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

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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'-GTTTTCCCCAGT-CACGACTTTTTTTTTTTT-3'), and PCR was done with primers M4 (5'-GTTTTCCCCAGTCACGAC-3') and S (5'GG(A/G/C/T)AA(C/T)AA(C/T)AG(G/A/G/C/T)CA(A/G/GCC-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.

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DISEASE NOTE

FIRST DESCRIPTION OF GRAPEVINE SYRAH VIRUS 1 IN VINEYARDS OF HUNGARY

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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 DefF and DefR 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'-TCCCAGCTTCAGGGTGAAATT-3') and GVQCP-R (5'-GCATTGCTGCGCATTGGAG-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.

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