SUMMARY & CONCLUSIONS

Rice is the principal food crop of India. The grain yield in this crop is severely affected due to various abiotic and biotic stress conditions. Among fungal pathogens that afflict rice crop, rice sheath blight fungus (*R. solani*) is considered as one of the major production constraints for rice in South East Asia where one third of the world’s population live and depend on rice as major staple food. The introduction of **IR-type semi-dwarfs** and the advancement of production technology particularly adoption of intensive cultural practices have led to the failure of the crop against sheathblight (ShB) disease.

Rice sheathblight fungus, *R. solani* has a wide host range and is highly variable in pathogenicity. In the absence of suitable morphological and physiological characteristics, the identification of the isolates of *R. solani* has proved very difficult impeding breeding efforts and deployment strategies for resistance. Traditionally the isolates have been grouped into anastomosis groups (AG) and intra specific groups (ISG). Although the anastomosis grouping concept correlates to some extent with pathogenicity, evidence from several studies suggests that there is considerable variation among the isolates from the same AG and the pathogenicity cannot be explained solely in terms of AG. The major objective of the present study was to characterize pathogenic variability in rice sheathblight fungus *R. solani* using proteins, isozyme polymorphism and **RAPD-PCR** profiles and an attempt was made to assess the genetic diversity existing in ShB fungus. Towards characterization of variability, 18 isolates of ShB fungus were collected from different rice growing regions of India. The results emanating from the present study are *summarised* as follows.

1. The virulence spectrum of all 18 isolates was examined on susceptible IR 50 and tolerant Swarnadhan, based on which the isolates could be grouped broadly as *avirulent*, moderately virulent and *virulent*. The highly significant values of the pathogenicity parameters studied, coupled with highly significant Spearman rank correlation coefficients showed that the variation of the isolates was not a chance phenomena, but inherent property of the isolates.
2. Simple correlation studies between the morphological characters and pathogenicity parameters indicate a positive correlation between sclerotial size and pathogenicity.

3. The variation in the total soluble protein banding patterns was very high and the banding patterns could not be used to differentiate the isolates.

4. Twelve, out of thirteen isozymes studied across the fungal isolates showed a total of 153 electrophoretic phenotypes. Isozyme polymorphs of acid phosphatase, glutamate dehydrogenase and leucine aminopeptidase were associated with virulence, whereas, a polymorph of the isozyme peroxidase was associated with avirulence.

5. The isozymes, 6-phosphogluconic dehydrogenase and esterases produced unique zymograms for each of the 18 isolates, thereby indicating suitability of these isozymes for protein based fingerprinting of the Indian rice sheath blight fungal isolates.

6. When the utility of isozyme polymorphism was critically examined, one isolate RS 319 with unknown level of virulence was identified as a virulent isolate with the isozymes acid phosphatase and leucine aminopeptidase. Using the polymorphisms of esterases, the isolate was identified as the isolate from Titabar, Assam.

7. Studies based on RAPDs generated by using random decamer primers depicted DNA polymorphs ranging from 0.34-1.64 kb range. All the nine random primers produced polymorphism indicating high level of genomic variability within the isolates studied. Only 3% of the total amplified fragments were shared by all the isolates tested.

8. Some bands were unique for the virulent isolates, whereas some others were specific for avirulent isolates. With the help of amplification of OPA10 primer, an isolate with unknown level of virulence was identified as the virulent isolate, which was later confirmed by standard glass housing screening.

9. RAPDs generated by the primers OPC01 and OPQ01 showed distinct profiles for each of the 18 fungal isolates, thereby providing DNA fingerprinting patterns for the isolates of ShB fungus.

10. Within these 18 fungal isolates, the similarity coefficients were all higher than 40%.
11. Dendrograms generated using the combined similarity coefficients across the primers afforded distinct grouping of the avirulent isolates from the virulent isolates at similarity level of about 50%. Similar results were obtained when similarity coefficients from the isozyme and RAPD studies were pooled.

12. The clustering of 18 fungal isolates resulted in a major cluster, which included all sixteen virulent isolates and a minor cluster which included two avirulent isolates.

In the present study, an attempt was made to study diversity in the collected sheathblight fungal isolates using morphological and pathogenic variability, isozyme and DNA polymorphisms. The study indicated existence of variation among isolates of *R. solani*, which could be suitably used to find stable sources of resistance among cultivated rice and also moderately resistant varieties to ShB of rice. Though, the fungal isolates studied were representative of all important rice growing regions of India, numerical increase of isolates for identification and characterization is important for understanding ISG and AG which in turn will give better appraisal of genetic diversity and distribution of pathogen.