New Disease Reports

First report of *Microidium phyllanthi* causing powdery mildew on chamber bitter in Vietnam

L.T.T. Tam [1]*, H.T. Hoai [1], L.P. Thao [1], N.T. Huong [1] and N.M. Khue [2]

[1] *Division of Plant Pathology, Plant Protection Research Institute, Duc Thang, Bac Tu Liem, Hanoi, Vietnam*; [2] *Plant Protection Department of Lai Chau province, Lai Chau, Vietnam*

*E-mail: hanhtamle10_2012@yahoo.co.uk

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Chamber bitter, *Phyllanthus urinaria*, is a widely used herbal medicine that has been reported to possess various biological activities with anticancer effects (Huang *et al*., 2003). Chamber bitter plants have been cultured intensively in large areas for commercial medical production in Vietnam and China. Powdery mildew was found on this species at the National Institute of Medicinal Material in Hanoi during winter 2013, as well as on other species in nearby fields. Whole plants were covered almost completely by white fungal colonies giving the impression of having been sprayed by powdered lime (Fig. 1). Disease incidence reached approximately 85% resulting in an approximately 60% loss in yield. Two representative specimens were deposited in the Plant Protection Research Institute Herbarium (Accession Nos. PPRI-PM054 and PPRI-PM055) in Hanoi.

Microscopic examination showed conidiophores had a catenescent form of conidiogenesis and were composed of 1-3 cells, measuring (76-)78-117(-120) µm long. Conidiophore foot-cells were curved with a twist at the base and measured 58-65(-68) x 4 µm (Fig. 2a, b). Conidia were produced in chains and were small, doliiform, ellipsoid to cylindrical in shape, measuring 15-20(-23) x 8-10 µm with a length/width ratio of (1.5-)1.8-2.7(-3.0). Conidia had no fibrosin bodies, but inclusion-like oil drops were present and germinated with *Microidium*-type germ tubes (Fig. 2c, d). No chasmothecia were found. Appressoria on mycelium had lobe or nipple shapes. The morphological characteristics were consistent with descriptions of *Microidium phyllanthi* (To-anun *et al*., 2005; Braun & Cook, 2012). To confirm the identity of the causal fungus, the complete ITS regions of rDNA from the above specimens were amplified with primer pairs ITS1/P3 (White *et al*., 1990; Kusaba & Tsuge, 1995) or HF1/ HR4 (Tam *et al*., 2015) and directly sequenced. The resulting sequences of 645 and 700 bp, respectively, were deposited in GenBank (Accession Nos. KM260738, KM260739, respectively). A GenBank BLAST search using the present data revealed that these ITS sequences shared 100% identity with those of *Microidium phyllanthi* (AB719943).

Pathogenicity was confirmed through inoculation tests by gently sweeping conidia with a pen brush from diseased leaves of chamber bitter onto young leaves of 10 two-month-old potted seedlings of *P. urinaria*. Ten non-inoculated seedlings were used as controls. Plants were maintained in a glasshouse at 24-26°C. Inoculated leaves developed symptoms after nine days, whereas the control plants remained symptomless. The fungus present on the inoculated leaves was morphologically identical to that observed on the original diseased leaves, with the same sequence being produced following the PCR protocol described above, fulfilling Koch's postulates.

According to Braun & Cook (2012), *M. phyllanthi* has a host range on other *Phyllanthus* species, including *P. acidus*, *P. amarus*, *P. niruri*, *P. reticulatus*, *P. rheedii* and *P. urinaria* with distribution in Africa (Ghana and Mauritius) and Asia (India, Indonesia, Sri Lanka, Taiwan and Thailand). To our knowledge, this is the first report of *M. phyllanthi* infection of *P. urinaria* in Vietnam. This report is significant as this disease is affecting commercial production for medical use of chamber bitter in Vietnam and control measures are being sought.

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Figure 1

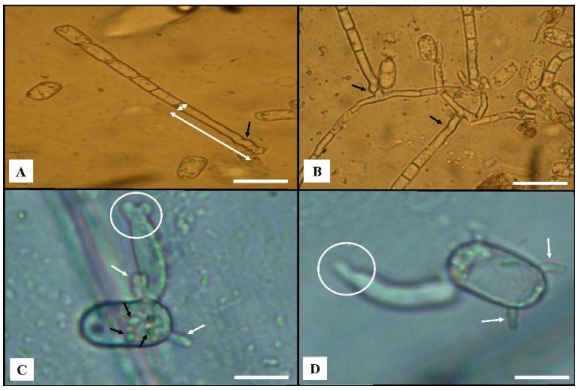

Figure 2

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