Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium compactum* Causing Fusarium Head Blight of Wheat in China

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Fusarium head blight (FHB), a devastating wheat disease caused by several species of *Fusarium*, threatens global wheat yield and quality (Erenstein et al. 2022). In August 2023, wheat spikes exhibiting clear FHB symptoms were observed in fields in Yunnan, China (24°16′46″N, 102°29′46″E), with an incidence rate of approximately 10%. Diseased wheat spikes exhibited a bleached, wilted appearance, with abundant orange sporodochia on the glumes, similar to previous reports (Osborne and Stein 2007). Twenty-four symptomatic spikes were collected from a single field, and sporodochia were washed with sterile water to prepare a spore suspension of 1×10^3 spores/ml, which was inoculated onto potato dextrose agar (PDA) to obtain monosporic cultures. Four reference strains (KUNCC 3418 to KUNCC 3420 and KUNCC 3431) were deposited at the Kunming Institute of Botany Culture Collection, Chinese Academy of Sciences (KUNCC). For species identification, four strains were cultured on PDA and carnation leaf agar (CLA) at 25°C, with incubation under a 12-h near-UV light/dark cycle on CLA and in complete darkness for 24 h on PDA. Colonies on PDA grew rapidly, appearing white and loosely flocculent. Abundant pale orange, translucent sporodochia formed on CLA. Sporodochial conidiogenous cells were monophialidic or polyphialidic, subulate to subcylindrical, and 9.5 to 12 × 3 to 3.5 µm. Sporodochial macroconidia were naviculate to fusiform, with an elongate, tapering apical cell and a foot-shaped basal cell, 3 to 6 septate, measuring 33 to 67.5 × 3.5 to 5.5 µm. The internal transcribed spacer (ITS), translation elongation factor 1-α (*tef1-α*), DNA-directed RNA polymerase II largest subunit (*rpb1*), second-largest subunit (*rpb2*), and calmodulin (*cam*) regions were amplified and sequenced using the primers ITS1/ITS4, EF-1/EF-2, rpb1-F7/G2R, rpb2-5F2/11aR, and CL1/CL2A, according to the methods described by Crous et al. (2021). These sequences were deposited in GenBank for *cam* (PP951603 to PP951606), ITS (PP946846 to PP946849), *tef1-α* (PP719217, PP731572 to PP731574), *rpb1* (PP719219, PP737839 to PP737841), and *rpb2* (PP719218, PP951607 to PP951609). BLASTn analyses of these sequences showed an identity range of 99.7 to 100% with the epitype strain NRRL 36323 of *Fusarium compactum* (GenBank: *cam* = GQ505560, ITS = MH855177, *tef-1α* = GQ505648, and *rpb2* = GQ505826), with base pair matches of 663/665 bp for *cam*, 488/488 bp for ITS, 641/641 bp for *tef1-α*, and 892/892 bp for *rpb2*. Both morphological and BLASTn analyses confirmed these isolates as *F. compactum* (Han et al. 2023; Leslie and Summerell 2006). Pathogenicity tests were performed by spraying 1 ml of spore suspension (1×10^8 spores/ml) of *F. compactum* strains onto spikes of the wheat cultivar Yunmai 126 at the flowering stage ($n = 9$). Controls ($n = 9$) were treated only with sterile water. Following treatment, the wheat spikes were covered with plastic bags and incubated at 25°C for 10 days. After 14 days, the inoculated spikes turned bleached and dry, showing FHB symptoms, whereas the wheat spikes in the control treatment remained asymptomatic. The pathogenic fungus reisolated from all diseased samples was confirmed as *F. compactum*. It has been frequently reported in association with crown and root rot of wheat, particularly in regions such as Turkey and Iran (Besharati et al. 2017; Tunali et al. 2008). To our knowledge, this is the first report of *F. compactum* on diseased wheat spikes in China. This finding provides valuable insights into the spread of *F. compactum*.

References:

Besharati, F. M., et al. 2017. Arch. Phytopathol. Pflanzenschutz. 50:123.
Crous, P. W., et al. 2021. Stud. Mycol. 98:100116.
Erenstein, O., et al. 2022. Global Trends in Wheat Production, Consumption and Trade. Springer International Publishing, Cham, Switzerland.
Han, S. L., et al. 2023. Stud. Mycol. 104:87.
Leslie, J. F., and Summerell, B. A. 2006. The *Fusarium* Laboratory Manual. Blackwell Publishing, Ames, IA.
Osborne, L. E., and Stein, J. M. 2007. Int. J. Food Microbiol. 119:103.
Tunali, B., et al. 2008. Plant Dis. 92:1299.

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