GENETIC DIVERSITY OF THE RICE SHEATH BLIGHT PATHOGEN POPULATION IN INDIA

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Rhizoctonia sheath diseases of rice, comprising sheath blight, sheath spot and aggregate sheath spot, cause significant yield losses in many rice-growing regions of the world. The emergence of Rhizoctonia sheath diseases as economically important rice diseases is of recent date and has been attributed to the intensification of rice-cropping systems with the development of new short-stature, high-tillering, high-yielding varieties, high plant densities, and an increase in nitrogen fertilization. These factors promote disease spread by providing a favorable microclimate for *Rhizoctonia* spp., due to a denser leaf canopy with an increased leaf-to-leaf and leaf-to-sheath contact.

Rice sheath blight, one of the most serious fungal diseases of rice, is caused by multinucleate *Rhizoctonia solani* Kühn (teleomorph *Thanatephorus cucumeris* (A.B. Frank) Donk), an ubiquitous pathogen. Fourteen anastomosis groups (AGs) have been described in *R. solani* to date. Several anastomosis groups are further subdivided into intraspecific groups (ISGs). Isolates of AG1 have been divided into 3 ISGs including IA, IB and IC based on host origin, symptoms, and cultural characteristics. Isolates of AG1-IA have been associated with the development of rice sheath blight. Sheath spot and aggregate sheath spot are caused by multinucleate *R. oryzae* Ryker & Gooch (teleomorph *Waitea circinata* Warcup & Talbot) and binucleate *R. oryzae-sativae* (Swada) Mordue *(*teleomorph C*eratobasidium oryzae-sativae* Gunnell & Webster), respectively. Both pathogens produce lesions on the leaf sheath very similar to those of sheath blight, and are known to occur in California, Argentina and Asia. In addition to the similarity of disease symptoms, distinguishing the various *Rhizoctonia* species in culture is difficult due to the lack of stable morphological characters on which to base a definitive classification of the genus *Rhizoctonia* and species assigned to it. Also, identification of the intraspecific groups of AG1 based on anastomosis grouping on a slide is not accurate because isolates of AG1-IA fuse well not only with other isolates of IA, but also with isolates of IB and IC. Isolates of *Rhizoctonia* spp. were obtained from rice leaves and leaf sheaths with sheath blight symptoms that had been collected from various rice cultivars in different geographic regions of India during 2000-2003. Characterization by conventional techniques and polymerase chain reaction (PCR) using species-specific primers showed that from 110 isolates, 99 were *R. solani* and 11 were *R. oryzae- sativae*. In restriction fragment length polymorphism analysis of PCR-amplified ribosomal DNA internal transcribed spacer region of *R. solani* isolates, no polymorphism was observed among 96 isolates belonged to anastomosis group (AG) 1-IA but they were differentiated from AG1-IB and AG1-IC isolates using two discriminant restriction enzymes (*Mse*I and *Mun*I).