CONCLUSION
Chapter 6
Conclusion

This thesis report the characterization of *Maganporthe oryzae* population and the molecular identification of *Pi9* blast resistance gene along with diversity study for *Pi9* alleles. This research is of particular importance in studying the effectiveness of *Pi9* blast resistance gene against the blast pathogen in North-East and Eastern India. The major research outcomes have been:

(i) *Pi9* gene exhibited complementary resistance spectrum and excluded all the pathotypes of the pathogen that are required for strategic resistant gene deployment.

(ii) Combination of *Pi9* and its allelic genes *Piz, Piz5* with *Pi1, Pi7, Pi19* and *Pi12* can exclude all the virulence of the pathogen and is expected to provide broad spectrum resistance across North-East and Eastern region of India.

(iii) *Pi9* blast resistance gene is one of the most important and effective gene in different gene combinations.

(iv) The data on mating type distribution and lineage diversity indicated that sexual recombination might be the one reason for lineage diversity in *M. oryzae* in fields of large rice-growing regions in North-East and Eastern states of India.

(v) Demonstrated that the *Avr* genes identification in the *M. oryzae* population and its corresponding *R* genes in the monogenic lines do not necessarily lead to resistance. The high frequency of virulent strains harbouring several *Avr* genes, suggest that there might be additional mechanisms in the pathogen to overcome host gene surveillance

(vi) Verification of the presence of *Pi9* blast resistance gene in the rice germplasm collected from North-East and Eastern India using gene based STS marker and also the validation of marker. The germplasm accessions identified having *Pi9* gene would allow us to use them as donors for *Pi9* in future breeding programs.
(vii) The microarray expression profiling study reveals that the defense response in compatible and incompatible rice- \textit{M. oryzae} interaction was quantitative in nature, with distinct transcriptional regulation mechanisms in various functional categories. This study enhanced our understanding of the complex network of transcriptional regulation during rice early response to the blast fungus.

(viii) The resistant germplasm having \textit{Pi9} allele is different from the \textit{Pi9} allele of susceptible germplasm but the nucleotide polymorphism is very low, greater in the LRR region and might be one of the reason for susceptibility. Since, blast pathosystems follows gene-for-gene system, low level of polymorphism at the LRR region of the \textit{Pi9} alleles point towards the intermediate level of evolutionary forces has acted on the \textit{Pi9} locus during the co-evolution of blast fungus.