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DISEASE NOTES

First Report of *Grapevine Pinot gris virus* in German Vineyards

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Grapevine Pinot gris virus (GPGV) was first identified in northern Italy in 2012 on grapevine variety Pinot gris showing chlorotic mottling and leaf deformation (Giampetruzzi et al. 2012). Since 2012, GPGV has been reported from other countries including Slovenia, Slovakia, the Czech Republic, Greece, France, Korea, the United States, Canada, and China. Since its discovery, the association of a specific symptomology with the presence of GPGV has been contradictory. GPGV was often reported in mixed viral infections, making it difficult to associate GPGV with disease etiology. Moreover, the virus was also detected in asymptomatic vines. These observations suggest the existence of latent isolates and/or variable susceptibility of grapevine genotypes. The pathogenesis of GPGV remains unclear; therefore, the studies of GPGV molecular variability and epidemiology are still of great importance. During a field survey conducted in 2015 in the state of Baden-Württemberg (Germany), symptoms resembling those caused by a viral infection (short internodes, zigzag growth of shoots, disturbed berry development) were observed in *Vitis vinifera* cv. Riesling vines in a commercial vineyard. Thirty vines were analyzed and were positive by RT-PCR using the GPGV- specific primer pair DetF/DetR (Saldarelli et al. 2015). The RT-PCR amplicons from three vines were cloned and sequenced. The three amplicons shared a high identity (99%). Sequence analysis results revealed a 99% nucleotide sequence identity with the Slovak isolate SK30 of GPGV (GenBank accession no. 543887400). Symptomatic leaves of these plants tested negative for Grapevine leafroll-associated viruses (GLRaV-1, -2, -3,- 4, and 7), *Grapevine fanleaf virus*, *Raspberry ringspot virus*, *Grapevine fleck virus*, *Arabis mosaic virus*, *Strawberry latent ringspot virus*, *Tomato black ring virus*, *Tomato ringspot virus*, *Tobacco ringspot virus*, and Grapevine red blotch-associated virus by ELISA and/or PCR. In order to check the presence of other viral pathogens or undetected divergent viral variants, small interfering RNAs isolated from one symptomatic Riesling plant were analyzed using next generation sequencing (NGS) performed by the Illumina platform. Besides GPGV, this analysis identified three other

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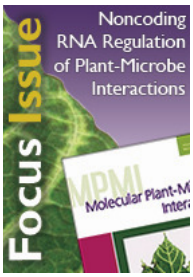
infecting agents (*Grapevine rupestris stem pitting-associated virus*, *Hop stunt viroid*, and *Grapevine yellow speckle viroid 1*). The full-length genome sequence of GPGV was obtained by combining the results of mapping of the Illumina reads on a reference GPGV genome, Sanger sequencing, and RACE PCR. This genome sequence, showing 94 to 98% nt identity to complete genome sequences (KF686810, KF134124, KF134125, KM491305, and NC_15782.1) was deposited in the GenBank database (KX522755). To our knowledge, this is the first official report of GPGV in Germany.



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Cited by

The recent importation of Grapevine Pinot gris virus into Australia
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