

## DISEASE NOTE

**FIRST REPORT OF *CHILLI RINGSPOT VIRUS* INFECTION OF *SOLANUM XANTHOCARPUM* IN CHINA**

J.Y. Hu<sup>1\*</sup>, J. Liu<sup>1\*</sup>, D.Z. Deng<sup>2</sup> and W.X. Yan<sup>2</sup>

<sup>1</sup>Ecological Security and Protection Key Laboratory of Sichuan Province, College of Life Science and Biotechnology, Mianyang Normal University, Mianyang 621000, P.R. China

<sup>2</sup>Sichuan Academy of Forestry, Chengdu 610081, P.R. China

\*These authors contributed equally to this work.

*Solanum xanthocarpum* (yellow-berried nightshade) is a common weed in southwest China. In August 2014, two *S. xanthocarpum* plants with leaves displaying ringspots were observed near Mianyang (Sichuan province, China). Total RNAs was extracted from symptomatic and symptomless leaves using Trizol (Invitrogen, USA), and first strand cDNA synthesis was primed with M14T (5'-GTTTTCCCAGTCACGAC(T)18-3') by SuperScript III Reverse Transcriptase (Invitrogen, USA). RT-PCR was performed using the potyvirus universal primers Sprimer (5'-GGX AAY AAY AGY GGX CAZ CC-3', X=A, G, C or T; Y=T or C; Z=A or G) and M4 (5'-GTT TTC CCA GTC ACG AC-3') (Chen *et al.*, 2001). A 1.6 kb DNA fragment was amplified from symptomatic but not from symptomless leaf samples. The amplified products were purified, cloned into the PMD19-T vector (TaKaRa, China) and sequenced. Sequencing results confirmed the presence of *Chilli ringspot virus* (ChiRSV) (GenBank accession No. KP310866) with 99% (JN008909.1) and 91% (DQ925438) nucleotide identity with comparable sequences of other ChiRSV isolates available in GenBank. To the best of our knowledge, this is the first report of ChiRSV on *S. xanthocarpum* in China.

Work supported by the Project of Panda protection and habitat restoration in Beichuan Qiang Autonomous County after Wenchuan earthquake, the Opening Project of Ecological Security and Protection Key Laboratory of Sichuan Province (071197147), the National Natural Science Foundation of China (No. 31170319).

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

Corresponding author: J.Y. Hu

Fax: +86.816 .2578582

E-mail: jinyaohu@126.com

Received January 15, 2015

Accepted January 21, 2015

## DISEASE NOTE

**FIRST REPORT OF *RHODOTORULA GLUTINIS*-INDUCED RED SPOT DISEASE OF *PLEUROTUS NEBRODENSIS* IN CHINA**

S. Wang<sup>1</sup>, C. Rong<sup>1</sup>, Y. Ma<sup>1,2</sup>, Y. Liu<sup>1</sup>, D. Zhang<sup>1</sup> and F. Xu<sup>1</sup>

<sup>1</sup>Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Science, Beijing Engineering Research Center for Edible Mushroom, Key Laboratory of Urban Agriculture (North), Beijing 100097 China

<sup>2</sup>College of Food Science and Technology, Shanghai Ocean University, Shanghai 201306, China

In September 2012, red spots located between the stipes and pilei of the fruiting bodies of *Pleurotus nebrodensis* whose growth had halted were observed in China. The internal transcribed spacer (ITS) and the D1/D2 domain of 26S rRNA gene from the putative pathogen, a bacterium isolated from diseased mushrooms, were amplified and sequenced (GenBank accession Nos KF314800 and KF314802). The neighbour-joining tree constructed with ITS sequences showed that those of the bacterium under study had the highest similarity (99.2%) with the comparable sequences of *Rhodotorula glutinis* CBS 20<sup>T</sup>, while the D1/D2 domain sequences were identical with those of the same bacterial species. Metabolic profiles of the bacterial isolate from diseased mushrooms closely resembled that of *R. glutinis* CBS 20<sup>T</sup> with one exception (negative for acid production from fermentation of D-ribose). Based on the above, the putative pathogen was identified as *R. glutinis*. Pathogenicity tests carried out with suspensions (approximately 1×10<sup>6</sup> CFU/ml) directly inoculated on the surface of young *P. nebrodensis* fruiting bodies resulted in the development within 3-5 days of red spots like those shown by naturally diseased mushrooms. Negative controls did not develop symptoms. A bacterium identical to that used for inoculation trials was re-isolated from symptomatic mushrooms, thus fulfilling Koch's postulates. *Rhodotorula* spp. are closely phylogenetically related to the genus *Sporobolomyces*, which was reported as the agent of the red spot disease of *Pleurotus eryngii* (Xu *et al.*, 2014). To the best of our knowledge, this is the first report of *R. glutinis*-induced red spot disease of *P. nebrodensis* in China.

Xu F., Wang S.X., Liu Y., Ma Y.W., Zhang D.P., Zhao S., 2014. First report of *Sporobolomyces symmetricus* induced red spot disease of *Pleurotus eryngii* in China. *Plant Disease* **98**: 693.

Corresponding author: F. Xu

Fax: +86.10.51503899

E-mail: xxu1022@163.com

Received January 24, 2015

Accepted January 25, 2015