Disease Note

Diseases Caused by Viruses

First Report of Vitis Cryptic Virus Infecting Mildew-Resistant Grapevine Interspecific Hybrids in France

T. Candresse,[1,†] C. Faure,[1] A. Calonnec,[2] P. Cartolaro,[2] and A. Marais[1]

[1] INRAE, UMR BFP, University of Bordeaux, Villenave d'Ornon 33882 CEDEX, France
[2] UMR 1065 SAVE, INRAE, Bordeaux Science Agro, ISVV, Villenave d'Ornon 33882 CEDEX, France

Plant Dis. 108:232, 2024; published online as https://doi.org/10.1094/PDIS-09-23-1751-PDN. Accepted for publication 10 October 2023.

Vitis cryptic virus (VCV), a deltapartitivirus identified in Japan in *Vitis coignetiae* (Nabeshima and Abe 2021), is known from only two other countries. It was detected in China (Fan et al. 2022) and in Russia, including in a *V. labrusca* and the Saperavi Severnyi interspecific hybrid (Shvets et al. 2022). There is no information on VCV pathogenicity, but deltapartitiviruses are generally not pathogenic. Fan et al. (2022) reported VCV graft transmission and chlorotic mottling symptoms developing on a graft-inoculated vine in spite of the fact that cryptic viruses are not known to move cell-to-cell or be graft-transmissible. In fall 2022, a few plants of the Prior interspecific hybrid (https://www.vivc.de) showed unusual red blotch and leaf curl in Bordeaux, France, prompting the high-throughput sequencing analysis of two plants using total leaf RNA. Following host genome subtraction, the ribodepleted RNASeq data were assembled de novo using CLC Genomics Workbench (Candresse et al. 2018) and contigs annotated by BlastX against the GenBank database. Rupestris stem pitting virus, grapevine Pinot gris virus, hop stunt viroid, and grapevine yellow speckle viroid 1 were identified. In addition, mycoviral contigs were identified, together with contigs for Rhopalosiphum padi virus and a divergent isolate of barley aphid RNA virus 10 (the latter only in one plant), and the two genomic RNAs of VCV. The VCV RNA1 contigs were 1,570 and 1,574 nucleotides (nt) long, respectively, and 100% identical, showing 97.1% nt identity to a Japanese isolate (LC746759). They integrated 6,480 and 4,613 reads (0.2 and 0.4% of total subtracted reads) for a coverage of 611× and 433×, respectively. The VCV RNA2 contigs were also 100% identical and shared 95.5% identity with a Japanese isolate (LC746761). They were 1,518 to 1,519 nt long, integrated 11,338 and 9,999 reads (0.4 and 0.9% of reads) for a coverage of 1,109× and 972×, respectively. The Prior VCV RNAs were deposited in GenBank (OR474475 and OR474476). Specific RNA2 primers, 5′-TTACAGGTTTGATTGGAATCATG-3′ and 5′-ATAGTAGGTCCAATCACTAATC-3′ (Tm 56°C), were used to confirm VCV presence in the original plants as well as in three other asymptomatic Prior vines. Amplicons 100% identical to the contigs were obtained from four of five plants. Two plants of Bronner, one of Prior parents, also tested positive. The rootstock (Fercal) of a VCV-infected Prior and two plants of another hybrid, Artaban (sampled in the same plot as Prior), tested negative. BlastN datamining identified VCV reads in RNASeq data from a range of wild grapevines including *V. acerifolia* (SRX2885763), *V. quinquangularis* (SRX1496837), *V. romanetii* (SRR3938616), *V. cinerea* (SRR10135144), *V. davidii* (SRR3255926), *V. amurensis* (SRX13387918), and *V. vinifera* subsp. *sylvestris* (HAOE01029819 and HAOE01001237). Although not experimentally verified, detection in wild *Vitis*, including *V. amurensis*, a Saperavi Severnyi, Bronner, and Prior progenitor, suggests VCV might have been introduced in these hybrids through crosses aiming to develop powdery and downy mildew-resistant varieties. To the best of our knowledge, this is the first report of VCV infection in grapevine in France. The symptoms that prompted this research have not recurred in 2023 and are not linked to VCV because the virus was also identified in symptomless Prior plants. The risk of introducing VCV in European grapevine through breeding efforts appears limited, but VCV may be present in fungal disease-resistant cultivars in a range of countries.

References:

Candresse, T., et al. 2018. Arch. Virol. 163:277.
Fan, X. D., et al. 2022. Plant Dis. 106:3006.
Nabeshima, T., and Abe, J. 2021. Viruses 13:827.
Shvets, D., et al. 2022. Viruses 14:1314.

The author(s) declare no conflict of interest.

Keywords: grapevine, pathogen detection, viruses and viroids

[†]Indicates the corresponding author.
T. Candresse; thierry.candresse@inrae.fr