Phytopathological note

FIRST REPORT OF *FUSARIUM FUJIKUROI* CAUSING SOFT ROT DISEASE OF DRAGON FRUIT IN BANGLADESH

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ABSTRACT

Karim, M. M., Rahman, M. Z., Islam, M. N., Kawser-E-Jahan, Rahman, M. M. E., Akhter, M. S., Faruk, M. I. and Rahman, M. M. 2022. First report of *Fusarium fujikuroi* causing soft rot disease of dragon fruit in Bangladesh. Bangladesh J. Plant Pathol. 38(1&2): 61-64.

A survey was carried out in dragon fruit orchards of Khagrachari hill district during the year 2016-17 to monitor and identify the diseases of dragon fruit and also for proper management of the diseases. The dragon fruits of the surveyed orchard were infected by soft rot disease and in some orchard it was up to10% of total dragon fruit plants. Morphological and molecular characterization, and pathogenicity test it was revealed that *Fusarium fujikuroi* was the causal agent of the soft rot disease of dragon fruit. The pathogen *Fusarium fujikuroi* causing soft rot disease of dragon fruit was seemed to be a new record in Bangladesh.

Key words: Soft rot, dragon fruit, *Fusarium fujikuroi*

The dragon fruit (*Selenicereus undatus)* cultivation is gaining popularity in Bangladesh due to its taste and high commercial value but cultivation is hampered due to the infection of different fungal diseases (Karim *et al*. 2019, Mahmud *et al*. 2020, Briste *et al*. 2022). Therefore, the survey was conducted to monitor and identify the diseases of dragon fruit and also to find out proper management of the diseases.

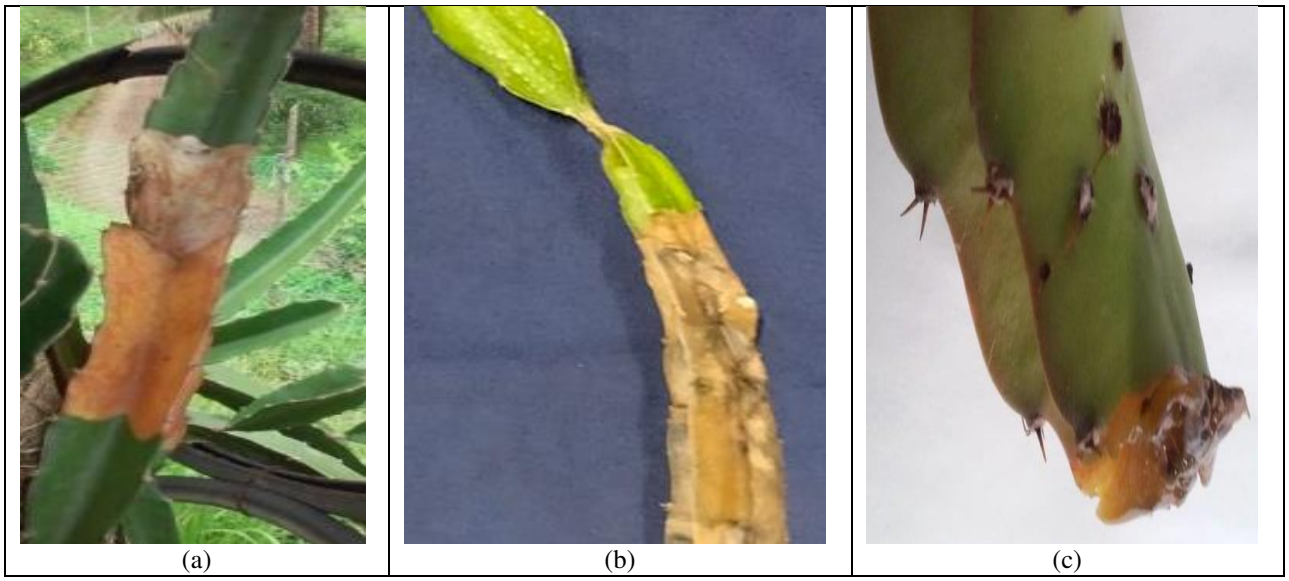
A survey was carried out in dragon fruit orchards of Khagrachari hill district during the year 2016-17. From this survey soft rot disease was identified from dragon fruit. In this study, 10 % of total plants were infected by soft rot disease (Fig. 1).

Infected plants parts of dragon fruit were collected and brought to the Plant Pathology Laboratory, BARI, Gazipur for identification and isolation of causal organisms. Pieces of the infected tissues were sterilized by 10% chlorox solution for 2-3 minutes, followed by several rinses with sterile distilled water, and placed on potato dextrose agar (PDA) in Petri plates at 25±1°C for 5 days. Three Fusarium isolates with identical morphology were selected and purified on fresh PDA plates using the hyphal tip culture method. After 7days of incubation the appearance of dense powdery aerial mycelia, and reproductive structures of fungi were examined under the compound microscope (BX 53 Olympus, Japan). The macroconidia were long, slender, almost straight, tapered apical cell, foot-shaped basal cell, 20.5–58.5 x 2.5–4.5 µm and 3–5 septa. The microconidia were club-shaped with a flattened base, 4.5–15.5 x 2.5–5.6 µm and without septation. The morphological features consistent with the description of *Fusarium fujikuroi* infecting red fleshed dragon fruit (Hawa *et al*. 2017).

Total genomic DNA of pathogenic fungi was extracted from mycelium using a commercial DNA isolation kit (Promega, USA). The rDNA was amplified and sequencing using specific primers (Internal Transcribed Spacer) *ITS*, ITS4 5' TCCTCCGCTTATTGATATGC-3'; ITS5 5'-GGAAGTAAAAGTCGTAACAAGG-3' and Translation Elongation Factor 1 alpha (*tef1-α*) EF1 5'-ATGGGTAAGGAAGACAAGAC-3') and EF2 (5'-GGAAGTACCAGTGATCATGTT-3' (White *et. al.* 1990, O'Donnell *et al*. 1998). After sequencing of *ITS* and *tef1-α* were assembled using Cap3, homology was evaluated with NCBI BLAST tool for comparison and identification of the isolates and deposited to GeneBank with the accession number ITS (OQ518895; OQ518896 & OQ518897) and *tef1-α* (OQ511504; OQ511505 & OQ511506). Moreover, the ITS and *TEF1* multi-locus phylogenetic analysis using maximum likelihood method with the MEGA 11 software confirmed that the isolates clustered with the *F. fujikuroi* clade (Fig. 2).

Pathogenicity test was conducted on symptomless, detached stem of dragon fruit according to Akhter *et al*. (2009). Mycelial plugs (6mm) taken from the margins of actively growing PDA colonies were placed on the dragon fruit stem which were previously wounded by sterile needle and kept the inoculated stem on the porcelain plate of the dedicator and sterile PDA plugs were used as controls. Three stems were inoculated by one identical isolate (FfDra1) and three stem were kept as a control. After two weeks of incubation at 25± 2°C with 90% relative humidity in 12h light/12h dark conditions, all inoculated stems showed stem rot symptom identical to the field symptom (Fig.1c). On the other hand, no such symptom was developed on the un-inoculated stem. The fungus was re-isolated from the symptomatic tissues and confirmed the pathogenicity of the isolated fungi.

Based on the morphological and molecular study and also pathogenecity test, the isolates were confirmed as *Fusarium fujikuroi* causing soft rot diseases of dragon fruit. The fungus *Fusarium fujikuroi* was seemed to be a new record for causing soft rot disease of dragon fruit in Bangladesh.



(a) (b) (c)

Figure 1. The soft rot disease symptom of dragon fruit observed in the field (a-b). Dragon fruit stem showing soft rot symptom after two weeks of incubation (c)

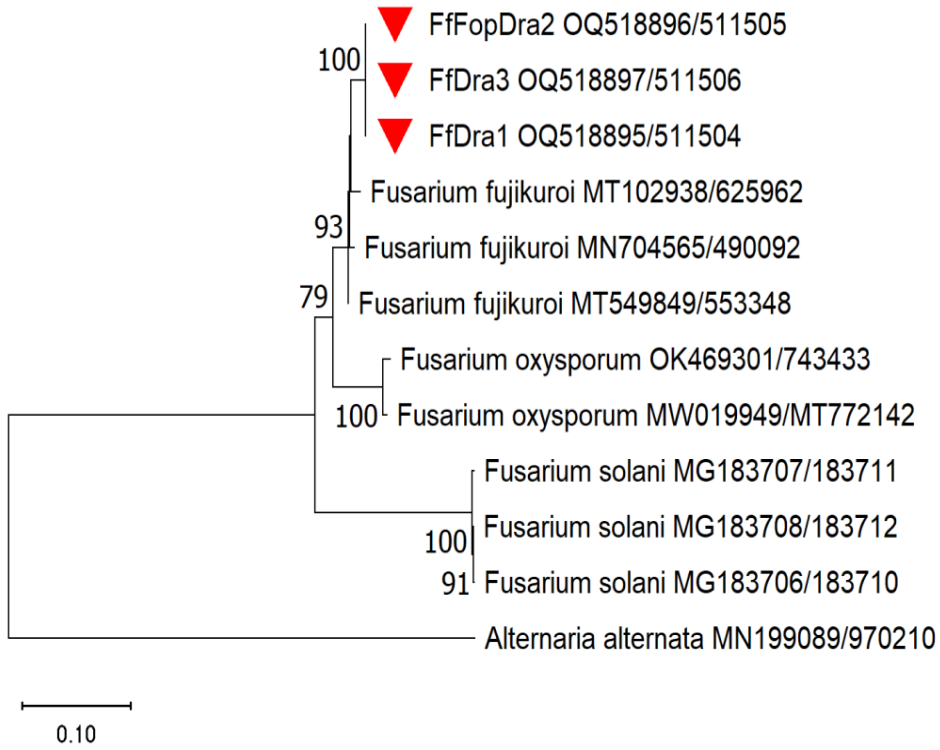


Figure 2. Phylogenetic tree constructed from concatenated rDNA-ITS/Tef1 alpha sequences. Reference nucleotide sequences of rDNA-ITS/Tef1 alpha of related Fusarium species are retrieved from NCBI

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