Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Collar and Stem Rot Caused by *Rhizoctonia solani* AG-1-IA on *Sesbania sesban* in India

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Sesbania sesban (L.) Merr. (family Fabaceae), commonly called “dhaincha” in India, is used as a cover crop, as green manure, in the paper industry, and as animal fodder. The leaves contain high amounts of pinitol, which is an antidiabetic agent (Misra and Siddiqi 2004). During July and August from 2017 to 2019, *Sesbania* plants exhibiting typical *Rhizoctonia*-like symptoms including collar rot, wilting, and necrotic lesions on stems were regularly observed at ICAR-Central Potato Research Institute Regional Station, Meerut, Uttar Pradesh. Disease incidence ranged between 5 and 10% in a *Sesbania* crop being grown on 25 ha in *Sesbania*–potato rotation. Ten diseased plants were collected from different fields and brought to the laboratory. Affected stem pieces (~5 mm) were surface sterilized with 2% NaOCl, washed twice in sterilized water, and air dried. Four diseased pieces per plate were inoculated on 2% water agar amended with 2% streptomycin sulfate and incubated at 28 ± 1°C in the dark. All four affected pieces began to produce *Rhizoctonia*-like colonies after 48 h of incubation, and eight isolates were purified and stored at 4°C for further use. The colonies of eight isolates were evaluated, and all were whitish during early growth and became light brown after 72 h. Dark-brown sclerotia appeared in a random pattern on PDA after 120 h. Microscopic observations showed that all isolates had hyphal branching at right angles with slight constriction at the base of the branch, presence of dolipore septum near the branching, and multinucleate individual hyphae compartments (Sneh et al. 1991). Based on morphological characteristics, it was identified as *Rhizoctonia solani*. All isolates were further characterized to determine anastomosis group (AG) by pairing with a known AG tester of *R. solani* AG-1-IA (ITCC 7650), AG-1-IB (ITCC 5650), and AG-3 (RS-20) procured from the Indian Type Culture Collection, Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, and ICAR-Central Potato Research Institute,

Shimla, Himachal Pradesh, India, respectively. All eight isolates showed positive anastomosis with a known AG-1-IA tester isolate; no anastomosis was observed with other known tester isolates (Carling 1996). A single ~265-bp amplicon was amplified with a primer specific to *R. solani* AG-1-IA group, confirming the AG-specific identity of the isolates (Matsumoto 2002). Amplification was not observed with AG-1-IB, AG-3, and AG-2 specific primers (Khodayari et al. 2009). The four selected isolates were molecularly characterized by amplifying the ITS and rDNA 5.8s regions by PCR using ITS1 and ITS4 primer pairs (White et al. 1990). BLASTn analysis of the four resulting sequences (GenBank MT105386, MT105387, MT105388, and MT105389) supported the identification of the isolates as AG-1-IA subgroup and showed 95.12, 98.93, 96.79, and 98.04%, respectively, sequence homology with known cultures of *R. solani* AG-1-IA isolated from rice in China (KC285893) and India (MK481078). To confirm pathogenicity, *Sesbania* plants were grown in pots and maintained in the greenhouse at 25°C with a 12-h-light/dark photoperiod. After 35 to 40 days of growth, the stems of 10 *Sesbania* plants were artificially inoculated with PDA plugs containing *R. solani* mycelia (Jia et al. 2007) and covered with aluminum foil. Plants inoculated with noncolonized agar plugs served as a control. After 96 h of incubation, all the plants inoculated presented typical collar and stem rot symptoms. No symptoms were observed in the control plants. *R. solani* was reisolated 100% from these 10 infected plants, fulfilling Koch’s postulates. *R. solani* AG-1-IA has been reported to cause sheath blight and banded leaf and sheath blight diseases of rice and maize, respectively (Ogoshi 1987). This is the first report of *S. sesban* infected by *R. solani* AG-1-IA and serving as a host for the pathogen. The result from our findings will be helpful for planning of crop rotations in an agro-ecosystem.

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