NEW REPORT

First report of *Choanephora infundibulifera* causing blossom blight of teasle gourd in India

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ABSTRACT: *Momordica subangulata* Blume subsp. *renigera* (G. Don) de Wilde is an important vegetable in India. In June 2015, blossom blight symptoms of *Momordica subangulata* subsp. *renigera* was first time noticed in the experimental plot of Directorate of Research, Bidhan Chandra Krishi Vishwavidyalaya, Kalyani, West Bengal, India. The disease severity ranged from 10-30% and the disease infection was also recorded from several other districts of West Bengal, India. The disease is caused by zygomycetous fungi, *Choanephora infundibulifera* (Currey) sacc. is the main causal organism of blossom blight disease. The temperature 28-30°C with high humidity (70-90%) prevalent during the rainy season (June-November) favoured the disease development. This is the first report of blossom blight of *Momordica subangulata* subsp. *renigera* caused by *Choanephora infundibulifera*.

Keywords: *Choanephora infundibulifera*, ITS, *Momordica subangulata*, monosporous, sporangiola

Momordica subangulata Blume subsp. *renigera* (G. Don) de Wilde (family-Cucurbitaceae) is the perennial vegetable with high food value and medicinal importance. It is native of Asia with extensive distribution in all the states of India. During June-November 2015, blossom blight of *Momordica subangulata* subsp. *renigera* was first time noticed in the experimental plot of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, West Bengal, India (Fig. 1). The disease severity ranged from 10-30% in the farm area. Symptoms appeared as black pin head like emerging sporangiola, formed a cushiony mat on blossom.

The peak disease infection was recorded from the month of June to September in 2015. Previously it was known that plant pathogenic zygomycetes are weak parasites (Agrios, 2005), but some zygomycetous fungi evolved their behavior in such a way that their complex adaptability prefers new host range as a substitution of their trend line. The genus *Choanephora*, a member of Zygomycetes is known to attack withering floral parts of many plants after fertilization and invades the fruits, causing a soft rot of primarily summer squash or pumpkin, pepper and okra (Agrios, 2005). Isolation of the pathogen was done from the infected plant part or

Fig. 1. Blossom blight of *Momordica subangulata* subsp. *renigera* with emerging sporangiola (A) Initial stage (B) Mature stage

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Fig. 2. (a) *Choanephora infundibulifera* culture on PDA, (b) Single sporangia

Fig. 3. The sequence generated on the present study showed a maximum likelihood search in RAxML with an alignment of the 16S rDNA region using MEGA version 6

singly emerging sporangia on PDA medium and maintained at $28 \pm 2^\circ\text{C}$. The pathogen preferred monsoon or rainy season with high moisture (70-90%). Creamish white colored culture shows yellow pigmentation at maturity due to β -carotene synthesis. Pathogenicity test of the isolate M.D-9 was confirmed by cross-inoculation of seven different isolates by single mycelial disc inoculation technique. Among three different isolates, host specific isolates M.D-2 and M.D-9 showed virulence.

To fulfill Koch's postulates and confirm its pathogenicity, detached leaf assay was performed in

respect of three isolates - M.D-9, Cow-6 and Br-2. Host specific isolate M.D-9, gave the highest virulence with sporulation and proved pathogenic.

Morphological studies revealed that sporangia were sub-globose in shape and $40.2\text{-}118.5\ \mu\text{m}$ in size. There are two types of sporangia i.e., monosporous and multisporous sporangia. Monosporous sporangia were elliptic, fusiform, or ovoid in shape, pediculate, striate, and $8.5\text{-}24.5 \times 6.5\text{-}13.5\ \mu\text{m}$ in size (Fig. 2). Sporangiospores were elliptic, fusiform or ovoid ($6.5\text{-}11.5 \times 10\text{-}30\ \mu\text{m}$), brown, with or without three or more thin appendages at both ends.

Based on morphological characterization the fungus was identified as *Choanephora infundibulifera*. The herbarium specimen of infected plant and culture of the isolate M.D-9 was deposited in HCIO (Herbarium Cryptogamae Indiae Orientalis, HCIO No. 52020) and ITCC (Indian Type Culture Collection, ITCC No. 7904) at ICAR-Indian Agricultural Research Institute, New Delhi, India.

For molecular characterization, genomic DNA was extracted from fungal mycelium of M.D-9 isolate using CTAB DNA extraction method (Wu *et al.*, 2001). Internal transcribed spacers (ITS) of the ribosomal DNA of M.D-9 isolate was amplified by using the primer pair, ITS-1 and ITS-4 (White *et al.*, 1990). The resulting sequence of 622 bp DNA was deposited in Genbank and assigned with the accession number KU745738. Homology searching with BLAST tool of NCBI-Gen bank fungal database (of ITS-r DNA region), exactly matches with publicly available *Choanephora infundibulifera* sequence. Results showed that the KT828740 (India) and JN 943007 (India) remains in the same cluster and nearest. The phylogenetic analysis was done by using MEGA version 6 (Fig. 3).

C. infundibulifera is a dioecious mucoraceous fungus. Previously *Choanephora* was considered as a weak pathogen or saprophyte, but day by day its improved infectious behavior, as well as increased host range (including different plant families), turned out to be a major pathogen in the domain of West Bengal's present agro-climatic situation. Although it has been previously reported on different crops to cause pod rot of *Vigna sinensis* (Kwon *et al.*, 2001b), blossom blight of

Petunia (Kwon *et al.*, 2001a), flower rot of *Hibiscus mutabilis* (Kwon and Park, 2002). Based on literature this is the first report of blossom blight of *Momordica subangulata* subsp. *renigera*.

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