

## GENETIC DIVERSITY OF *RHIZOCTONIA SPP.* ASSOCIATED WITH SHEATH DISEASES OF RICE IN INDIA

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The *Rhizoctonia* sheath disease complex, comprising *R. solani*, *R. oryzae* and *R. oryzae-sativae* (telemorphs are *Thanatephorus cucumeris*, *Waitea circinata* and *Ceratobasidium oryzae-sativae* respectively) cause significant yield losses in rice. *R. solani*, a ubiquitous pathogen, incites rice sheath blight is one of the two most serious fungal diseases of rice world-wide. Among 14 anastomosis groups (AGs) that have been described in *R. solani* to date, isolates of AG 1- IA have been mostly associated with the rice sheath blight pathogen. *R. oryzae* and *R. oryzae-sativae*, causal agents of sheath spot and aggregate sheath spot respectively, both produce lesions on the leaf sheath very similar to those of sheath blight. As a consequence, the diagnosis of these diseases by visual observation is extremely difficult and often inaccurate. Accuracy in distinguishing these pathogens is also essential to ensure the success of the extensive breeding programmes and to develop rice varieties with resistance to sheath diseases. As well as the similarity of disease symptoms, distinguishing the 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. Therefore, the aim of this study was to identify genetic variation among the *Rhizoctonia* species responsible for sheath disease and to determine clonality in these populations. In this study, the genetic diversity of field populations of *R. solani* and *R. oryzae-sativae* in 4 states of India was examined using somatic compatibility and amplified fragment length polymorphism (AFLP) criteria. A sample of 110 isolates of *Rhizoctonia* from rice were used in AFLP analysis and somatic compatibility grouping (SCG) was done for 60 isolates including 55 *R. solani* AG 1- IA isolates and 5 *R. oryzae-sativae* isolates with pairing these isolates in all possible combinations on PDA plus activated charcoal and examined for their resulting somatic interactions. Seven distinct somatic compatibility groups were identified in the AG 1- IA samples and only one SCG was found among *R. oryzae-sativae* isolates. AFLP results showed that *R. solani* AG 1-IA isolates are clearly separated from another group of multinucleate *Rhizoctonia* and from *R. oryzae-sativae* isolates. Also, AFLP analysis indicated that each of the 5 *R. oryzae-sativae* isolates had a distinct AFLP phenotype, whereas 39 AFLP phenotypes were found among the 55 isolates of *R. solani* AG 1- IA. Non of the *R. oryzae-sativae* isolates were somatically compatible or shared a common AFLP phenotype with any AG1- IA isolate. Clones (cases where two or more isolates were somatically compatible and shared the same AFLP phenotype) were identified only in the AG 1- IA population. Five clones represented 28% of the AG 1- IA population. All seven SCG of AG 1- IA isolates were associated with more than one AFLP phenotype. The ability to survey a large number of loci with AFLP analysis