

## Exploring Stress Metabolism of Crops for Enhanced Food Security

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The society is facing three inter-connected challenges of food (crop) production, climate change and energy security. The world population is projected to be increased to approximately 9.0 billion by year 2050. Therefore, securing the food demand of the increased population by way of enough crop production with limited agricultural land would be the major challenge in front of humankind. Moreover, various kinds of stresses are posing additional threat to global crop production. Broadly these stresses can be divided in two categories, abiotic and biotic stress. Abiotic stress includes, drought, flooding, hypoxia/anoxia, heavy metals, metalloids, salinity, extreme temperature and excess light, radiation, etc., whereas, biotic stress is mainly caused by pathogen attack and herbivory. These stresses greatly diminish the crop yield by adversely affecting crop metabolism [1].

The severity of stresses on crop production has aroused a great deal of concern around the globe. Hence, understanding the stress metabolism of crops has become the major focus of plant biology research [1]. The toxic actions of various stresses occur through different stress specific processes, such as, alteration/deactivation of vital enzymatic activities, inhibition of nutrient uptake, disruption of structure and function of photosynthetic apparatus, osmotic disbalance, physiological drought, etc. Despite having stress-specific toxic actions, all kind of stresses lead to develop a condition called as oxidative stress, which occurs due to increased toxicities of reactive oxygen species. Generation of reactive oxygen species is a generalized phenomenon reported from almost all aerobic forms even during normal conditions. But stresses are known to increase the formation of reactive oxygen species in living cells. Therefore, plant cell needs to maintain a dynamic equilibrium between the formation and scavenging of reactive

oxygen species to cope up with oxidative damage. Characterization of oxidative metabolism is another important focus in crop related research. Substantial information has been accumulated on various aspects of oxidative stress in plants during stress conditions [2,3]. Stresses activate the accumulation of several molecules, especially, compatible solute in plant cells. Hyper-accumulation of proline, glycine betaine, mannitol, etc., have been reported as frequently observed phenomenon in plant cells exposed to various types of stresses. Compatible solutes, especially proline, are known to confer tolerance to plants against a variety of stresses either by maintaining osmotic balance and/or scavenging reactive oxygen species [4-6]. Our understanding about various types of stresses in crops has improved significantly during post-genome era. Availability of information about whole genome sequences of several plants including crops e. g. Rice, Maize, Chickpea has greatly supported to understand the stress-responsive genes/proteins. The combination of Omics technologies (genomics, proteomics, metabolomics) helped to discover stress-regulated transcripts and their regulatory elements [7]. Subsequent discovery of gene silencing has provided another effective tool to characterize the genetics of stress responses in crops. Despite significant progress on various aspects of stress-crop interaction, further research is required to completely understand the whole stress response system of plants by integration of our knowledge on. genomics, proteomics, and metabolomics.

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## Bibliography

1. Tripathi BN. "Stress metabolism of plants". *Protoplasma* 245 (2010): 1.
2. Bhatt I and Tripathi B N. "Plant Peroxiredoxins: Catalytic Mechanisms, Functional Significance and Future Perspectives". *Biotechnology Advances* 29 (2011): 850-859.
3. Hong SH., *et al.* "Functional switching of ascorbate peroxidase 2 of rice (OsAPX2) between peroxidase and molecular chaperone". *Scientific Reports* 8 (2018): 9171-9180.
4. Singh V., *et al.* "Proline improves copper tolerance of chickpea". *Protoplasma* 245 (2010): 173-181.
5. Tripathi BN., *et al.* "Mechanism of Cu and Cd-induced Proline Hyper-accumulation in *Triticum aestivum* (Wheat)". *Journal of Plant Growth Regulation* 32 (2013): 799-808.
6. Singh V., *et al.* "Interaction of Mg with heavy metal (Cu, Cd) in *T. aestivum* with special reference to oxidative and proline metabolism". *Journal of Plant Research* 129 (2015): 487-497.
7. Garg B., *et al.* "Transcript profiling identifies novel transcripts with unknown functions as primary response components to osmotic stress in wheat (*Triticum aestivum* L.)". *Plant Cell, Tissue and Organ Culture* 113 (2013): 91-101.

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