Disease Note

DETECTION OF *TURNIP MOSAIC VIRUS* INFECTING MACA IN YUNNAN, SOUTHWEST OF CHINA

Y.Y. Yin [1,2], X. Lu[1], T.T. Li[1], Z.J. He[2], M. Guo[2] and M. Ding[1]

[1]Institute of Biotechnology and Germplasm Resources, Yunnan Academy of Agricultural Sciences, Kunming, Key Laboratory of Agricultural Biotechnology of Yunnan Province, Key Lab of the Southwestern Crop Gene Resources and Germplasm Innovation, Ministry of Agriculture, Kunming, 650223, P.R. China
[2]Institute of Alpine Economic Plant, Yunnan Academy of Agricultural Sciences, Lijiang, 674100, P.R. China

Maca (*Lepidium meyenii*), also known as Peruvian ginseng, is a herbaceous biennial plant of the crucifer family native to the high Andes. During a survey in November 2014, maca plants showing dwarfing and thickening of the main leaf veins, were observed in Huize county of Yunnan province (Southwest China). The incidence of symptomatic plants was approximately 50% and aphids were observed in the fields. Two symptomatic plants were collected and tested for the presence of viruses. Flexuous filamentous particles 700-750 nm in length were observed with the electron microscope in leaf dips suggesting the presence of an aphid-transmitted potyvirus. To investigate this hypothesis, total RNA was extracted using TRIzol reagent (Invitrogen, USA) and tested by RT-PCR (Chen *et al*., 2001). The first strand cDNA synthesis was conducted using *Potyviridae* universal primer M4-T (5'-GTTTTCCCAGTCACGACTTTTTTTTTTTTTT-3'), and PCR was done with primers M4 (5'-GTTTTCCCAGTCACGAC-3') and S (5'-GG(A/G/C/T)AA(C/T)AA(C/T)AG(C/T)GG(A/G/C/T)CA(A/G)CC-3'). An amplicon of approximately 1.7 kb was obtained from both diseased samples, indicating the presence of a potyvirus. The RT-PCR products were cloned into pGEM-T Easy vector (Promega, USA) and sequenced. Sequences of 1,689 bp of two isolates were identical and shared 100% nucleotide sequence identity with an isolate of *Turnip mosaic virus* (TuMV) from China (CHN12) (GenBank accession No. AY090660). The sequence of this maca isolate (TuMV-maca) was deposited in GenBank as accession number KP637171. To our knowledge, this is the first report of TuMV infecting maca.

This work was supported by Special Fund for Agro-scientific Research in the Public Interest (Project nr. 201303028).

Chen J., Chen J.P., Adams M.J., 2001. A universal PCR primer to detectmembers of the Potyviridae and its use to examine the taxonomicstatus of several members of the family. *Archives of Virology* **146**:757-766.

Corresponding author: M. Ding
E-mail:mingd73@163.com

Received October 12, 2015
Accepted October 27, 2015

Disease Note

FIRST DESCRIPTION OF GRAPEVINE SYRAH VIRUS 1 IN VINEYARDS OF HUNGARY

N. Czotter[1], E. Szabó[1], J. Molnar[2], L. Kocsis[3], T. Deák[4], Gy. Bisztray[4], G.E. Tusnády[2], J. Burgyán[1] and É. Várallyay[1]

[1]NARIC, Agricultural Biotechnology Institute, Gödöllő, Hungary
[2]HAS, Research Center of Natural Sciences, Institute of Enzymology, Budapest,
[3]University of Pannonia, Georgikon Faculty, Department of Horticulture, Keszthely,
[4]BCE, Institute of Viticulture and Oenology, Department of Viticulture, Budapest

Grapevine Syrah virus 1 (GSyV-1) was first identified in a Californian vineyard of *Vitis vinifera* cv. Syrah (Al Rwahnih *et al*., 2009). Since then, its presence has been reported from Chile, Washington (USA), Canada, France, Italy, Slovakia and Czech Republic (Glasa *et al*., 2015). During a survey of Hungarian vineyards for virus infections, leaf samples were collected from 20 vineyards in May 2014. Small RNA libraries of each vineyard were produced and sequenced using an Illumina platform. Bioinformatics analysis of the resulting reads strongly suggested a frequent occurrence of GSyV-1 (15 out of 20 vineyards). Validation by RT-PCR using primers DetF and DetR designed in the methyltransferase gene (Al Rwahnih *et al*., 2009) resulted in the amplification of a 296 bp product in 10 samples, representing five vines from distant grape-growing regions of the country. Another RT-PCR assay with primers GVQCP-F (5-TCCCAGCTTCAGGGTGAATT-3') and GVQCP-R (5'-GCATTGCTGCGCATTGGAGG-3') that amplify the coat protein (CP) gene revealed the GSyV-1 specific 720 bp product in all of the predicted samples. Twelve GSyV-1-derived PCR products were purified, sequenced and the sequences were deposited in GenBank. Comparison of the partial methyltransferase gene sequences (KT005394-KT005397) showed 93-97% nucleotide identity, while the partial CP gene sequences (KT005398-KT005405) showed 92-98% nucleotide identity to the reference genome (FJ436028). Their comparison with Slovak and Czech strains showed 94-97% and 70-98% identity, respectively, confirming a high variability of European GSyV-1 strains (Glasa *et al*., 2015). To our knowledge this is the first report of GSyV-1 in Hungary. Further studies are needed to determine the significance and relevance of this finding.

W*ork supported by the KTIA_AIK_12-1-2013-0001 project.*

Al Rwahnih M., Daubert S., Golino D., Rowhani A., 2009. Deep sequencing analysis of RNAs from a grapevine showing Syrah decline symptoms reveals a multiple virus infection that includes a novel virus. *Virology* **387:** 395-401.

Glasa M., Predajna L., Soltys K., Sabanadzovic S., Olmos A., 2015. Detection and molecular characterisation of Grapevine Syrah virus-1 isolates from Central Europe. *Virus Genes* **51:** 112-121.

Corresponding author: E. Varallyay
E-mail: varallya@abc.hu

Received October 12, 2015
Accepted October 15, 2015