

Emerging Role of Metabolic Pathways in Abiotic Stress Tolerance

Mukesh Jain*

National Institute of Plant Genome Research (NIPGR), Aruna Asaf Ali Marg, New Delhi – 110067, India

Keywords: Abiotic stress; Gene expression; Metabolic pathways; Stress tolerance; Genetic engineering

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.

*Corresponding author: Mukesh Jain, National Institute of Plant Genome Research (NIPGR), Aruna Asaf Ali Marg, New Delhi-110067, India, Tel: +91-11-26735182; Fax: +91-11-26741658; E-mail: mjain@nipgr.ac.in

Received April 02, 2013; Accepted June 09, 2013; Published June 15, 2013

Citation: Jain M (2013) Emerging Role of Metabolic Pathways in Abiotic Stress Tolerance. J Plant Biochem Physiol 1: 108. doi:10.4172/2329-9029.1000108

Copyright: © 2013 Jain M. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

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.

Acknowledgements

Financial support from core grant of NIPGR and Department of Science and Technology, Government of India is gratefully acknowledged.

References

- Godon C, Lagniel G, Lee J, Buhler JM, Kieffer S, et al. (1998) The H₂O₂ stimulon in *Saccharomyces cerevisiae*. *J Biol Chem* 273: 22480-22489.
- Liu H, Colavitti R, Rovira II, Finkel T (2005) Redox-dependent transcriptional regulation. *Circ Res* 97: 967-974.
- Fukao T, Xu K, Ronald PC, Bailey-Serres J (2006) A variable cluster of ethylene response factor-like genes regulates metabolic and developmental acclimation responses to submergence in rice. *Plant Cell* 18: 2021-2034.
- Baxter CJ, Redestig H, Schauer N, Reipsilber D, Patil KR, et al. (2007) The metabolic response of heterotrophic *Arabidopsis* cells to oxidative stress. *Plant Physiol* 143: 312-325.
- Jung KH, Seo YS, Walia H, Cao P, Fukao T, et al. (2010) The submergence tolerance regulator Sub1A mediates stress-responsive expression of AP2/ERF transcription factors. *Plant Physiol* 152: 1674-1692.
- Ray S, Dansana PK, Giri J, Deveshwar P, Arora R, et al. (2011) Modulation of transcription factor and metabolic pathway genes in response to water-deficit stress in rice. *Funct Integr Genomics* 11: 157-178.
- Rathinasabapathi B (2000) Metabolic engineering for stress tolerance: installing osmoprotectant synthesis pathways. *Anal Bot* 86: 709-716.
- Rontein D, Basset G, Hanson AD (2002) Metabolic engineering of osmoprotectant accumulation in plants. *Metab Eng* 4: 49-56.
- Reguera M, Peleg Z, Blumwald E (2012) Targeting metabolic pathways for genetic engineering abiotic stress-tolerance in crops. *Biochim Biophys Acta* 1819: 186-194.
- Hare PD, Cress WA, van Staden J (1997) The involvement of cytokinins in plant-responses to environmental-stress. *Plant Growth Regulation* 23: 79-103.
- Cutler SR, Rodriguez PL, Finkelstein RR, Abrams SR (2010) Abscisic acid: emergence of a core signaling network. *Annu Rev Plant Biol* 61: 651-679.
- Goossens A, Häkkinen ST, Laakso I, Seppänen-Laakso T, Biondi S, et al. (2003) A functional genomics approach toward the understanding of secondary metabolism in plant cells. *Proc Natl Acad Sci U S A* 100: 8595-8600.
- Sasaki-Sekimoto Y, Taki N, Obayashi T, Aono M, Matsumoto F, et al. (2005) Coordinated activation of metabolic pathways for antioxidants and defence compounds by jasmonates and their roles in stress tolerance in *Arabidopsis*. *Plant J* 44: 653-668.
- Wang ZY, Xiong L, Li W, Zhu JK, Zhu J (2011) The plant cuticle is required for osmotic stress regulation of abscisic acid biosynthesis and osmotic stress tolerance in *Arabidopsis*. *Plant Cell* 23: 1971-1984.
- Franke RB, Dombrink I, Schreiber L (2012) Suberin goes genomics: use of a short living plant to investigate a long lasting polymer. *Front Plant Sci* 3: 4.
- Carter CJ, Bednarek SY, Raikhel NV (2004) Membrane trafficking in plants: new discoveries and approaches. *Curr Opin Plant Biol* 7: 701-707.
- Rosa M, Prado C, Podazza G, Interdonato R, Gonzalez JA, et al. (2009) Soluble sugars--metabolism, sensing and abiotic stress: a complex network in the life of plants. *Plant Signal Behav* 4: 388-393.
- W Patrick J, C Botha F, G Birch R (2013) Metabolic engineering of sugars and simple sugar derivatives in plants. *Plant Biotechnol J* 11: 142-156.
- Bailey-Serres J, Fukao T, Ronald P, Ismail A, Heuer S, et al. (2010) Submergence tolerant rice: SUB1's journey from landrace to modern cultivar 3: 138-147.
- Fernie AR, Schauer N (2009) Metabolomics-assisted breeding: a viable option for crop improvement? *Trends Genet* 25: 39-48.
- Kliebenstein D (2009) Advancing genetic theory and application by metabolic quantitative trait loci analysis. *Plant Cell* 21: 1637-1646.
- Schauer N, Semel Y, Balbo I, Steinfath M, Reipsilber D, et al. (2008) Mode of inheritance of primary metabolic traits in tomato. *Plant Cell* 20: 509-523.
- Ruan CJ, Teixeira da Silva JA (2011) Metabolomics: creating new potentials for unraveling the mechanisms in response to salt and drought stress and for the biotechnological improvement of xero-halophytes. *Crit Rev Biotechnol* 31: 153-169.
- Wentzell AM, Rowe HC, Hansen BG, Ticconi C, Halkier BA, et al. (2007) Linking metabolic QTLs with network and cis-eQTLs controlling biosynthetic pathways. *PLoS Genet* 3: 1687-1701.
- Kanehisa M, Goto S (2000) KEGG: kyoto encyclopedia of genes and genomes. *Nucleic Acids Res* 28: 27-30.
- Liang C, Jaiswal P, Hebbard C, Avraham S, Buckler ES, et al. (2008) Gramene: a growing plant comparative genomics resource. *Nucleic Acids Res* 36: D947-953.
- Hancock T, Mamitsuka H (2010) Amarkov classification model for metabolic pathways. *Algorithms MolBiol* 5: 10.
- Hancock T, Takigawa I, Mamitsuka H (2010) Mining metabolic pathways through gene expression. *Bioinformatics* 26: 2128-2135.

Citation: Jain M (2013) Emerging Role of Metabolic Pathways in Abiotic Stress Tolerance. *J Plant Biochem Physiol* 1: 108. doi:10.4172/2329-9029.1000108

Submit your next manuscript and get advantages of OMICS Group submissions

Unique features:

- User friendly/feasible website-translation of your paper to 50 world's leading languages
- Audio Version of published paper
- Digital articles to share and explore

Special features:

- 250 Open Access Journals
- 20,000 editorial team
- 21 days rapid review process
- Quality and quick editorial, review and publication processing
- Indexing at PubMed (partial), Scopus, EBSCO, Index Copernicus and Google Scholar etc
- Sharing Option: Social Networking Enabled
- Authors, Reviewers and Editors rewarded with online Scientific Credits
- Better discount for your subsequent articles

Submit your manuscript at: <http://www.omicsonline.org/submission/>