

Emerging Role of Metabolic Pathways in Abiotic Stress Tolerance

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Abiotic stress factors, such as drought, salinity, temperature extremes (high and low) and submergence cause significant yield losses. In the past decade, advances in 'omics' technologies has enhanced our genetic and molecular understanding of plant response to various abiotic stresses. Currently, numerous stress-responsive genes have been identified and functionally analyzed in transgenics. However, very limited success has been achieved in producing abiotic stress-tolerant cultivars. Therefore, there is a great need to identify novel genes/pathways for effectively improving plant tolerance to abiotic stresses. Recently, metabolic pathways involved in abiotic stress responses have gained attention of researchers, a better understanding of which can help achieve this target. In this review, a brief overview of recent finding highlighting the importance of metabolic pathways in abiotic stress responses is presented.

It is well established that metabolic changes is the key part of response to oxidative stress in microbes [1,2]. Recent gene expression studies have shown that genes involved in several metabolic pathways are affected under abiotic stress conditions in plants also [3-6]. In a comprehensive study in Arabidopsis cells, a profound effect of oxidative stress was observed on central metabolic pathways, such as tricarboxylic acid cycle, glycolysis and oxidative pentose phosphate pathway [4]. Further, a coordinated transcriptional response of the genes involved in metabolism was found to reconfigure metabolic fluxes to cope with metabolic hiatus. Interestingly, the overall metabolic response of Arabidopsis cells was found similar to the microbes [4], which suggest that knowledge from microbial system can also be transferred to plants to identify the key regulators of stress responses.

Many of metabolic pathways are involved in production of osmoprotectants, such as sugars (trehalose, sucrose and fructan), amino acids (tryptophan and proline) and ammonium compounds (polyamines and glycinebetaine). These molecules accumulate in plants under stress conditions as adaptive mechanism, which can provide stress tolerance. The manipulation of genes associated with production of such osmoprotectants has been used to improve stress tolerance in crop plants [7-9]. Other most important metabolic pathways are those involved in scavenging of reactive oxygen species (ROS) generated in response to abiotic stresses. ROS are toxic compounds, which cause damage to cellular components. The genetic engineering of enzymes (peroxidase and catalase) involved in detoxification of ROS can improve tolerance to abiotic stresses. Hormone metabolism has also emerged as key factor in regulating plant stress response. Although exact mechanism is still unknown, the enzymes involved in metabolism of auxin, cytokinin, ethylene and abscisic acid have been implicated in different stresses [10,11]. In fact, levels of some of these hormones are known to regulate the production of many secondary metabolites and osmoprotectants [12,13]. The pathways involved in biosynthesis of cell wall components, such as cellulose and suberin, also play important role in stress adaptation [14,15]. Carbohydrate and lipid metabolism pathways are also important targets of research as some of their components have been found to be regulated by abiotic stresses [16,17]. A few studies have already demonstrated that alteration of levels of

soluble sugars and plant sterols can improve stress tolerance in plants [17,18]. It has been shown that increased carbohydrate metabolism can act as escape strategy for plants under submergence stress in an attempt to grow above water and resume photosynthesis [19].

Recently, metabolomics has been proposed as a complimentary approach to the genomics-assisted selection for crop improvement [20,21]. A few mQTLs have already been identified in Arabidopsis, tomato and *Populus* and have been shown to have intermediate heritability [22,23]. The integration of QTL mapping with gene expression and metabolite profiling showed a complex relation among them [24]. In the same study, it was also found that major regulators of gene expression variation for aliphatic and indolic glucosinolate synthesis metabolic pathways, are biosynthetic genes not the transcription factors. Although substantial efforts are required in this direction, the present investigations may be taken as proof-of-concept studies for identification of mQTLs for abiotic stress tolerance.

The complexity of metabolism/metabolic pathways poses a challenge in identifying the key regulatory components of metabolic pathways involved in abiotic stress responses. A few databases of known metabolic pathways in different organisms are available and few models have been proposed [25-28], which can help investigate the key metabolic pathways involved in a particular biological response. Although better and user-friendly databases and tools are required, the existing databases and models can also be used to elucidate the key metabolic pathways and functional components responsible for abiotic stress responses. The availability of such tools can provide platform for system-level annotations and understanding of role of individual genes in overall metabolic network of an organism.

Metabolic engineering is the manipulation of specific enzymatic reactions for improvement of cellular properties. A few studies have already demonstrated the potential of metabolic engineering for enhancing stress tolerance in plants. So far, the focus of such studies has been on the manipulation of a single gene involved in a specific metabolic pathway. However, considering the complexity of abiotic stress trait, the manipulation of single gene may not be very effective. Therefore, it would be more advantageous to engineer multiple enzymatic reactions of the same or different metabolic pathways to generate abiotic stress tolerant plants. A few successful examples already exist in the literature, which used this strategy to generate plants with better stress tolerance [9]. These studies demonstrate the enormous potential of simultaneous manipulation of multiple steps of single pathway or multiple pathways.

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Further, the identification of master regulators of critical metabolic pathways, such as transcription factors, can also provide an effective strategy for development of stress-tolerant plants via manipulating a single gene only.

In conclusion, the importance of metabolic pathways in abiotic stress response is clear now. Metabolomics is now being increasingly used to reveal plant stress responses. Therefore, there is a great need of systematic in-depth investigations to define their exact role and identify the major enzymes/pathways involved. Future pioneering studies in model plants can pave the way to identify the key regulators as target for genetic engineering of stress tolerance in crop plants. It has also been envisaged that metabolic fingerprinting can be used as a breeding tool for development of plants with best potential to tolerate abiotic stresses.

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