INTRODUCTION

Rice ( *Oryza sativa*) is the principal food crop on which two-thirds of the world’s population subsists wholly or partially. Human consumption accounts for 85% of the total production of rice, compared with 60% for wheat and 25% for maize (IRR1, Rice Almanac, 1993). Rice crop is grown under an extremely wide range of climatic conditions. Notwithstanding the high yielding cultivars generated that made several developing countries self-sufficient in food production, sustainable rice production is often seriously threatened by combination of stresses, both abiotic (such as drought, floods, low and high temperatures) and biotic (such as insects, pests, diseases and weeds). Rice crop is affected by several diseases like blast, sheath blight, bacterial blight and tungro which cause great damage to the crop.

Sheath blight disease (ShB) of rice, caused by the basidiomycetous fungus *Rhizoctonia solani* Kuhn has acquired alarming proportions both in temperate and tropical rice growing areas. This disease is aggravated since the introduction of high yielding varieties in 1960’s, as the high tillering capacity of improved cultivars, the greater density of plants, higher rates of Nitrogen fertiliser application and systems of minimal cultivation have resulted in greater incidence (Lee and Rush, 1983; Ou, 1985). The disease is considered second in importance after blast. Various estimates of crop losses due to sheath blight have been made. They usually vary from negligible to 50% (Lee and Rush, 1983).

Current control of ShB in rice depends upon chemicals, cultural management and use of so-called tolerant cultivars, all of which may be used in an integrated manner. Use of chemicals for control of this disease is hindered by high cost or potential damage to the environment. Cultural methods are not an ideal solution to the ShB control in rice as the measures such as crop rotation involve hidden losses that are unacceptable to specialist growers or those with few alternative crops. The use of resistant cultivars has been one of the most effective and economic means of combating several diseases in rice. But so far no commercially acceptable level of resistance to ShB pathogen has been found in rice germplasm. Though the knowledge of existing relative resistance in the available
Introduction

rice germ plasm help in the efforts of breeding for resistance, a more appropriate approach for genetic enhancement of resistance to this disease is to engineer the resistance genetically, for which basic information on variability in sheath blight fungus is very important.

Isolates of *Rhizoctonia solani* show tremendous variation in characteristics such as morphology, pathogenicity and host specificity (Ogoshi, 1987). In spite of the economic importance of the fungus, very little is known about the genetic variation within the fungus. Information regarding the variability within the fungal population is important for better understanding of disease development and for prediction of future disease outbreak. The genetic variability of the pathogen complicates breeding for resistance and deploying available cultivars effectively. Knowledge of pathogen can contribute both to resistance breeding efforts and to the development of strategies for deployment of resistance. An improved understanding of pathogen population also facilitates researchers to determine which resistance gene or gene combinations will be most effective in protecting the crop from disease.

A method based on anastomosis group (AC) has been used for identification and classification of sheath blight isolates. Although AC concept correlates to some extent with pathogenicity, there is considerable reported variation among the isolates from the same AG (Vilgalys and Gonzalez, 1990). However, due to the lack of stable morphological or physiological markers in this fungus, there is no information by which this variation is generated. Lack of markers has also hindered the studies on the population dynamics and the epidemiology of the pathogen. Development of markers should be very useful for assessing the level of variation within the different groups and for identifying the mechanisms responsible for variation. Studies using markers like proteins, isozymes, RFLPs, RAPD-PCR etc., have revealed a hitherto unsuspected level of variation in a number of species of phytopathogenic fungi and the mechanisms of variation in those species (Michelmore and Hubert, 1987). Thus taking a holistic view based on the facts that (a) rice is the principal food crop in India (b) sheath blight is an important fungal disease that afflicts rice crop and (c) the knowledge of variability of the pathogen is essential for breeding/engineering resistance, present studies were undertaken with the following objectives.
i) to characterise pathogenic variability in rice sheath blight fungus *Rhizoctonia solani* at molecular level using proteins, isozyme polymorphism and RAPD-PCR profiles

ii) to understand the genetic relatedness among the different isolates of *ShB*.

and iii) to establish association, if any, of these variations with pathogenecity of rice sheath blight fungus.

The results of the experimental studies carried out towards these objectives and the conclusions drawn are presented in this thesis.