



First report of grapevine leafroll-associated virus 3 in wild vines (*Vitis vinifera* subsp. *sylvestris*) in Tunisia

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Wild grapevines (*Vitis vinifera* subsp. *sylvestris*) form scattered populations mostly in the Northwest and Northeast of Tunisia. Wild grapevines may represent natural reservoirs for pathogens including viruses and can play an important role in their spread to cultivated grapevines. Previous studies showed the presence of grapevine rupestris stem pitting-associated virus (GRSPaV) and grapevine virus A (GVA) in Tunisian wild grapevines (Selmi et al. 2017, 2018). Grapevine leafroll-associated virus 3 (GLRaV-3) belongs to the genus *Ampelovirus*, in the family *Closteroviridae*, has a worldwide distribution, and is widely distributed in Tunisian vineyards. To study the presence of GLRaV-3 in wild grapevines, a survey was carried out in the mountain forests of northern Tunisia. Dormant canes from 68 accessions (male and female specimens) were collected and tested for the presence of GLRaV-3 by RT-PCR using specific primers (Ling et al. 1998) to amplify a 546 bp fragment of the heat-shock protein 70 homolog (HSP70h) gene. Results showed that 10.3% (7 of 68) of the samples tested were infected by GLRaV-3. To confirm the presence of GLRaV-3 in wild Tunisian grapevines, RT-PCR amplicons from two positive accessions were sequenced and sequences were compared with those available in GenBank. The Tunisian GLRaV-3 isolates VS25 (HG996442) and VS50 (HG996439) showed respectively 96% and 98% nucleotide sequence identity

with isolate NY1 (AF037268) representing Group I. To our knowledge, this is the first report of GLRaV-3 in wild grapevines in Tunisia.

Data availability The sequencing data generated in this study were deposited in the Genbank and will be freely available to any researcher.

Declarations

Informed consent All authors have approved the submission of this manuscript.

Conflict of interest The authors declare that they have no conflict of interest.

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