

# Integrating Information from Genes and Genomics for Climate Resilient Crops

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Climate change and abiotic stress affects agriculture and crop production adversely. Wheat is a temperate crop and prone to various abiotic stresses therefore mapping and characterizing ESTs offers a manageable approach to understand the complex architecture and functioning of the wheat transcriptome. Tolerance to heat stress is a complex phenomenon and controlled by multiple genes, hence a program on functional genomics of heat stress has been initiated to understand the transcriptional profile of the sensitive and tolerant cultivars of wheat under heat stress by subtractive hybridization, both at the vegetative and reproductive stages. Heat tolerance related gene transcripts were identified based on their putative functions and validated by cDNA microarray and northern/RT-PCR analysis, with the aim to unravel the complexity associated with heat stress response in wheat. A common response to high temperature stress is the synthesis of Heat Shock Proteins (HSPs). HSP encoding genes are found to be under the control of Heat Shock Factors (HSF), transcription factors that regulate the expression of HSP genes. One such gene, a chloroplastic small heat shock protein (sHSP26) was found essential for tolerance to heat stress. Transgenic *Arabidopsis* plants over-expressing wheat HSP26 were more tolerant to high temperature induced damage to the photosynthetic machinery, and the antisense transgenic plants were found to be severely sensitive to heat stress. Similarly, a newly identified heat shock factor (HSF) possesses the characteristic domains of class A type plant HSFs and shows high similarity to rice OsHsfA2d. The transcription factor activity of TaHsfA2d was confirmed through transactivation assay in yeast. Transgenic *Arabidopsis* plants overexpressing TaHsfA2d not only possess higher tolerance towards high temperatures but also showed considerable tolerance to salinity stress. They also showed higher yield and biomass under constant heat stress conditions. Analysis of putative target genes through quantitative RT-PCR showed higher and constitutive expression of several abiotic stress responsive genes in transgenic *Arabidopsis* plants over-expressing TaHsfA2d. TaHsfA2d can also functionally complement the T-DNA insertion mutants of AtHsfA2, although partially. These observations suggest that TaHsfA2d may be useful in molecular breeding of crop plants, especially wheat, to improve yield under abiotic stress conditions.

The discovery of novel genes, determination of their expression pattern in response to abiotic stress and an improved understanding of their roles in stress adaptation (obtained by functional genomics) will provide the basis of effective engineering strategies leading to greater stress tolerance and management in agriculture. Thus with the advent of genomics, a new era of plant sciences is beginning which helps not only in gene discovery and functional analysis of novel genes, but also aid in mining efficient alleles for introgression in desired plants for crop improvement and generation of agriproduct diversification.