

DISEASE NOTE

FIRST REPORT OF *LEEK YELLOW STRIPE VIRUS* IN FOREIGN AND POLISH GARLIC PLANTS IN CENTRAL POLAND

M. Chodorska, E. Paduch-Cichal, E. Kalinowska, O. Gaczkowska, M. Lis, B. Sierant and M.S. Szyndel

Warsaw University of Life Sciences - SGGW, Faculty of Horticulture and Landscape Architecture, Department of Plant Pathology, Nowoursynowska 159, 02-776, Warsaw, Poland

Leek yellow stripe virus (LYSV), genus *Potyvirus*, family *Potyviriidae* (King *et al.*, 2011) is the most common and important virus infecting a wide range of *Allium* worldwide. The aim of this study was to detect and identify LYSV in leek and garlic plants originating in central Poland, and also materials from Belgium, Egypt, and Spain purchased in Polish markets in April 2014. Randomly collected 178 samples were tested by a double-antibody sandwich enzyme linked immunosorbent assay (DAS-ELISA), according to the manufacturer's instructions (DSMZ, Braunschweig, Germany). All leek plants tested negative for LYSV, whereas 31 of 120 garlic bulbs tested positive. The presence of LYSV was confirmed by reverse transcription (RT)-PCR using total RNA extracted with the silica capture method (Boom *et al.*, 1990; Malinowski, 1997) and primers 1-LYSV/2-LYSV (Parrano *et al.*, 2012) designed to amplify a part of the N-terminal domain of the coat protein (CP) gene of the virus (363 bp). A sequence of the partial CP genes of the 12 LYSV isolates was submitted to GenBank (Accession Nos KM032272-KM032283). BLAST analysis of Polish sequences showed 96-99% identity at the nucleotide and amino acid levels. Sequences of Egyptian isolates, first representatives from this locations, showed 92 and 95% nucleotide and amino acid identities, respectively. However Spanish isolates revealed 95% and 97% nucleotide and amino acid identities, respectively. To the best of our knowledge, this is the first report of LYSV in foreign and Polish garlic plants available for purchase in central Poland. The accurate identification of viruses present in garlic plants, especially in imported plant material, will help to use the appropriate strategies to reduce viral incidence in garlic-growing areas.

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Corresponding author: M. Chodorska
Fax: +48.225932043
E-mail: maria_chodorska@sggw.pl

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FIRST REPORT OF GUMMOSIS OF MANGO TREES CAUSED BY *NEOFUSICOCCUM PARVUM* IN SICHUAN, SOUTHWEST CHINA

Q.L. Li^{1,2}, T.J. Deng³, S.P. Huang^{1,2}, T.X. Guo^{1,2}, J.Y. Mo^{1,2} and T. Hsiang⁴

¹Institute of Plant Protection, Guangxi Academy of Agricultural Sciences, Nanning, Guangxi, 530007, China

²Guangxi Key Laboratory of Biology for Crop Diseases and Insect Pests, Nanning, Guangxi, 530007, China

³Plant Protection Station of Guangxi Province, Nanning, Guangxi, 530022, China

⁴School of Environmental Sciences, University of Guelph, Guelph, Ontario, N1G 2W1, Canada

Mango (*Mangifera indica*) is an important fruit crop in southern China, and gummosis is one of the most important diseases. In September 2012, symptomatic branches were collected in Panzhihua, Sichuan province. On potato dextrose agar, isolates of similar morphological characteristics were consistently recovered from surface-sterilized branch pieces. The fungus was identified as *Neofusicoccum parvum* based on morphology and DNA sequence comparisons (Costa *et al.*, 2010). Conidia were hyaline, thin walled, spindle-shaped to ellipsoid, nonseptate, and ranged from 15 to 23.5 × 4 to 7 μm (average 19.5 × 5.6 μm). The rDNA internal transcribed spacer region, a partial sequence of the β-tubulin gene, and the translation elongation factor 1-α gene of one isolate (L13), showed 100% identity to *N. parvum* (GenBank accession Nos GU997685, HM480386 and HQ859955). Pathogenicity of three isolates was tested in three green twigs and three 3-year-old branches in mango orchards of Guangxi Academy of Agricultural Sciences, Guangxi, China. Five wounds were made for each location with a sterilized needle. Mycelial plugs were placed at wounds and then covered with parafilm. Control twigs were inoculated with uncolonized PDA plugs. Two weeks later, typical brown lesions were observed on inoculated branches, and gum exuded from infected tissues wound. No symptoms were seen on the controls. Koch's postulates were fulfilled by re-isolation of *N. parvum* from diseased branches. In China, the disease was mainly associated with *Lasiodiplodia theobromae* (Li *et al.*, 2013) and *Botryosphaeria dothidea* (Mo *et al.*, 2013). To our knowledge, this is the first report of *N. parvum* causing mango gummosis in China.

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Corresponding author: J. Mo
Fax: +86-0771-3243874
E-mail: mojianyou@gxaas.net

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