**Title: Elucidating the Molecular Diversity Pattern of Major Bacterial Blight R-Genes and Identification of Candidate Bacterial Blight Resistance Genes in Rice**

**Abstract:**

 In this thesis, we investigated the natural variation in genes which are involved in bacterial blight resistance. The aim of this study was to identify alternate source and form of resistance which will make elite susceptible rice varieties stand strongly against virulent *Xoo* strains. Phenotypic screening of 104 accessions including wild species, cultivars, landraces and introgression lines for resistance against five different *Xoo* strains DX011, DX127, DX020, DX015, and DX133 revealed that the wild accessions were highly resistant towards BB than the cultivated species. Through marker analysis two resistant forms of *xa5* alleles were identified from *O. sativa* cultivar which may be useful for developing BB resistant lines. Polymorphisms of four BB resistance *R* genes *Xa21, Xa26, Xa27* and *xa5* were determined as quantified by average pair wise difference across all sites denoted by ‘π’.

Along the entire gene sequence, it was commonly observed that intron and non-coding region exhibited higher diversity for entire four locus. The allelic diversity was higher in *O*. *nivara* than *O*. *sativa*. In natural habitat there are more chances of intermixing genetic components in wild species by out crossing which increases the intensity of allelic diversity. Transition bias >1 was observed in all the genes which suggest that transition pattern of substitution is favoured over transversion during the course of evolution. During *Xoo* infection in wild rise *O*. *nivara* 81832 and *O*. *longistaminata* OL 1, out of 13 genes analysed, only seven genes were differentially expressed. These genes were constitutively expressed in both resistant and susceptible plants. *OsBAKI*, *RPLD* isoforms, *EI10P8* and *EI1K8* were found to induce and may be targeted for developing BB resistant lines. The proteome analysis was performed only in *Xoo* infected and water infiltrated resistant wild rice and only the up-regulated proteins were identified. Some of the protein identified in this study might play important roles in plant disease resistance, although further studies are required to verifiy the detailed localization and regulation of these proteins.