In-sillico characterization of phosphoglucose isomerase (PGI) gene in *Triticum aestivum*

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Food security is a major concern in India; hence, it is necessary to devise strategies to enhance food grain production. Heat tolerance is a complex trait, with scant knowledge about its genetics, physiology and molecular biology. Activity assays for enzymes involved in grain starch synthesis can be one approach to address this trait. Phosphoglucose isomerase enzyme, also known as glucose-6-phosphate isomerase (GPI), has a major role in glucogenesis i.e. starch synthesis. It has also been reported that there is 50% reduction in starch synthesis with 50% reduction in PGI enzyme, which leads to reduction in grain size. Hence, characterization of the PGI gene is important to know in detail its role in starch synthesis. The protein sequence of PGI enzyme of wheat (*Triticum aestivum*) was downloaded from the protein database of NCBI, and analyzed to find the respective gene in *T. aestivum*. Three homologous gene copies of PGI were present on 1A, 1B and 1D chromosome of *Triticum aestivum*. The orthologous gene copies were also traced in grass family. Multiple Sequence Alignment tool was used for gene as well as protein sequences analysis in homologous as well as orthologous copies of PGI. To further study the gene sequence, gene structures (introns and exons) of homologous as well as orthologous PGI were constructed. Finally, to analyse the structure and function of the homologous and orthologous genes, 3D protein structure were predicted with the help of I-Tasser software which helped in understanding the mode of action of different PGI genes.

Mining for heat stress responsive genes by RNA-Seq based comprehensive gene expression analyses in chickpea (*Cicer arietinum* L.)

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Chickpea (*Cicer arietinum* L.), an important legume crop, is adversely affected by abiotic stresses such as heat, drought and salinity. Amongst these stresses, heat stress is the main abiotic stress that has an adverse impact on almost all aspects of plant development, growth, reproduction and yield. Development of genomic resources is a pre-requisite to develop heat-tolerant chickpea varieties. In this context, RNA-Seqbased transcriptome analysis was performed on vegetative (leaves and roots) and reproductive (leaves, roots and flowers) tissues of six contrasting heat responsive (tolerant - ICCV 92944, ICC 1356, ICC 15614 and sensitive - ICC 5912, ICC 4567, ICC 10685) genotypes. A total of ~514 million reads were generated and alignment of these reads against the available chickpea genome assembly resulted in mapping of 469 (92.9%) million reads. Furthermore, gene expression analysis resulted in identification of 7,670 significantly differentially expressed genes, including 874 novel genes between contrasting genotypes. A set of 56 stress responsive genes belonging to APETALA2/Ethylene Responsive Factor (AP2/ERF), Heat Shock Protein (HSP) and 90 families are selected for further validation using quantitative real time PCR. Moreover >22,456 single nucleotide polymorphisms (SNPs)/INDELs were identified between parental genotypes of two mapping populations (ICC15614 × ICC 4567 and ICC 1356 × ICC 4567). Novel differentially expressed genes along with the marker resources identified in this study should help breeders in developing heat tolerant chickpea varieties in efficient manner.