Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium* Wilt Disease on Watermelon Caused by *Fusarium oxysporum* f. sp. *niveum* in Malaysia

Muhammad Ziaur Rahman,^{1,2} Khairulmazmi Ahmad,^{1,†} Yasmeen Siddiqui,^{3,†} Norsazilawati Saad,¹ Tan Geok Hun,⁴ Erneeza Mohd Hata,¹ Osmah Rashed,¹ Md Imam Hossain,¹ and Abdulaziz Bashir Kutawa^{1,5}

¹ Department of Plant Protection, Faculty of Agriculture, University Putra Malaysia, 43400, Serdang, Selangor, Malaysia

² Plant Pathology Division, Bangladesh Agricultural Research Institute (BARI), Gazipur-1701, Bangladesh

³ Laboratory of Sustainable Agronomy and Crop Protection, Institute of Plantation Studies (IKP), University Putra Malaysia, 43400, Serdang, Selangor, Malaysia

⁴ Department of Agriculture Technology, Faculty of Agriculture, University Putra Malaysia, 43400, Serdang, Selangor, Malaysia

⁵ Department of Biological Sciences, Federal University Dutsin-Ma, P.M.B 5001, Dutsin-Ma, Katsina State, Nigeria

Funding: Funding for this research work was provided by NATP Phase II (National Agricultural Technology Program), BARC, Dhaka, Bangladesh with grant no. 6282515. Plant Dis. 105:4169, 2021; published online as <https://doi.org/10.1094/PDIS-04-21-0780-PDN>. Accepted for publication 24 May 2021.

Fusarium wilt disease incited by *Fusarium oxysporum* f. sp. *niveum* is the utmost devastating soil-inhabiting fungal pathogen limiting watermelon (*Citrullus lanatus*) production in Malaysia and globally. The field disease survey of *Fusarium* wilt was carried out during December 2019 and November 2020, in three major production areas (three farmer fields per location) in peninsular Malaysia, namely Mersing, Serdang, and Kuantan, and disease incidences of 30 and 45% were recorded for the two years, respectively. Infected watermelon plants showed symptoms such as vascular discoloration, brown necrotic lesions to the soil line or the crown, one-sided wilt of a plant, a runner, or the whole plant. Pieces of infected root and stem tissues (1 to 2 cm) were surface sterilized with 0.6% NaOCl for 1 min followed by double washing with sterile water. The disinfected tissues were air-dried and transferred onto semiselective Komada's medium (Komada 1975) and incubated for 5 days. The fungal colonies produced were placed on potato dextrose agar (PDA) to attain a pure culture and incubated at 25 ± 2°C for 15 days. The pure fungal colony was flat, round, and light purple. Macroconidia were straight to slightly curved, 18.56 to 42.22 µm long, 2.69 to 4.08 µm wide,

predominantly 3 septate, and formed in sporodochia. Microconidia were 6.16 to 10.86 µm long and 2.49 to 3.83 µm wide, kidney-shaped, aseptate, and were formed on short monophialides in false-heads. Chlamydospores were single or in pairs with smooth or rough walls, found both terminally or intercalary. To confirm their pathogenicity, 2-week-old watermelon seedlings (cv. New Beauty) were dipped into spore suspension (1×10^6 spores/ml) of representative isolates of JO20 (Mersing), UPM4 (Serdang), and KU41 (Kuantan) for 30 s and moved to 10 cm diameter plastic pots containing 300 g sterilized soil mix. Disease symptoms were assessed weekly for 1 month. Control seedlings were immersed in sterile distilled water before transplanting. The inoculated seedlings showed typical *Fusarium* wilt symptoms like yellowing, stunted growth, and wilting, similar to the farmer field infected plants. However, control seedlings remained asymptomatic. The pathogen was successfully reisolated from the infected seedlings onto Komada's medium, fulfilling Koch's postulate. For PCR amplification, primers EF-1 and EF-2 were used to amplify the *tef1-α* region. A BLASTn analysis of the *tef1-α* sequences of the isolates JO20 (accession no. MW315902), UPM4 (MW839560), and KU41 (MW839562) showed 100% similarity, with e-value of zero, to the reference sequences of *F. oxysporum* isolate FJAT-31690 (MN507110) and *F. oxysporum* f. sp. *niveum* isolate FON2 790-2 (MN057702). In the *Fusarium* MLST database, isolates JO20, UPM4, and KU41 revealed 100% identity with the reference isolate of NRRL 22518 (accession no. FJ985265). Though isolate FJ985265 belongs to f. sp. *melonis*, earlier findings had revealed *F. oxysporum* f. sp. are naturally polyphyletic and making clusters with diverse groups of the *F. oxysporum* species complex (O'Donnell et al. 2015). The isolates JO20, UPM4, and KU41 were identified as *F. oxysporum* f. sp. *niveum* based on the aligned sequences of *tef1-α* and molecular phylogenetic exploration by the maximum likelihood method. To the best of our knowledge, this is the first report of *F. oxysporum* f. sp. *niveum* as a causative pathogen of *Fusarium* wilt disease of watermelon in Malaysia. Malaysia exports watermelon year round to countries like Singapore, Hong Kong, The United Arab Emirates, and The Netherlands. The outburst of this destructive soil-borne fungal pathogen could hinder watermelon cultivation in Malaysia. Thus, growers need to choose multiple management tactics such as resistant varieties, cultural practices (soil amendments and solarization), grafting, cover crops, and fungicide application to control this new pathogen.

References:

Komada, H. 1975. Rev. Plant Prot. Res. 8:114.
O'Donnell, K., et al. 2015. Phytoparasitica 43:583.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Fusarium oxysporum* f. sp. *niveum*, *Fusarium* wilt, watermelon, Malaysia

[†]Indicates the corresponding authors.
K. Ahmad; khairulmazmi@upm.edu.my, and
Y. Siddiqui; yasmeen@upm.edu.my