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NEW DISEASE REPORT

Occurrence of grapevine Pinot gris virus in commercial table grapes in Peru

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In the 2022–2023 season, Peru maintained its status as the world's leading exporter of table grapes, exporting 593,000 tons comprised of more than 53 varieties. The varietal change and the increase of new producing areas has brought several phytosanitary problems, including those of viral aetiology. Since 2022, occasional grapevines in commercial vineyards in Ica (southern Peru), the main producing area in the country, have been observed with complex symptoms including short internodes, stunting and deformation of the leaves (Fig. 1) and chlorotic mottling on leaf blades (Fig. 2). At fruiting, symptoms included heterogeneity in berry development (Fig. 3), delayed ripening and consequently reduced yield.

A total of 52 samples, consisting of both leaf and shoot segments, from diseased (12%) and asymptomatic (88%) grapevines



FIGURE 1 Grapevine showing short internodes, stunting and deformation of the leaves

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FIGURE 2 Grapevine leaves showing chlorotic mottling



FIGURE 3 Bunch of grapes showing heterogeneity of berry development

from 22 different cultivars in 26 orchards located in the Ica region were collected between February to October 2024. RNA was isolated using the NucleoSpin RNA Plant kit (Macherey-Nagel, Germany) and RT-PCR was done using a GPVG-specific primer pair, DetF (5'-TGGTCTGCAGCCAGGGGACA-3') and DetR (5- TCACGACCGGCAGGGAAGGA 3'), which amplify a 588 bp product associated with-a region located between the movement and coat proteins of the viral genome (Morelli *et al.*, 2014).

GPGV isolates were detected in two samples: MC1_GPGV (asymptomatic grapevine cv. Moscatel) and MC2_GPGV (diseased grapevine cv. Sweet Celebration). Bidirectional sequencing of the isolates was performed using the Sanger method and the obtained sequences were compared with those in GenBank using BLAST. MC1_GPGV (PQ444178) and MC2_GPGV (PQ461689) had a nucleotide sequence identity of 98.76% (MN458411.1) and 99.05% (OR892451.1) with GPGV, respectively. Phylogenetic analysis of the MC1_GPGV and MC2_GPGV sequences showed that both accessions were grouped in different clades. MC1_GPGV could be more closely related phylogenetically to a virus reported in France in 2019 (MN458414, MN458416, MN458411), while MC2_GPGV seems closer to a viral strain reported in Russia in 2023 (OR892451) (Fig. 4). The marked variability between the accessions indicates that MC1_GPGV and MC2_GPGV evolved independently from a common ancestor or have originated in different geographic regions, consistent with the numerous reports of this virus worldwide. In South America, GPGV has been reported in Argentina, Brazil, Chile and Uruguay (Zamorano *et al.*, 2019; Debat *et al.*, 2020) in the last five years, and has been found in symptomatic and asymptomatic grapevine plants worldwide (Saldarelli *et al.*, 2015).

It has been reported that latent GPGV infections have no significant impact on grapevine yield, losses only occuring in symptomatic plants and depending on the severity of the infection (Messmer *et al.*, 2024). GPGV may be a phytosanitary issue to the Peruvian grapevine industry because it is easily transmitted by grafting and by eriophyid mite vectors (Malagnini *et al.*, 2016). Additionally, the virus has evolved considerable genetic variability which has led to the emergence of new and potentially pathogenic variants (Tarquini *et al.*, 2019).

To our knowledge, this is the first report of GPGV in Peru, which provides further evidence for its wide geographical distribution and the broad range grapevine cultivars which host the virus.

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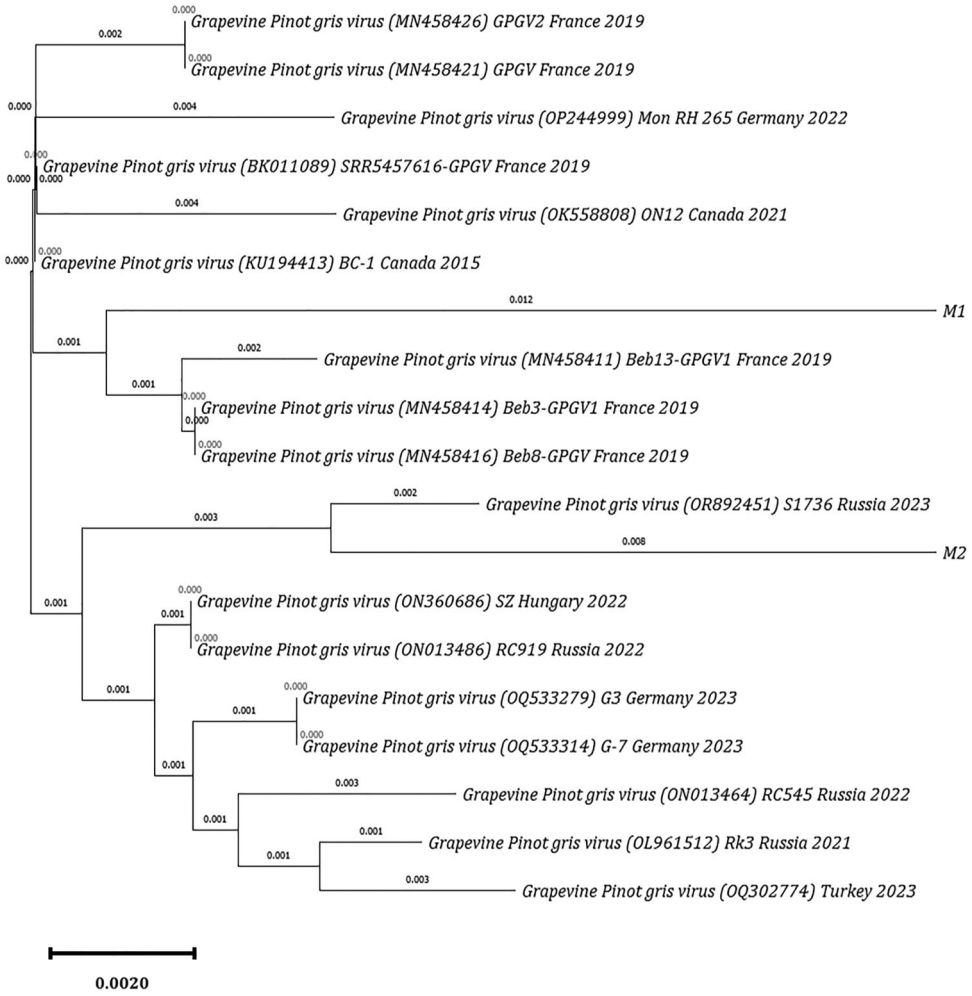

FIGURE 4 Phylogenetic tree showing the location of Peruvian GPGV isolates in relation to other accessions

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