

DISEASE NOTE

**FIRST REPORT OF *GRAPEVINE VIRUS E*
FROM GRAPEVINES IN CHINA****X.D. Fan, Y.F. Dong, Z.P. Zhang, F. Ren,
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A survey to assess the presence and incidence of *Grapevine virus E* (GVE) in China was carried out in 2011 and 2012 by testing dormant canes of 192 grapevine samples collected from the Chinese provinces of Liaoning (183 samples), Xinjiang (8 samples), and Jilin (1 sample). Total RNA was extracted from cortical scrapings according to Foissac *et al.* (2001) and submitted to RT-PCR using GVE-specific primers designed on the viral movement protein (GVE-MP1 5'-TGTGGGGTGCATAGTCATAGGTTT-3' and GVE-MP2 5'-GCTTTTGACTCCATTGGCTTTCTC-3') and coat protein (GVE-CP15'-GTGGGTGAACCACTCAAGGT-3' and GVE-CP2 5'-AGACCACTTGCGGCTCTTTA-3') genes. Ten of 192 tested samples (5.2%) resulted positive with both primer sets. Considering that *Grapevine virus A* and *B* (GVA and GVB) infected 4.7% and 1.6% of the samples, respectively, GVE resulted the most common vitivirus in our survey. The 992-bp and 478-bp long PCR products amplified from a Chinese table grape cultivar (Guifeimeigui) were cloned and sequenced. These sequences comprised the complete CP and putative nucleic acid binding protein genes, as well as the partial sequence of the MP gene. Comparisons with GenBank sequences revealed 99% identity of this Chinese GVE isolate (GenBank accession No. JX570675 and JX570674) with the South African strain (GU903012). Further molecular analysis revealed that all GVE-infected vines hosted also one or two other viruses, including *Grapevine leafroll associated virus -1, -2, -3* and *Grapevine rupestris stem pitting associated virus* (GRSPaV). The presence of mixed infections did not allow to establish a direct relationship between GVE and disease symptoms, except for an observed aggravation of leafroll symptoms, that needs further studies. To the best of our knowledge, this is the first report of GVE in China.

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Foissac X., Svanella-Dumas L., Dulucq M.J., Candresse T., Gentit P., 2001. Polyvalent detection of fruit tree tricho-, capillo- and foveaviruses by nested RT-PCR using degenerate and inosine containing primers (DOP RT-PCR). *Acta Horticulturae* **550**: 37-44.

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**FIRST REPORT OF WEB BLIGHT ON
LAVENDER (*LAVANDULA OFFICINALIS*)
CAUSED BY *RHIZOCTONIA SOLANI*
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In summer 2012, a blight was observed on leaves and stems of several 90-day-old plants of *Lavandula officinalis* grown in a farm located near Albenga (northern Italy). Semi-circular, water soaked lesions appeared on the leaves, starting from the basal ones. *Rhizoctonia solani* was consistently isolated from diseased tissues. Three isolates of *R. solani* were successfully anastomosed with *R. solani* isolate AG-1 (ATCC 58946) (Carling, 1996). Characteristics of mycelium and sclerotia were typical for subgroup IB. The internal transcribed spacer (ITS) region of rDNA was amplified using the primers ITS1/ITS4 and sequenced (GenBank accession No. KC493639). BLASTn analysis (Altschul *et al.*, 1997) of the amplified product 661 bp in size showed 99% homology with the sequence of *Thanatephorus cucumeris* (telomorph *R. solani*) JQ692294. The pathogenicity of one isolate was demonstrated by placing mycelium disks on the leaves of 42 lavender plants which were then covered with plastic bags. The first symptoms developed two days post inoculation and *R. solani* was reisolated from affected plants. This is the first report of *R. solani* on *L. officinalis* in Italy.

Altschul S.F., Madden T.L., Schaffer A.A., Zhang Z., Miller W., Lipman D.J., 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programme. *Nucleic Acids Research* **25**: 3389-3402.

Carling D.E., 1996. Grouping in *Rhizoctonia solani* by hyphal anastomosis reactions. In: Sneh B., Jabaji-Hare S., Neate S., Dijst G. (eds). *Rhizoctonia* Species: Taxonomy, Molecular Biology, Ecology, Pathology and Disease Control, pp. 37-47. Kluwer Academic Publishers, Dordrecht, The Netherlands.

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