevine associated jivivirus 1 infecting grapevines in Brazil

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## Abstract

Grapevines can host up to 86 virus species, some of which affect plant vigor, production and fruit quality (Fuchs, 2020). In 2014, a *Vitis vinifera* cv. Semillon vine showing yellow speckles and mild leafroll symptoms in Bento Gonçalves, RS, Brazil, was investigated for viruses (Silva et al., 2017), resulting in the detection of grapevine enamovirus 1, grapevine yellow speckle viroid 1 and hop stunt viroid. Total nucleic acids (TNA) extracts from this sample were enriched for dsRNA (Valverde et al., 1990), prepped with TruSeq Stranded mRNA kit (Illumina, USA), then subjected to high throughput sequencing (HTS) on the Illumina HiSeq 2000 platform. The HTS yielded 13,214 Mbp raw reads, which were trimmed and the host derived sequences subtracted with Trimmomatic and Burrows-Wheeler Aligner softwares, respectively. The remaining reads were subjected to taxonomic

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assignment with the Kaiju webserver, preliminarily indicating 26 reads related to citrus virga-like virus (Matsumura et al., 2017). De novo assembled contigs built by SPAdes generated five contigs that were subjected to tBLASTx searches against the NCBI viral RefSeq. Four sets of primers were designed to sequence the gaps between these contigs and the PCR amplicons were sequenced by Sanger method resulting in two long contigs. A third long contig related to citrus jingmen-like virus (Matsumura et al., 2017) was also retained for further analysis. BLASTn analyses of the assembled virus contigs showed that they are closely related to grapevine associated jivivirus 1 (GajV-1) (Chiapello et al, 2020). The derived partial tripartite genomic sequences of GajV-1 isolate SEM-BR from Brazil (GenBank acc. nos. MT657278-MT657280) covered 84.4% (3424 nt), 40.3% (1289 nt) and 73% (1555 nt) of RNAs 1, 2 and 3 of isolate DMG 109 from Italy (MN520745-MN520747), respectively. The pairwise nt sequence identities between both isolates were 99.3% (RNA1), 97.1% (RNA2) and 100% (RNA3), indicating that they are highly identical to each other. To confirm the HTS results, fresh TNA extracts from SEM-BR and four newly sampled vines were screened by RT-PCR using specific primers F (5'GGACGAAGTCACAACCAACACAGTTT3') and R (5'CGCGAGTAGGTCTGACAACTTTCATTAT3'), designed based on GajV-1 RNA1. The resulting 478 bp amplicons were sequenced (MT657281-MT657285) and found to share 99.4%-99.8% nt identities with the corresponding sequences of GajV-1 SEM-BR (MT657278). To assess graft-transmissibility of GajV-1, Semillon scions of SEM-BR source vine were grafted onto 14 GajV-1-free 1103P rootstocks. Six of 14 recipient plants (all asymptomatic)

tested positive for GajV-1 by RT-PCR 106 days after grafting. Additionally, RT-PCR screening of a Brazilian grapevine collection block resulted in the detection of GajV-1 in nine of 33 tested vines of different accessions (27.3%). The GajV-1 positive vines included eight commercial cultivars (Ancelotta, Aragonez, Merlot, Semillon, Michele Palieri, Malvasia, Viognier, and Pinot Nero). This is the first report of GajV-1 in Brazil, a virus that was recently described in Italy and Spain (Chiapello et al, 2020). Our results also demonstrated the graft-transmissible nature of the virus but it is unclear if GajV-1 is associated to grapevine plant cells or strictly to a possible grapevine fungal endophyte. Additional studies on the GajV-1 prevalence in commercial vineyards in Brazil and possible effects of the virus on grapevines are necessary. References: Chiapello, M., et al. 2020. *Annals of Applied Biology* 176:180. <https://doi.org/10.1111/aab.12563> Fuchs, M. 2020. *J. Plant Pathol.* <https://doi.org/10.1007/s42161-020-00579-2> Matsumura, E.E., et al. 2017. *Viruses* 9:92. <https://doi.org/10.3390/v9040092> Silva, J.M.F., et al. 2017. *Virus Genes* 53:667. <https://doi.org/10.1007/s11262-017-1470-y> Valverde, R.A., et al. 1990. *Plant Dis.* 74:255. [https://www.apsnet.org/publications/plantdisease/backissues/Documents/1990Articles/PlantDisease74n03\\_255.PDF](https://www.apsnet.org/publications/plantdisease/backissues/Documents/1990Articles/PlantDisease74n03_255.PDF)

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