

Heat stress biology of rice plants

Anil Grover

Department of Plant Molecular Biology, University of Delhi South Campus, Benito Juarez Road, Dhaula Kuan, New Delhi-110021, India (email: anil.anilgrover@gmail.com)

Our work shows that the transcriptional profile of rice (*Oryza sativa* L.) is significantly modulated within 10 min of heat stress (HS₁₀): analysis of differentially expressed genes (DEGs) revealed that 1,556 genes were rapidly up-regulated (\geq twofold, $P < 0.05$) at HS₁₀ as compared to 600 down-regulated genes. The transcriptional profile shows that the response of rice to heat stress involves signal perception and transduction, activation/ synthesis of heat shock factors, genomic and proteomic alterations, ROS metabolism and a host of other proteins associated with biochemical, cellular and physiological processes and 'unknown' functions.

Genome-wide gene families of rice Hsp20, Hsp40, Hsp70 and Hsp100 as well as heat shock factors (Hsfs) were analysed. Rice ClpB/Hsp100 family proteins are constituted of three isoforms localized in three different cell compartments namely cytoplasm (ClpB-c), chloroplast (ClpB-p) and mitochondria (ClpB-m).

Our present focus is to analyse the role of ClpB/Hsp100 proteins in governing heat stress response in Arabidopsis and rice plants.