

IDT9-059 | Heat induced differential proteomic changes reveal molecular mechanisms responsible for heat tolerance in chickpea

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Understanding the molecular differences in plant genotypes contrasting for heat sensitivity can provide useful insights into the mechanisms that confer heat tolerance in plants. We focused on comparative physiological and proteomic analyses of heat sensitive (ICC16374) and tolerant (JG14) genotypes of chickpea (*Cicer arietinum* L.) when subjected to heat stress at anthesis. Heat stress reduced seed germination, leaf water content, chlorophyll content and membrane integrity with a greater impact on sensitive genotype than on the tolerant ones that had higher total antioxidant capacity and osmolyte accumulation, and consequently less oxidative damage. Comparative gel-free proteome profiles indicated differences in the expression levels and regulation of common proteins that are associated with heat tolerance in contrasting genotypes under heat stress. Several crucial heat induced and heat responsive

proteins were identified and categorized based on ontology and pathway analysis. The proteins which are essentially related to the electron transport chain in photosynthesis, amino acid biosynthesis, ribosome synthesis and secondary metabolite synthesis may play key roles in inducing heat tolerance. In addition, our study also provides evidence that the foliar application of nitric oxide (NO) donor can enhance heat and drought stress tolerance by modulating a number of proteins in chickpea. Understanding the active metabolic adjustments in tolerant genotype under stress and inducing the stress tolerance in sensitive genotype by exogenous NO application offers a comprehensive and systematic approach to tackle heat and drought stress in chickpea. This study potentially contributes to improved stress resilience by offering valuable insights on the mechanisms of heat and drought tolerance in chickpea.

IDT9-060 | Exploring the behavior of transporter proteins in response to abiotic stress through genomics and microarray analyses

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Plants respond to stress conditions through various physiological mechanisms like redistribution of nutrients to critical tissues, production of metabolites for free radical scavenging, and osmotic adjustments. Transporter proteins are the key components of such processes and their diversity contributes to the plant's ability to survive under stresses. The Major Facilitator Superfamily is one of the largest superfamilies of secondary active transporters that transport diverse molecules such as sugars, sugar-alcohols, vitamins, amino-acids, oligopeptides and nucleosides. We identified members of this superfamily in *Arabidopsis thaliana* and *Vitis vinifera* through protein homology search and domain annotation, and classified them into 21 families based on the type of substrate they potentially transport. Analyses of microarray data revealed that 52% of them were transcribed in six different tissues, suggesting their role in

cellular transport and distribution of metabolites across plant tissues. However, about 30% of these were differentially regulated under heat and salinity stress conditions; half of these comprised sugar porters and amino-acid transporters known for maintaining the osmotic balance and turgor pressure under water-stress. Surprisingly, we observed simultaneous up- and down-regulation of transporters of the same family in same tissue under same condition, suggesting contrasting effect of solutes of similar class of molecules, opposite transport directions of co-localized transporters or different behaviors of transporters in different cell types in a tissue. Further studies on these transporters with the combined implementation of transcriptomics and mutant studies could lead to better prediction of their roles in metabolic fluxes in a plant under abiotic stresses.