



Agro-ecological variations of sheath rot disease of rice caused by *Sarocladium oryzae* and DNA fingerprinting of the pathogen's population structure

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ABSTRACT. To examine the impact of regional and seasonal variations on the incidence and severity of sheath rot, a major seed-borne disease of rice caused by *Sarocladium oryzae*, data on incidence and severity were collected from 27 selected fields in the Gazipur, Rangpur, Bogra, Chittagong, Comilla, Gopalganj, Jessore, Manikgonj, and Bhola districts of Bangladesh in rain-fed and irrigated conditions. Cultural variability of 29 pathogen isolates obtained from 8 different locations was studied on potato dextrose agar (PDA) and genetic variability was determined by DNA fingerprinting using variable number tandem repeat-polymerase chain reaction markers. Overall, disease incidence and severity were higher in irrigated rice. Disease incidence and severity were highest in the Bhola district in rain-fed rice and lowest in irrigated rice. Mycelial growth of 29 representative isolates was found to vary on PDA and the isolates were

divided into 6 groups. The range of the overall size of conidia of the selected isolates was 2.40-7.20 x 1.20-2.40 μm . Analysis of the DNA fingerprint types of the 29 isolates of *S. oryzae*, obtained from the amplification reactions, revealed 10 fingerprinting types (FPTs) that were 80% similar. FPT-1 was the largest group and included 13 isolates (44.8%), while FPT-2 was the third largest group and included 3 isolates. Each of FPT-3, 4, 5, and 6 included only 1 isolate. We observed no relationship between cultural and genetic groupings.

Key words: Incidence; Lineage group; Molecular markers; Rice; Sheath rot disease