

DISEASE NOTE

FIRST REPORT OF POWDERY MILDEW ON *LAGENARIA SICERARIA* CAUSED BY *PODOSPHAERA XANTHII* IN INDIA

A.K. Nayak and B.K. Babu

Microbial Genomics and Diagnostics Lab., Microbiology and Plant Pathology Division, Regional Plant Resource Centre, Bhubaneswar-751015, Odisha, India

The bottle gourd (*Lagenaria siceraria*, family Cucurbitaceae) is a medicinal plant (Sirohi and Sivakami, 1991) widely cultivated throughout India. In December 2014, powdery mildew symptoms were observed on *L. siceraria* in different fields of the Odisha state (India), i.e. circular white mycelial patches 1 to 2 mm in diameter on the upper surface of the leaves, which coalesced and developed into larger circular or irregular spots on both leaf surfaces. Infected leaves dried and eventually dropped. Conidiophores were 110-220×11-13.5 µm in size and produced 3 to 5 immature conidia in chains with a crenate outline. Foot cells were 40-75 µm long, straight, cylindrical, slightly constricted at the basal septum. Conidia were hyaline, ellipsoid-ovoid, 25-40×17-22 µm in size and had distinct fibrosin bodies. These morphological traits suggested this fungus to be a species of the genus *Podosphaera*, likely corresponding to *Podosphaera xanthii* (Braun and Cook, 2012). For confirmation, the internal transcribed spacer (ITS) region of rDNA from conidia was amplified with primers ITS 1/ ITS 4 and sequenced according to Babu *et al.* (2015). The resulting 182 bp sequence (GenBank accession No. KU376473) was analysed by BLAST homology search against GenBank database revealing 100% similarity with *P. xanthii* (KX061106, KR779870). Pathogenicity was determined by inoculating conidial suspension onto young leaves of five healthy potted *L. siceraria* in a greenhouse at 25-28°C (>80% humidity). Five non inoculated plants served as control. Symptoms like those shown in the field developed 5-7 days post inoculation only on inoculated plants from which *P. xanthii* was reisolated. To our knowledge, this is the first report of *P. xanthii* as the cause of powdery mildew disease on bottle gourd in India.

Babu B.K., Sharma R., 2015. Taq Man real-Time PCR assay for the detection and quantification of *Sclerospora graminicola*, the causal agent of pearl millet downy mildew. *European Journal of Plant Pathology* **142**:149-158.

Braun U., Cook R.T.A., 2012. Taxonomic Manual of the *Erysiphales* (Powdery Mildews), CBS Biodiversity Series No. 11. CBS, Utrecht, Netherlands.

Saha P., Mazumber U.K., Haldar P.K., Islam A., Kumar R.B.S., 2011. Evaluation of acute and sub chronic toxicity of *Lagenaria siceraria* aerial part. *International Journal of Pharmaceutical Sciences and Research* **2**: 1507-1512.

Sirohi P.S., Sivakami N., 1991. Genetic diversity in cucurbits. *Indian Horticulture* **36**: 45-46.

Corresponding author: B.K. Babu
E-mail: kishorebanadam@gmail.com

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DISEASE NOTE

FIRST REPORT OF *CITRUS DEPRESSA* AS A NEW NATURAL HOST OF *XANTHOMONAS CITRI* subsp. *CITRI* PATHOTYPE A IN TAIWAN

C.J. Huang¹ and H.F. Ni²

¹Department of Plant Medicine, National Chiayi University, 60004, Taiwan

²Department of Plant Protection, Chiayi Agricultural Experiment Station, Taiwan Agricultural Research Institute, Chiayi, 60044, Taiwan

Citrus depressa is an indigenous citrus species in Taiwan. Not much is known about diseases occurring on *C. depressa*. A leaf spot disease of *C. depressa* was first observed in Chiayi City, Taiwan, in 2015 and 2016. Symptoms were brownish necrotic spots, surrounded by a yellowish halo. Leaf blight was not observed. Bacteria were isolated from surface-sterilized leaf spot samples, and two *Xanthomonas*-like yellow isolates, CJHCd003 and CJHCd004, were purified and stored at -80°C in 20% glycerol. Leaves of *C. depressa*, sweet orange (*C. sinensis* cv. Liucheng), mandarin (*C. reticulata* cv. Ponkan), grapefruit (*C. paradisi*), and Mexican lime (*C. aurantiifolia*) were infiltrated with bacterial suspensions (1×10⁶ CFU/ml). *C. depressa* inoculated leaves exhibited necrotic spots surrounded with a yellowish halo ten days post inoculation similar to those observed in natural infections. The same bacterium could be consistently re-isolated from the inoculated leaves and confirmed by PCR with 4/7 primers (Hartung *et al.*, 1993), fulfilling Koch's postulates. The control leaves remained disease-free. Multilocus sequence analysis of seven housekeeping genes (16S rDNA, *fusA*, *gap-1*, *gltA*, *gyrB*, *lacF*, and *lepA*) (Almeida *et al.*, 2010; Ngoc *et al.*, 2010) fully identified the two isolates from *C. depressa* as pathotype A strains of *X. citri* pv. *citri* with 100% sequence identity (Ngoc *et al.*, 2010; Zhang *et al.*, 2015). Furthermore, these strains caused typical erumpent, callus-like tissue at inoculated sites on the other citrus leaves tested, indicating that these strains belong to pathotype A strains of *X. citri* subsp. *citri*. To our knowledge, this is the first report of *C. depressa* as a newly discovered natural host of *X. citri* subsp. *citri* pathotype A in Taiwan.

Almeida N.F., Yan S., Cai R., Clarke C.R., Morris C.E., Schaad N.W., Schuenzel E.L., Lacy G.H., Sun X., Jones J.B., Castillo J.A., Bull C.T., Leman S., Guttman D.S., Setubal J.C., Vinatzer B.A., 2010. PAMDB, a multilocus sequence typing and analysis database and website for plant-associated microbes. *Phytopathology* **100**: 208-215.

Hartung J.S., Daniel J.F., Pruvost O.P., 1993. Detection of *Xanthomonas campestris* pv. *citri* by the polymerase chain reaction method. *Applied and Environmental Microbiology* **59**: 1143-1148.

Ngoc L.B.T., Verniere C., Joun E., Ah-You N., Lefeuvre P., Chiroleu F., Gagnevin L., Pruvost O., 2010. Amplified fragment length polymorphism and multilocus sequence analysis-based genotypic relatedness among pathogenic variants of *Xanthomonas citri* pv. *citri* and *Xanthomonas campestris* pv. *bilvae*. *International Journal of Systemic and Evolutionary Microbiology* **60**: 515-525.

Zhang Y., Jalan N., Zhou X., Goss E., Jones J.B., Setubal J.C., Deng X., Wang N., 2015. Positive selection is the main driving force for evolution of citrus canker-causing *Xanthomonas*. *ISME Journal* **9**: 2128-2138.

Corresponding author: C.J. Huang
E-mail: chienjui.huang@mail.ncyu.edu.tw

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