

Enhancing resilience to Climate Change in Rainfed Agriculture— Role of Imaging and Genomic Tools

Abiotic stresses such as drought, elevated temperatures and salinity – both individually, or more commonly, in combination are major constraints to crop productivity in rainfed agriculture. Along with these, the impending climate change catastrophes represent a serious threat for sustainable agriculture. These abiotic stresses cause numerous deleterious effects on plants which include reduced cellular osmotic potential, inhibition of cell division and expansion, reduced membrane integrity, and impaired cellular function and disruption of ion homeostasis.

Plant responses to abiotic stresses involve the multifaceted activation of a range of tolerance mechanisms. A number of adaptive traits have been identified with tolerance to water limited environments such as matching the phenology to the available water supply, early vigor, osmotic adjustment, transpiration efficiency, grain growth, leaf area retention etc. Different

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physiological mechanisms contributing to heat tolerance in the field are higher membrane thermo stability, stay green, and heat avoidance as indicated by canopy temperature depression and high stomatal conductance. Similarly of a number of plant responses to salt stress over production of compatible solutes, Na⁺/K⁺ ratio, ROS, stomatal closure are the most important ones. These adaptive traits in response to various abiotic stresses have the ability to directly or indirectly control yield over a time-scale influencing either water use efficiency and partitioning to the grain.

In recent years, crop physiology and genomics along with imaging tools for non-destructive analysis have led to new insights to abiotic stress tolerance providing new avenues for crop improvement. Marker assisted selection is another molecular tool which gained considerable importance in developing abiotic stress tolerant genotypes. For developing crop genotypes with enhanced multiple tolerance, it is of paramount significance to understand plant responses to abiotic stresses that disturb the homeostasis equilibrium at cellular and molecular level in order to identify a common

mechanism for tolerance. An integrated approach for developing crop cultivars with better adaptation to multiple stresses involves use of metabolic and molecular tools for identification of stress signaling pathways and tolerance mechanisms.

Plant metabolites implicated in multiple abiotic stress responses comprise compounds such as polyols mannitol and sorbitol; glycine betaine; sugars such as sucrose, trehalose and fructan; or amino acids such as proline which serve as osmo-protectants under drought and salt stresses. A variety of epicuticular waxes protect plants from excess water loss during drought and serves as a mechanical barricade to confront pathogens. The saturation level of membrane fatty acids can significantly alter chilling tolerance. Many small molecules protect plants from oxidative damage associated with heat stress. Ascorbic acid, glutathione, tocopherols, anthocyanins and carotenoids protect plant tissues by scavenging active oxygen intermediates generated during oxidative stress. The plant defense response is connected with the production of phytoalexins, activation of the general phenylpropanoid



pathway and induction of lignin biosynthesis. Methyl salicylate, methyl jasmonate and other small molecules induced in stress can also serve as signaling molecules activating defense and acclimation responses.

Advances in forward and reverse genetic approach have elucidated genes and gene products that are involved in gene expression, signal transduction, and stress tolerance under various kinds of abiotic stresses. Transcriptomic approach has the potential to identify a large number of genes not previously shown to have a role in regulating stress responses. The importance of micro RNA (mRNA) has to be emphasized in transcriptome analyses. However, in the transcriptome profile, it is imperative to scrutinize which mRNAs are translated, degraded, or temporarily stored during stress treatments. It is central to explain the purpose of newly recognized stress-responsive protein-coding and non-coding RNAs to comprehend the multifaceted abiotic stress responses of plants. Integrated metabolome and transcriptome analyses have exposed that numerous vital metabolic pathways are regulated at the transcriptional level.

Early endeavors to develop transgenics for abiotic stress tolerance were concerned with genes responsible for alteration of a single metabolite so as to bestow increased tolerance to various abiotic stresses. Stress proteins with recognized functions such as water channel proteins, key enzymes for osmolyte biosynthesis, detoxification enzymes, and transport proteins were the early objectives of plant transformation.

The identification of interactions between stresses, discovery of traits that impart tolerance to these stresses and studying the

underlying candidate genes offer opportunities to increase productivity gains. Deployment of biotechnological tools towards crop improvement is now closer to reality than a few years ago.

The era of post genomics has been ushered in with vast knowledge about the genome sequences of various crop species during recent years. It is now increasingly easier to sequence and map genomes, giving scientists access to information. Nevertheless, converting this vast information to field application has remained a bottle neck. In this context, High-throughput automated imaging is a promising tool for efficient non-destructive phenotyping of multiple morphological and physiological plant traits. Genotype-phenotype associations are crucial for trait discovery for abiotic stresses. These approaches will help generate high precision, high-throughput and multi-dimensional phenotype data for modeling and prediction of plant growth and structural development.

Combination of abiotic stresses that climate change can affect the agricultural productivity especially in rainfed agriculture. Although, the adverse impacts of multiple abiotic stresses affect all growth stages of crop but often, reproductive stage is the most affected. Stress tolerance mechanisms have been understood at various levels viz., morphological, biochemical, physiological, metabolic and molecular levels. Application of advanced and precise phenotyping typing as well as genome editing tools in crop improvement programs for enhanced abiotic stress tolerance needs meticulous planning. Further, application of crop modeling facet will support better crop management under climate change and climate variability.

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