Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Paramyrothecium foliicola* Causing Leaf Spot on *Vigna radiata* in China

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Mung bean (*Vigna radiata* L.) is an important legume crop cultivated widely in China (Nair et al. 2013). In September 2018, a severe foliar disease occurred on some mung bean cultivars (Jilv0816, Baolv200810-1, Liaolv10L708-5, and Zhonglv5) in Shijiazhuang (38°03'N, 114°29'E), Hebei Province, China. Initially, lesions were circular to irregular, with dark brown margins and pale centers. Later, tiny dark stroma with oval or irregular shape were observed on spots. The infected field was about 0.067 ha with 50 to 70% disease incidence, but with no significant yield losses. Several leaves with necrotic spots were collected and cut into 2- to 3-mm pieces, surface sterilized with 2% NaClO for 2 min, rinsed three times in sterile distilled water, and incubated on potato dextrose agar (PDA) at 25°C in darkness for 7 days. Three of 10 obtained single spore isolates, QB1, QB2, and QB3, were used for further studies. Colonies had abundant white aerial mycelia and produced black sporodochia bearing masses of viscid spores on PDA after 7 to 10 days. Conidia were aseptate, hyaline, and cylindrical, with the size of 5.6 to 7.5 × 1.6 to 3.3 μm ($n = 50$). Conidiophores branched repeatedly. These morphological characteristics resembled that of *Paramyrothecium*-like isolates (Lombard et al. 2016). Given that *Paramyrothecium roridum*, *P. foliicola*, and *P. nigrum* were all reported to cause leaf spot on leafy vegetables and ornamental crops, five loci (the internal transcribed spacer [ITS], translation elongation factor 1- α [*tef1*], β -tubulin [*tub2*], 28S rRNA [LSU], and calmodulin [*cmdA*])

were amplified and sequenced for molecular analysis (Matić et al. 2019). The resulting sequences were deposited in GenBank under accession numbers MK335967 and MT415351 to MT415364. Among the five loci, ITS and LSU sequences showed 99 to 100% (584/590, 545/546 base pairs) similarity with *P. foliicola* type strain CBS113121 (NR_145074.1; KU846324.1) by BLASTn analysis, whereas the *tef1*, *tub2*, and *cmdA* sequences exhibited high identity (99%) (398/404 bp, 323 to 324/326 bp, 555 to 558/560 bp) with *P. foliicola* strain Bas4_m2 (MH939239.1, MH824739.1, MH807772.1) (Matić et al. 2019). The phylogenetic tree of the five concatenated loci showed that our isolates cluster with *P. foliicola*, although they show slight differences from other *P. foliicola* strains. Based on morphology and molecular analysis, the pathogen was identified as *P. foliicola*. Pathogenicity tests of the three isolates were performed by spraying 2 ml of 1.0×10^6 /ml spore suspension on each 3-week-old seedling of mung bean cultivar 'Jilv 7' ($n = 5$ for each isolate), whereas the controls were inoculated with sterile water ($n = 3$). All inoculations were incubated in a moist chamber at 25°C with a 12-h light cycle. The experiment was repeated twice. After 7 to 10 days, symptoms with necrotic brown spots were observed on plants inoculated with *P. foliicola* but not on controls. The pathogen was reisolated from randomly selected diseased leaves and identified as *P. foliicola* by morphology and DNA sequencing of *tub2* and *cmdA* loci. No pathogens were isolated from controls. Although *P. roridum* has been reported to cause mung bean leaf spot in India (Singh and Narain 2008; Singh and Shukla 1997), to our knowledge, this is the first report of *P. foliicola* causing leaf spot on mung bean in China. This finding suggests a potential threat to mung bean production in China, and further studies should focus on epidemiology and control of this disease.

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