

EPPO Datasheet: *Badnavirus venavitis*

Last updated: 2022-02-07

IDENTITY

Preferred name: *Badnavirus venavitis*

Taxonomic position: Viruses and viroids: Riboviria: Pararnavirae: Artverviricota: Revtraviricetes: Ortervirales: Caulimoviridae

Other scientific names: *GVCV*, *Grapevine vein clearing virus*
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EU Categorization: Quarantine pest ((EU) 2019/2072 Annex II A)

EPPO Code: GVCV00



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Notes on taxonomy and nomenclature

In 2004, a new and severe virus-like disease was reported on Chardonnay vines in a Missouri vineyard, resulting in significant reduction of vine vigour and yield with symptoms resembling those of fanleaf disease (see Symptoms). This syndrome was named Grapevine vein clearing complex (GVCC) (Qiu *et al.*, 2007). The pathogen(s) involved could be transmitted via cuttings and grafting. Chardonnay, Cabernet Franc and Baco 22A vines that were grafted with the buds from the original diseased Chardonnay vines exhibited distinct vein-clearing symptom. Reverse transcription polymerase chain reaction (RT-PCR) tests indicated the association of grapevine fanleaf virus, tomato ringspot virus and grapevine Rupestris stem pitting-associated virus with the disease (Lunden *et al.*, 2010). Other reports of similar symptoms were made at this time, and based on this symptomatology, this syndrome of vein clearing and decline was speculated to be associated with a nepovirus. In 2011, virus-derived small interfering RNA (vsiRNA) high-throughput sequencing demonstrated the association of the vein clearing syndrome with a *Badnavirus* in the Caulimoviridae family. This was the first report of a DNA virus infecting grapevine and the virus was named Grapevine vein clearing virus (GVCV) (Zhang *et al.*, 2011, Singh *et al.*, 2012).

HOSTS

The cultivated grape *Vitis vinifera* and its hybrids with other *Vitis* species (e.g. used for rootstocks) are hosts of GVCV. A survey initiated in 2017 throughout Missouri and involving over 400 leaf samples collected randomly from 25 grape cultivars found that GVCV was exclusively detected in white-berried cultivars (Schoelz *et al.*, 2021). For example, GVCV has already been detected in the following cultivars: Cayuga, Chardonel, Chardonnay, Riesling, Valvin Muscat, Vidal, Vidal Blanc, Vignoles and Viognier (Qiu & Schoelz, 2017; Schoelz *et al.*, 2021). However, some infected red-berried cultivars such as Cabernet Franc, Cabernet Sauvignon and Noiret have also been reported (Qiu & Schoelz, 2017). Some cultivars are reported to be resistant (see Control).

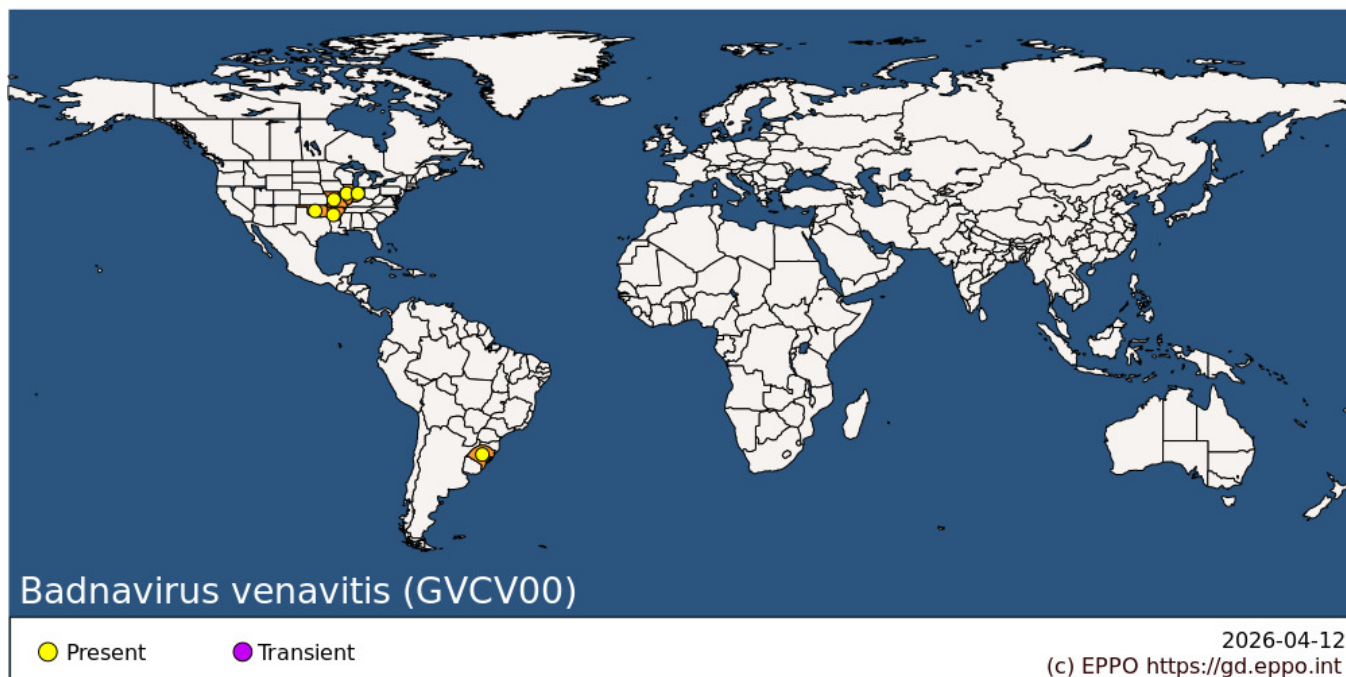
GVCV has also been detected in wild *Vitis rupestris*, leading to the identification of two divergent GVCV variants (Beach *et al.*, 2017). Moreover, GVCV was identified in wild *Vitis cinerea*, *V. palmata*, and *V. vulpina*, as well as in *Ampelopsis cordata* (heart-leaf pepper vine) collected in the Midwest area of the USA (Petersen *et al.*, 2017; Uhls *et al.*, 2021). It is hypothesized that GVCV could have originated from *A. cordata* or from unidentified wild perennial hosts in the midwestern region of the USA, spreading to nearby cultivated vines fairly recently (Cieniewicz *et al.*, 2020).

Host list: *Ampelopsis cordata*, *Vitis cinerea*, *Vitis hybrids*, *Vitis palmata*, *Vitis rupestris*, *Vitis vinifera*, *Vitis vulpina*

GEOGRAPHICAL DISTRIBUTION

GVCV is considered as an emerging virus in the USA, widespread in the Midwest region. Outside the USA, it has

only been reported so far in Brazil (Fajardo *et al.*, 2017).



North America: United States of America (Arkansas, Illinois, Indiana, Missouri, Oklahoma)

South America: Brazil (Rio Grande do Sul)

BIOLOGY

As is the case for most other plant viruses, GVCV is easily graft-transmissible (Guo *et al.*, 2014). Certain members of the genus *Badnavirus* are reported to be seed-transmitted (Bhat *et al.*, 2016; EFSA PLH, 2019), but this is considered to be exceptional and no information specific to GVCV is available. Members of genus *Badnavirus* are generally not reported to be pollen-transmitted (EFSA PLH, 2019). As is the case for other non-phloem-limited grapevine viruses, it is assumed that the virus spreads in the plant over 6-12 months (i.e. over one growing season and a winter dormancy) depending on the phenology and physiological state of the vines; older vines being probably less sensitive to the virus infection.

The large expansion of viticulture in the Midwest region of the USA in the 1980s has created interfaces between cultivated grapevines and ecosystems with wild *Vitis* and *A. cordata* hosting GVCV. The presence of genetically diverse isolates of GVCV in cultivated grapevine and wild *Vitis* suggests ongoing viral population exchanges between cultivated agro-ecosystems and their wild counterparts.

Observation of clusters of symptomatic vines suggested a transmission via an insect vector. Moreover, badnaviruses are known to be transmitted either by mealybugs or, in a few cases, by aphids. Vineyard observations validated the hypothesis of an association between GVCV spread dynamics and aphids' abundance. Furthermore, *Aphis illinoisensis*, the grapevine aphid, which is ubiquitous in the Midwest region of the USA, has been shown to be able to transmit GVCV from *A. cordata* to the cultivated variety Chardonnay, which then developed typical vein clearing symptoms. Presence of GVCV in both the stylets and whole body of aphids suggests a semipersistent or a circulative non propagative transmission mode of the virus (Uhls *et al.*, 2021). Given the high (31%) infection rate recorded in wild populations of *A. cordata* in Missouri, this wild grapevine relative has been suspected as the natural reservoir from which the aphid *A. illinoisensis* acquired the virus and transmitted it to cultivated grapevines (Cieniewicz *et al.*, 2020). Grape aphids in North America are heteroecious and alternate between *Viburnum prunifolium* and *Vitaceae* species (Baker, 1917). Spring migrants typically fly up to 20 km from *V. prunifolium* to their grapevine hosts, a pattern which appears to be consistent with the local epidemic pattern of GVCV in wild plants and in vineyards (Petersen *et al.*, 2019). A recent large-scale survey of GVCV in wild *Vitaceae* (*A. cordata*, *V. cinerea*, *V. palmata*, *V. vulpina*) and in *A. illinoisensis* aphids in Missouri showed that identical GVCV variants were found in grape aphids sampled from wild and cultivated *Vitaceae*, indicating that viruliferous aphids likely migrate and disperse GVCV variants among wild and cultivated *Vitaceae* (Uhls *et al.*, 2021).

DETECTION AND IDENTIFICATION

Symptoms

The symptoms of GVCV are dependent on grapevine phenology and evolve during the growing season. On a single GVCV-infected grapevine, some shoots may exhibit typical symptoms, while other parts of the vine may remain symptomless. The most visible symptoms on young leaves are a translucent vein clearing of secondary and tertiary veins, followed as the season progresses by mosaic, mottling and crinkling patterns with leaf edge rolling. Chlorotic and mosaic symptoms appear on old leaves. A zigzag shoot growth and short internodes can be seen on young shoots with small and distorted leaves particularly on the Chardonnay variety. Berries on the infected grapevines are deformed, discoloured, do not fully develop or do not ripen well and have a hard texture. Shoots of severely affected vines do not develop well and are stunted. Plant decline with severe yield losses, leading to the death of some plants, occurs in the years following the appearance of the first symptoms (Qiu and Schoelz, 2017).

Besides the typical vein clearing on young leaves, GVCV symptoms in wild *V. rupestris* progress to necrotic spots or veinal necrosis on mature leaves. Other infected wild *Vitis* and *A. cordata* often exhibit no symptoms or mild symptoms, although some infected *A. cordata* plants show mild vein clearing and mottle symptoms (Petersen *et al.*, 2019).

Morphology

GVCV virions have been visualized through electron microscopy (Zhang *et al.*, 2016). They are bacilliform without any envelope, 30 nm in width with a modal particle length of 130 nm. The GVCV-CHA reference genome (GenBank NC_015784) consists of a double-stranded, circular DNA molecule of 7 753 bp. Three large open reading

frames (ORFs) are predicted on the plus-strand of the genome, whose functions have not yet been fully characterized. ORF I and ORF II encode proteins of unknown function with predicted sizes of 24.2 and 14.3 kDa, respectively. ORF III encodes a polyprotein with a predicted size of 219.2 kDa. On the basis of conserved functional motifs, this polyprotein has been proposed to contain domains corresponding to a movement protein, the virus coat protein, a protease, a reverse transcriptase and an RNase H (Zhang *et al.*, 2011, 2015). The comparison of complete genomic sequences of GVCV isolates has shown whole genome variation to be within a 10% range so far, with ORF II being the genome's most variable part (Beach *et al.*, 2017). GVCV isolates do not appear to cluster phylogenetically according to geographical location or grapevine cultivar (Guo *et al.*, 2014).

Detection and inspection methods

A procedure for inspection of places of production of *Vitis* plants for planting is provided in Standard PM 3/85 (EPPO, 2018). Risks of confusion with symptoms of other pests should be taken in account, since symptoms such as deformation of leaves with mosaic, yellowing and translucent veins, abnormal and zigzag shoot growth and short internodes, depending on the grapevine variety, the season and putatively on the GVCV variant, might be attributed to nepoviruses.

GVCV infection can be detected by grafting on indicator grapes such as Cabernet Franc or Baco 22A, the former reacting with obvious vein clearing symptoms that are more pronounced than for the latter (Qiu and Schoelz, 2017).

There is currently no serological detection test available. Polymerase chain reaction is the conventional method of choice for the detection of GVCV. Four sets of primers have been designed to cover GVCV molecular diversity (Qiu and Schoelz, 2017). Very recently, hyperspectral imagery has been employed to identify and classify grapevines inoculated with GVCV at the early asymptomatic stages. A statistical approach was then used to discriminate reflectance spectra patterns between healthy and GVCV-infected vines enabling the specific detection of GVCV-infected grapevine seedlings (Nguyen *et al.*, 2021).

PATHWAYS FOR MOVEMENT

Given the high rate of transmission of GVCV through vegetative propagation practices, the main pathway for long-distance movement is the circulation and trade of infected grapevine propagation materials. The trade of 'wild' *Vitaceae* for use as ornamentals is also to be considered since several of these species have been found to be infected by GVCV in their native range, including *A. cordata* which has high infection rates (Petersen *et al.*, 2019). A minor pathway for entry could involve the movement of viruliferous winged *Aphis illinoisensis* or associated with non-regulated host plants. In this respect the recent introduction of *A. illinoisensis* in several European countries is of particular note (Havelka *et al.*, 2011; Mifsud and Pérez Hidalgo, 2011; Pérez Hidalgo *et al.*, 2011).

PEST SIGNIFICANCE

Economic impact

GVCV infection has been shown to affect many aspects of vine physiology, from leaf metabolism to fruit development and ripening. Economic losses can be severe and are a consequence of a reduction in fruit and wine quality as well as reductions in vegetative growth and canopy development (Qiu and Schoelz, 2017, EFSA PLH, 2019). As of 2021, seven vineyards have been removed in Missouri as a consequence of GVCV infection (Uhls *et al.*, 2021). However, it seems that spread of GVCV from wild *Vitis* (mainly *A. cordata*) to cultivated grapevines in the Midwest of the USA has occurred fairly recently, making it difficult to precisely estimate the economic impact of the vein clearing disease.

Infections have mainly been reported in white-berried cultivars (see Hosts), whereas most red-berries cultivars are suspected to be resistant (see Control): In Missouri, GVCV was absent from red-berried cultivars but detected at levels of 33% in Vidal, 24% in Chardonel and 20% in Valvin Muscat (Schoelz *et al.*, 2021).

Control

Most red-berried cultivars are suspected to be resistant (Schoelz *et al.*, 2021). In particular, cultivars Chambourcin (Guo *et al.*, 2014) and Norton (Qiu *et al.*, 2020) have been shown to be fully resistant to GVCV after grafting infected scions onto these varieties. However, some other red-berried cultivars have been suggested to be tolerant, i.e. showing mild symptoms or no symptoms (Qiu & Schoelz, 2017); still others, such as Cabernet Franc and Cabernet Sauvignon are known to be susceptible.

There is no curative treatment available to control the vein clearing disease in vineyards so that all control strategies are based on prophylaxis or, possibly, on control of grape aphid vectors. In this context, a key control element is of course the use of GVCV-free planting materials. Thus, implementation of GVCV testing in certification and quarantine programs to prevent the spread of this virus are well established or should be considered.

In Midwest vineyards in the USA, it has been suggested that roguing symptomatic vines and replanting with vines derived from GVCV-free propagation stocks may minimize losses. The control or removal of wild *Vitaceae* populations, in particular *A. cordata*, that may serve as a significant inoculum reservoir could possibly be of interest as it would reduce alternative GVCV inoculum sources and the number of hosts for grape aphids (Petersen *et al.*, 2019). Similarly, if eradication measures are taken, these should include attention to wild *Vitaceae* species if any grow nearby.

Phytosanitary risk

The phytosanitary risk is essentially linked to infected grapevine propagation material and seen as a significant risk given the clear pathogenicity and potential for negative impact of GVCV, and the importance of grapevine growing in the EPPO region. Should the virus be introduced, the possibility of local vector mediated spread already exists with the presence of *Aphis illinoisensis* in a range of countries in the Mediterranean area. *A. illinoisensis* is expected to be able to further expand its range to all the grape-growing areas of the Mediterranean and even those of South-Eastern and Central Europe (Havelka *et al.*, 2011). Very recently, *A. illinoisensis* has been reported for the first time in France on grapevines in the Provence Alpes Côte d'Azur region (Mouttet and Balmes, 2021). Therefore, it is expected that GVCV could establish and spread in many Mediterranean grapevine growing countries, causing symptoms and having negative impacts on *Vitis* fruit yield and/or quality (EFSA PLH, 2019).

PHYTOSANITARY MEASURES

Adapted from the measures drafted for other viruses of *Vitis* (e.g. grapevine red blotch virus; EPPO, in preparation), phytosanitary measures to import *Vitis* plants for planting into the EPPO region could require that these plants are produced in a pest free area, or in a pest free place/site of production established according to EPPO Standard PM 5/8 *Guidelines on the phytosanitary measure 'Plants grown under physical isolation'* (EPPO, 2016). The physical isolation should prevent both the virus and the vector from entering the place/site of production. Further options consisting of treating the consignment for the vector, and importing either varieties known to be fully resistant to GVCV infection, or combining the absence of GVCV symptoms during the growing period and testing of the consignment for GVCV, could be further investigated.

A number of EPPO countries already ban the import of *Vitis* plants for planting (other than seeds) (e.g. EU countries: Annex VI, points 10 of Regulation 2019/2072 (EU, 2019)). Host plants for planting could also be imported through post-entry quarantine (in the framework of a bilateral agreement). High Throughput Sequencing (HTS) procedures could also be implemented for such post-entry quarantine testing which would enable to detect all regulated exotic viruses, including GVCV, from imported plants in a single test.

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Datasheet history

This datasheet was first published online in 2022. It is maintained in an electronic format in the EPPO Global Database. The sections on 'Identity', 'Hosts', and 'Geographical distribution' are automatically updated from the database. For other sections, the date of last revision is indicated on the right.



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