Abstract

The global population is expected to exceed 10 billion by 2050, posing a significant challenge to the agriculture sector in fulfilling increased demands of food production. This necessitates the adoption of sustainable strategies to ensure global food security. Among staple food crops, *Oryza sativa* (rice) is a cornerstone of global food production, serving as a dietary staple for nearly half of the world's population. However, its productivity is severely constrained by biotic and abiotic stresses. Biotic stress includes pathogenic bacteria, fungi, and other organisms, while abiotic stresses such as drought, such as drought, and heat can result in yield losses of up to 90-100%. To mitigate these impacts, *O. sativa* possesses an intrinsic defense mechanism involving stress-responsive genes and proteins. Despite this, current interventions, including the use of pesticides and conventional breeding techniques, often provide only temporary relief. In response, the integration of computational tools with advanced breeding strategies has emerged as a promising avenue to enhance the resilience and productivity of *O. sativa* under stress conditions. This holistic approach has the potential to address the limitations of traditional methods and contribute to sustainable food production systems.

This thesis addresses the challenges posed by biotic and abiotic stresses in *O. sativa* by focusing on the identification, characterization, and analysis of stress-tolerant genes and proteins through computational approaches. The study has three primary objectives. First, it aims to identify novel disease-resistance proteins in *O. sativa Japonica* through *in silico* methods, targeting bacterial leaf blight (BB) and rice blast (RB) diseases, which are major biotic stressors affecting productivity of *O. sativa*. Second, it seeks to predict disease-resistance proteins in *O. sativa* and its related species by evaluating and comparing the performance of various deep learning (DL) and machine learning (ML) algorithms, thereby identifying the most effective computational frameworks for accurate protein prediction. Lastly, the research involves drought-responsive transcriptomic and genome-wide studies of *Prosopis cineraria*, a drought-resilient leguminous tree from the Indian Thar Desert, to uncover drought-tolerance genes that could potentially enhance drought resilience in *O. sativa*. Together, these objectives aim to contribute to sustainable strategies for improving the stress resilience of *O. sativa*.

In line with the objectives outlined above, five novel disease-resistance proteins were effective against BB and RB diseases in *O. sativa* were identified through a comprehensive *in silico* approach. These proteins were characterized using gene network construction, structural modeling, functional annotation, and phylogenetic analysis. The identified proteins exhibited key roles in disease-resistance mechanisms and showed evolutionary relationships with well-established resistance proteins. Furthermore, gene expression profiling revealed their differential expression under infections by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) and *Magnaporthe oryzae*, the causative agents of BB and RB diseases, respectively. These findings offer valuable insights for the development of disease-resistant varieties of *O. sativa*.

To extend the scope of disease-resistance protein identification in *O. sativa* and related species, various ML and DL models were employed. These models were rigorously trained, tested, evaluated, cross-validated, and compared for predictive performance. Among these, the DL-based Multi-Layer Perceptron model outperformed others, demonstrating precise prediction of disease-resistance proteins. The study thus provides computational frameworks and candidate proteins that can aid in breeding novel disease-resistant varieties of *O. sativa*.

In addition, drought-tolerance genes from *P. cineraria*, a resilient tree species from the Indian Thar Desert, were explored to identify robust orthologs that could enhance drought resilience in *O. sativa*. Transcriptomic analyses under drought, highlighted the APETALA2/Ethylene Responsive Factor (AP2/ERF) superfamily as key genes induced under drought, compelling us to conduct a genome-wide analysis of

this superfamily in *P. cineraria*. Comparative studies revealed significant copy number variations (CNVs) of *AP2/ERF* genes between drought-tolerant (DT) and drought-sensitive (DS) species, such as *O. sativa Japonica*, *Arabidopsis thaliana*, and *Pisum sativum*. Structural analyses of *P. cineraria* AP2/ERF proteins indicated stronger interactions between the DNA-binding AP2 domain of *P. cineraria* and the target *cis* element GCC box/dehydration-responsive element (DRE), as compared to orthologs from DS species. Additional investigations into amino acid variations and hydrogen bonding within AP2/ERF proteins among *O. sativa Japonica*, *O. sativa Indica*, and *P. cineraria* demonstrated substantial differences. Notably, DT *P. cineraria* AP2/ERFs contained polar amino acids at the variation positions and more hydrogen bonds compared to the orthologs from DS species *O. sativa* and *A. thaliana*, suggesting stronger DNA binding by AP2/ERF orthologs of DT species.

In conclusion, this thesis presents a comprehensive *in silico* investigation of stress-tolerant genes and proteins in *O. sativa*, providing breeders with novel genetic resources for developing stress-resilient varieties of *O. sativa*. Overall, these findings contribute to enhancing the productivity and resilience of *O. sativa*, thereby advancing global food security efforts.