

Chaperone Regulator: Characterization the Role of Heat-Responsive Transcription Factor Gene in Augmenting the Expression of HSPs and Total Antioxidant Potential of Wheat under Heat Stress

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Abstract—Terminal heat stress is one of the major problems in wheat growth and yield. It causes disintegration of photosystem, denaturation of enzymes, defunct pollen, and pseudo seed setting problem in agriculturally important crops. The mechanism of thermotolerance has yet not been elucidated. Transcription factors are protein, which perform their role at transcriptional level by affecting the transcription process of SAGs. Here, we have identified 38 novel transcription factor genes from wheat cv. HD2985 using *de novo* assembly. Based on the digital fold expression, we cloned TaHD97 of ~1.1 kb from wheat cv. HD2985. The nucleotide sequence was submitted in NCBI GenBank with accession no. KP259293. CD search revealed the presence of HSF DNA binding domain in the sequence. Expression analysis of cloned TF showed significant variations in the expression in response to heat stress; relative expression was observed very high in HD2985, as compared to HD2329 cv. of wheat. Tissue specific expression profiling showed up-regulation of TaHD97 in leaves, as compared to stem, and endosperm, whereas downregulation was observed in root. Expression analysis of targets of TaHD97 showed very high relative expression of HSP17 and HSP90 under HS; abundance of transcripts was observed more in HD2985, as compared to HD2329. A positive correlation was established between the TaHD97 and their respective targets under HS. The cloned novel TF can be used as a suitable candidate gene for the breeding program or for manipulating the thermotolerance of wheat using genetic engineering tool in order to develop climate-smart wheat crop.

Keywords: TFs, Heat stress, Wheat, Chaperones, sHSPs, TAP, Thermotolerance.