Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Basal Rot of Dragon Fruit Caused by *Fusarium oxysporum* in Bangladesh

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Dragon fruit (*Hylocereus polyrhizus*) is a high-value newly introduced fruit crop in Bangladesh. It has drawn considerable public attention due to its appealing flesh color, sweet taste, and fruit qualities. Recently, basal rot of dragon fruit plants was observed in several farmer's fields, nurseries, and the research field of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), and about 10 to 15% of plants were infected in each location. Initially, the symptoms appeared in the basal part near the soil as brown lesions, which gradually extended to the upper stem and finally became soft and watery. Infected plants were collected from Kapasia of Gazipur district (latitude 24.266, longitude 90.633) to isolate the causal organism. Isolations were carried out following the procedure reported by Briste et al. (2019). Briefly, infected plant parts were surface sterilized in 2% NaOCl for 1 min followed by 70% ethanol for 5 min and rinsed three times with sterile double distilled water. A large piece of a surface-sterilized plant was cut into small pieces (2 × 2 mm) from the margin of the necrotic lesion and placed on half-strength potato dextrose agar (PDA) and incubated for 7 days at 25°C. The BTFD1 and BTFD4 isolates were purified from single spores, resulting in white colonies with a growth rate of 1 cm/day on PDA. Colonies produced single-celled microconidia from unbranched, short monophialidic conidiophores and septate macroconidia as well as chlamydospores in PDA, which is consistent with *Fusarium oxysporum*. To confirm the identity of the isolates, the internal transcribed spacer (ITS1, 5.8S rRNA, and ITS2) and translation elongation factor-1

alpha (EF-1α) were amplified using primers ITS-1/ITS-4 and EF1-728F/EF1-986R, respectively (Surovy et al. 2019). The ITS sequences of the isolates BTFD1 and BTFD4 (GenBank accession nos. MN727096 and MN727095, respectively) showed 100% similarity with the sequence from *F. oxysporum* strain JJF2 (MN626452). Sequence identity for EF-1α (GenBank accession nos. MN752123 and MN752124, respectively) was 100% with the sequence from *F. oxysporum* strain CAV041_EO (MK783088). The isolates (BTFD1 and BTFD4) were identified as *F. oxysporum* based on the aligned sequences of ITS and EF-1α and on molecular phylogenetic analyses by maximum likelihood tree and maximum parsimony tree methods. The isolates were stored at 4°C on dried filter paper as well as in an ultra-low temperature freezer (−80°C) at Institute of Biotechnology and Genetic Engineering, BSMRAU, Bangladesh, and are available on request. To ensure pathogenicity, isolate BTFD1 was grown on PDA and incubated at 25°C for 7 days, and 250 ml of conidial suspension (with 1 × 10⁵ conidia/ml) was prepared. Twelve 3-month-old healthy dragon fruit plants were inoculated. Pathogenicity tests were carried out in two sets using three replications in each set. In one set, only the basal part of the plants was dipped into the conidial suspension, and in another set the whole plant was dipped into the conidial suspension for 2 h. Sterile distilled water was also used in another set of plants as a control. The inoculated plants were placed on wet tissue in a plastic box (31 × 24 × 8 cm), covered, and incubated at 25°C. After 10 days, all inoculated plants in both sets developed rot symptoms similar to those observed in the field, whereas the control plants remained healthy. The pathogen was successfully reisolated from the inoculated symptomatic parts on half-strength PDA medium and had morphology as characterized before, thus fulfilling Koch's postulates. This disease has been reported in Argentina and Malaysia (Hafifi et al. 2019; Wright et al. 2007). To the best of our knowledge, this is the first report of *Fusarium* basal rot of dragon fruit in Bangladesh caused by *F. oxysporum*.

References:

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