Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium sacchari* Causing Sugarcane Wilt in Bangladesh

S. K. Paul,¹ N. U. Mahmud,² D. R. Gupta,² M. N. Alam,³
M. Chakraborty,² and M. T. Islam^{2,†}

¹ Department of Agronomy, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh

² Institute of Biotechnology and Genetic Engineering, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh

³ Bangladesh Sugarcrop Research Institute, Ishurdi 6620, Pabna, Bangladesh

S. K. Paul and N. U. Mahmud contributed equally.

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Wilt is one of the destructive fungal diseases of sugarcane (*Saccharum officinarum* L.) affecting production in many sugarcane growing regions including Bangladesh. In July 2018, sugarcane plants showing wilting symptoms including withered, dried leaves and shriveling stalks with brown to pinkish discoloration in internal tissues (Viswanathan 2013) were collected from sugarcane fields in the Gazipur district (23°54'41" N, 90°23'20" E) of Bangladesh. The average disease incidence was 17% in 60 ha of sugarcane fields that were sampled for diseased plants with visible symptoms. Ten infected stalks (30 cm) were collected from five severely infected fields. The stalks were surface sterilized with 70% ethanol for 1 min followed by 0.2% sodium hypochlorite for 3 min and then rinsed three times with distilled water. Small pieces (2 mm × 2 mm) of the inner discolored tissue were cut with a sterile scalpel and placed on half strength potato dextrose agar (PDA) medium followed by incubation for 7 days at 25°C. A total of 10 isolates were recovered from the infected sugarcane stalks and were purified by the single spore culture method. Isolates produced floccose and cottony colonies with white mycelia and dark violet pigmentation on the lower surface of the PDA plate. Microconidia were oval, generally, without septations, measuring 5 to 9.6 µm long and 1.8 to 3.7 µm wide. Macroconidia were not found on PDA. Conidiophores produced mono- or polyphialides and conidia were arranged in false heads on conidiophores, which is consistent with *Fusarium sacchari*

(Duan et al. 2019). For molecular identification, DNA was extracted from two representative isolate BTFSS1 and BTFSS6. The internal transcribed spacer (ITS) region, translation elongation factor 1-α (TEF-1α) gene, and RNA polymerase II (RPB2) genes were amplified using primers ITS1/ITS4, EF1α-F/EF1α-R, and 5F2/11aR, respectively. Obtained ITS sequences (GenBank accession nos. MT176492.1 and MT177209.1) showed 99.8% similarity with the sequences from *F. sacchari* strain olowEKT1 (MK072727.1). The sequence identity of TEF-1α (MW558264.1 and MW507839.1) was 99.36% with the sequence of *F. sacchari* strain FF031 (MK152501.1), and RPB2 (MW558265.1 and MW507840.1) was 99.42% with the sequence of *F. sacchari* strain FF001 (MK152508.1), respectively. The isolates BTFSS1 and BTFSS6 were identified as *F. sacchari* based on the sequence alignment of ITS, TEF-1α, and RPB2 and on molecular phylogenetic analyses by the maximum likelihood method. To confirm the pathogen as a causal agent of sugarcane wilt, pathogenicity tests were conducted by the plug method (Viswanathan et al. 2011). Ten plants (cv. BSRI Akh 42) were inoculated with 1×10^5 conidia ml⁻¹ conidial suspension of the isolate BTFSS1. A borehole (5-mm-diameter) was made on the third or fourth internode from the base of the sugarcane plant in which the conidial suspension was placed and the bore place was sealed with cane tissues. Control plants were inoculated with deionized distilled water. All canes were cut longitudinally to evaluate the symptoms at 15 and 30 days after inoculation. Inoculated stalks exhibited tissue discoloration similar to those observed in infected sugarcane fields, whereas the control remained nonsymptomatic. Pathogens were reisolated from the artificially inoculated cane and confirmed by morphological and molecular tests. Sugarcane is the second important cash crop and the only source of white sugar in Bangladesh (Rahman et al. 2016). This is the first confirmed report that *F. sacchari* is the causal pathogen of sugarcane wilt in Bangladesh.

References:

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[†]Indicates the corresponding author.
M. T. Islam; tofazzalislam@yahoo.com