Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Microdochium nivale* and *M. majus* Causing Brown Foot Rot of Wheat in China

F. Xu, R. J. Shi, J. J. Zhang, Y. L. Song,[†] L. L. Liu, Z. H. Han, J. M. Wang, Y. H. Li, C. H. Feng, and L. J. Li

Institute of Plant Protection, Henan Academy of Agricultural Sciences; Key Laboratory of Integrated Pest Management on Crops in Southern Part of North China, Ministry of Agriculture and Rural Affairs of the People's Republic of China, Zhengzhou 450002, Henan, China

Funding: Funding was provided by the National Key R&D Program of China (2017YFD0201700). Plant Dis. 106:1523, 2022; published online as <https://doi.org/10.1094/PDIS-08-21-1722-PDN>. Accepted for publication 26 October 2021.

Microdochium nivale and *M. majus* not only cause seedling blight of wheat (*Triticum aestivum* L.) in cold dry soils, but also cause foot rot and ear blight of wheat under favorable conditions (Haigh et al. 2009). In May 2017, 2019, and 2020, a serious foot rot of wheat with an incidence of 92, 45, and 51% was observed in the field in Xiangcheng County (33.43° N, 114.84° E), Tanghe County (32.43° N, 112.66° E), and Linzhou City (36.13° N, 113.75° E), Henan Province, respectively. Serious brown lesions on the lower leaf sheaths were visible. The pathogens were isolated from brown leaf sheaths on potato dextrose agar (PDA) after being surface-sterilized (70% EtOH for 30 s followed by 3% NaClO for 1.5 min) and rinsed three times in sterile distilled water. After 5 d, mycelia were transferred to fresh PDA, and nine representative isolates (G17ZK2-1, G17ZK2-2, G17ZK2-3, g19TH10-4, g19TH10-5, g19TH10-6, G20LZ1-6, G20LZ1-7, and G20LZ1-8) were further purified by hyphal tipping. Species were identified based on morphological characteristics, and sequence analysis of partial sequences of the translation elongation factor-1 α (TEF), RNA polymerase II subunit (*RPB2*) gene, and β -tubulin gene (Abdelhalim et al. 2020). Among the nine isolates, six belonged to *M. majus* and three belonged to *M. nivale*. Sequences of six isolates of *M. majus* and three isolates of *M. nivale* were deposited in GenBank with accession numbers MW428296 to MW428298, MZ734119 to MZ734121, and MZ734139 to MZ734141 (TEF); MW384889, MW428291, MW428292, MZ734203 to MZ734205, and MZ734161 to MZ734163 (*RPB2*); and MW428293 to MW428295,

MZ501004 to MZ501006, and MZ501024 to MZ501026 (β -tubulin). For all the genes, isolates revealed 98 to 100% similarity to *M. majus* and *M. nivale* accessions. Microscopy of the six *M. majus* isolates showed that the conidia were falcate, straight to curved, apex pointed or obtuse to sub-acute, lacking basal differentiation, with one to six septa, 3.6 to 5.0 $\times$ 15.0 to 30.5 μ m (av. = 4.5 $\times$ 23.2 μ m; n = 60). The three *M. nivale* isolates showed that the conidia were hyaline, one to three septa, 2.4 to 4.4 $\times$ 11.9 to 26.0 μ m (av. = 3.5 $\times$ 14.7 μ m; n = 60). Perithecia of *M. majus* are dark brown, globose, and 95.2 to 190.5 $\times$ 95.2 to 228.6 μ m (av. = 144.4 $\times$ 152.5 μ m; n = 30). Asci are clavate, 6.8 to 11.0 $\times$ 68.2 to 77.3 μ m (av. = 8.6 $\times$ 72.0 μ m; n = 30), and contain eight ascospores. Mature ascospores are ellipsoidal and 3.8 to 4.9 $\times$ 11.5 to 19.2 μ m (av. = 4.0 $\times$ 15.2 μ m; n = 30), with 1 to 3 septa. These morphological characteristics were consistent with previous descriptions of these two species (Glynn et al. 2005). For pathogenicity tests, mycelia of *M. nivale* and *M. majus* was prepared using the modified procedure of Zhang et al. (2015). Two-week-old healthy wheat seedlings (cv. 'Aikang 58') were inoculated using 1 ml of prepared mycelia to one seedling, which was sprayed on soil. Control seedlings were inoculated with 1 ml of distilled water containing 0.2% gelatin. After 10 days under 15/10°C, 16h/8h, all the inoculated plants had developed brown spots while control plants remained healthy. The pathogens were reisolated from inoculated plants and identified as *M. nivale* and *M. majus* based on morphological characteristics and molecular methods described above. Although there are reports of *M. majus* associated with brown foot rot of wheat in Anhui Province and *M. nivale* associated with seedling blight of oat in Gansu Province (Chen et al. 2021; Tai et al. 2019), to our knowledge, this is the first report of brown foot rot of wheat caused by *M. nivale* and *M. majus* in China.

References:

- Abdelhalim, M., et al. 2020. Eur. J. Plant Pathol. 156:885.
- Chen, H., et al. 2021. Plant Dis. 105:704.
- Glynn, N. C., et al. 2005. Mycol. Res. 109:872.
- Haigh, I. M., et al. 2009. Eur. J. Plant Pathol. 124:65.
- Tai, J., et al. 2019. Plant Dis. 103:587.
- Zhang, W., et al. 2015. Mycologia 107:80.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: brown foot rot, cereals and grains, *Microdochium majus*

[†]Indicates the corresponding author.
Y. Song; songyuli2000@126.com