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Thesis Abstract

Thesis title: Genetic dissection of terminal heat tolerance in wheat

The present study in wheat was undertaken to dissect the genetic basis of terminal heat stress tolerance. This study was planned with the following three major objectives involving GWAS, bioinformatics of AGPase gene and expression analysis of genes involved in starch biosynthesis under controlled and heat stress conditions.

For GWAS analysis, a set of 273 SWRS wheat genotypes was used along with 12,646 GBS SNP markers and phenotypic data on 11 traits was recorded at Meerut and Powerkheda under timely and late sown conditions. Total 21 MTAs were commonly identified in all the three methods under LS and 21 MTAs other MTAs were commonly identified under TS and LS. Genomic prediction (GP) estimated using rrBLUP ranged from moderate (>0.4) to low for all the traits at both the locations. In summary, the results of the GWAS and GP analysis improved our understanding about the genetics of thermotolerance in wheat and also provided information about the relative importance of different traits for evaluation of genotypes for heat tolerance. Important MTAs identified during the present study may be the targets for molecular breeding for heat tolerance leading to development of heat tolerant wheat cultivars. The candidate genes identified during the present study may also be used for development of gene-based markers after validation using qRT-PCR/overexpression studies; these may also be and for further molecular dissection of the genetics of heat tolerance in wheat.

In the second objective, the true orthologs of AGPasé genes along with its structural and functional evolution among monocots and dicots. Overall, the comparative study revealed the structural conservation of LS and SS of AGPase, although some variation was observed in the length, number and phases of introns; N-terminal regions were relatively more variable. Among the two domains (ADP_Glucose_PP and LbH_G1P_AT_C) in each of the LS and SS, the domain ADP_Glucose_PP (with many more ligand binding sites carrying a conserved "LGGG" motif) perhaps plays an important role in the regulation of the AGPase activity. Some specific features of the LS and SS also suggested a species-specific evolution among monocots and dicots. Promoter and expression analysis revealed endosperm to be the main site of expression among cereals and leaves in *Arabidopsis*. Expression analysis also suggested that the expression of the genes for AGPases is regulated in a temporal manner during abiotic stresses.

In the third objective, the results of the expression analysis matched with the expected changes in starch content for both the cultivars at 14 days after anthesis (DAA) where the reduction in starch content was largely attributed to the decline in the expression of starch biosynthesis genes. However, the results did not completely match at 21 DAA and 28 DAA. Therefore, future studies involving enzyme activities and detailed starch estimation (amylose, amylopectin, starch granules) will surely lead us to better insights. The results also clearly indicated a very complex genetic mechanism of heat stress tolerance in thermotolerant genotypes and hence further detailed investigations are needed to gain a better insight into the molecular basis of heat tolerance n wheat.

Overall, the results all the three objectives provide better insights in order to understand the genetics of heat tolerance in wheat.

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