Omics Study for Abiotic Stress Responses in Plants

Abstract

Abiotic stresses, such as drought, temperature extremes and salinity, are the major constraints on crop yield and quality in fields. Transcriptomics, proteomics and metabolomics have been employed to improve understanding of the biological processes and molecular/cellular mechanisms involved in plant stress responses. Over the last several decades, in the light of research carried out using different omics approaches, various stress related mechanisms have been proposed for the development of tolerant varieties. Integrated use of functional genomics helps in understanding the relationship between an organism’s genome and their phenotype under different environmental conditions. By exploiting available genetic information and continuously improving techniques and strategies, integrated functional genomics alongside bioinformatics will provide a foundation for further in-depth functional studies of stress tolerance in plants.

Keywords
Abiotic stress; Metabolomics; Plants; Proteomics; Transcriptomics

Abbreviations
NGS: Next Generation Sequencing; NIPGR: National Institute of Plant Genome Research; CTDB: Chickpea Transcriptome Database; SSH: Subtractive Suppression Hybridization; mRNA: Messenger RNA; PTMs: Post-Translational Modifications; GABA: Gamma Amino Butyric Acid; TCA: Tricarboxylic Acid; BCAAs: Branched Chain Amino Acids; SAGE: Serial Analysis of Gene Expression

Introduction

In fields, plants are frequently subjected to various environmental stresses such as water deficit, freezing, heat and salt stress. These environmental stresses responsible for the large gap existing between the potential yield and real and harvest yield in several crops worldwide [1]. As plants are sessile in nature, they have developed different strategies to adapt and grow under rapidly changing environments. These strategies involve rearrangements at the molecular level, during gene expression starting from transcriptional regulation to mRNA processing, translation, protein modification or its turnover. Under stress condition, plants show stress specific regulation of transcription that affects their transcriptome [2-5]. These transcriptionally regulated genes have different functions, such as transcription, translation, signaling, metabolism and general stress response. Generally, seedling and reproductive stages are more susceptible to stress. Thus, stress response studies during these growth stages reveal novel differentially regulated genes or proteins with important functions in plant stress adaptation. In the past few decades, a great deal of research has been conducted with regards to deciphering the mechanism of multi-stress tolerance in crop plants. A large number of candidate genes, proteins and pathways have been identified using omics approaches (Figure 1). Omics refers to a study of large sets of molecules in biology, for detection of genes (genomics), mRNA (transcriptomics), protein (proteomics), and metabolites (metabolomics). Though plant biologists have unveiled several stress related molecular mechanisms, we are still a step away from understanding the plants entire response to multiple stresses in fields. While advancement in microarray and deep-sequencing technologies lead to rapid accumulation of genomic and transcriptomic data under different abiotic stresses [6,7], the limited depth of quantitative proteomics has inhibited similar progress in post-transcriptional gene regulation. To date, transcript levels are routinely used as the only measure for gene expression in high-through put approaches. Several studies, however, have reported a low correlation between transcript and protein levels,
highlighting the importance of post-transcriptional processes as the limited predictive value of transcripts for protein expression [8-12]. Recent developments in research technologies have shown that understanding of plant stress responses using genomics, transcriptomics, proteomics and metabolomics studies, requires quantitative information at every step of gene expression. Several research groups have shown the relevance of post-transcriptional and translational regulatory mechanisms in the plant adaptation process to different abiotic threats, including light [13,14], heavy metal intoxication [15], dehydration [16,17] and salinity stress [18].

Despite all the recent developments, our understanding of post-transcriptional gene regulation and its effects on protein-complex stoichiometry are lagging behind. Transcriptomic technologies have advanced tremendously in recent years. RNA-seq has shown to be an excellent method to obtain unbiased transcriptome data that correlate well with micro array analyses [19]. Though not as advanced as transcriptomic techniques, the mass spectrometry methods for high-throughput put analyses of proteome are also advancing rapidly. However, whilst these technologies are currently applied to answer many research questions in various model systems, there are relatively few comparative studies involving these technologies. Complementary analysis of the proteome and metabolome combined with a comprehensive transcriptome provides an important validation tool for the expression of key genes. Dissecting the relationship between differentially expressed transcriptome, proteome and metabolome will potentially help us to understand the molecular mechanisms underpinning abiotic stress tolerance in plants. By investigating transcript-protein-metabolite correlations, and change of correlation between the normal and stressed state, we can identify biological processes that are strongly regulated by abiotic stresses in plants. Furthermore, these studies will provide a comprehensive data set for quantitative systems-level analyses.

Transcriptomics: A Key to Understanding Abiotic Stress Responses in Plants

Transcriptomic approaches have paved the way to understanding plant responses to abiotic stresses. Recently, transcriptome analysis by next generation sequencing (NGS), RNA-seq for sRNAs and their use in genomics research, have greatly improved plant genomic resources [20-25]. Li et al. [26], identified 5365 differentially expressed probe sets (2-fold as cutoff) in the switch grass cultivar Alamo, under heat stress, utilizing switch grass Affymetrix gene chips. By comparative transcriptome analysis in response to heat stress, they identified 16 common genes in four monocots-switch grass, rice, wheat and maize. Interestingly, most of them were associated with protein refolding processes; therefore, these genes can be used as valuable biomarkers for identifying heat sensitive plant germplasm. Wakasa et al. [27], have done RNA sequencing-mediated expression profiling of transgenic rice plants, produced by homologous recombination, in which endogenous genomic OsSREI (ER stress sensor/transducer) was replaced by missense alleles defective in ribonuclease activity. This study provided valuable information about the ER stress response in rice plants and led to the discovery of new genes related to ER stress. Instead of just one type of stress study that is generally conducted under laboratory conditions, plants grown in the field are exposed to a combination of stresses, which require agonistic or antagonistic responses, or a number of potentially unrelated responses to a certain single stress condition. Rasmussen et al. [28], analyzed such responses by comparing transcriptome changes in 10 Arabidopsis thaliana ecotypes under different stresses and their combinations. This study revealed that 61% of the transcriptome changes in response to double stresses were not predicted from the responses to single stress treatments. They have also shown that plants prioritized between potentially antagonistic responses for only 5% to 10% of the responding transcripts. In light of this research, authors have delineated co expression network modules responding to single and combined stresses. RNA-seq analysis of Chenopodium quinoa under four water treatments (field capacity to drought) showed an overlap between drought stress tolerance and other abiotic stress mechanisms [29].

Kudapa et al. [30] used several Sanger EST collections of chickpea, together with sequence data from two different NGS (Next Generation Sequencing) platforms (Illumina and FLX/454) of chickpea, to produce a more extensive chickpea transcriptome assembly (CaTA v2). Additionally, NIPGR (National Institute of Plant Genome Research, India) have developed the Chickpea Transcriptome Database (CTDB), which will provide comprehensive information about the chickpea transcriptome (http://www.nipgr.res.in/ctdb.html). Apart from NGS, subtractive cDNA suppression hybridization (SSH) technology has also proved to be very helpful in transcriptomic studies in unveiling stress responses [31]. Molina et al. [6,7], used high resolution power of Super SAGE (Serial Analysis of Gene Expression) coupled to the Roche 454 Life/AGP GS FLX Titanium NGS technology, to characterize the complete transcriptome of drought and salt-stressed chickpea plant's roots and nodules under stress condition.

Transcriptomic sequencing of chrysanthemum plants under dehydration stress using the Illumina sequencing also provided better understanding of the molecular mechanisms of dehydration stress responses [32]. Zhu et al. [33], applied a comparative microarray analysis approach to study the transcriptome changes of cotton under five abiotic stresses. Their study unveiled the functional genes and stress related pathways, and also suggested a crosstalk of responsive genes or pathways to multiple abiotic stresses in cotton seedlings.

Transcriptomic technologies have the potential to provide deep coverage and unbiased representation of transcript abundance, which is very important in non-model plants lacking genome sequence information [34]. However, the frequent incongruity between protein levels and the abundance of cognate gene transcripts suggested the need of complementary analysis of the proteome for further validation of candidate genes and pathways [35].

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Proteomics: A Closer Look at Translatome Regulating Cellular Responses

Most functional genomics studies rely on transcriptome analysis across changing external conditions to identify transcripts that are differentially regulated, and often it is hypothesized that changes in transcript levels may lead to corresponding changes in protein levels. However, it has been shown by several groups that protein levels do not always necessarily correspond to mRNA levels [36,37]. Anderson and Selhamer [38] reported that the correlation coefficient in quantity between mRNA and protein abundance is relatively low. Protein level can be modulated by changing either the rate of synthesis or the stability of the messenger RNA (mRNA or transcript), or the synthesis or stability of the protein itself [39]. Translatome refers to the pool of all RNAs that are associated with ribosomes purified via an affinity tag. Study of the translatome or proteome can confirm the presence of the protein, and provides a direct measure of the quantity present. Precise analysis of the translatome/proteome and metabolome is essential for understanding the fundamentals of stress physiology and biochemistry. Proteins, the functional translated portion of the genome, play an essential role in plant stress response. Proteomic studies provide us with a finer picture of the protein networks and metabolic pathways primarily involved in stress tolerance mechanism. Identifying master regulator proteins that play key roles in the abiotic stress response pathway is fundamental in providing opportunities for developing genetically engineered crop plants to allow us to understand the stress response. Halbeisen and Gerber [40], compared the transcriptome with the translatome in yeast cells, exposed to different stresses, to determine the discrepancy between transcript and protein levels. Their analysis suggested that transcriptome and translatome show a strong coordinated response, particularly under severe stress. While, under mild stress conditions about 2% of all expressed messages showed differential regulation, and therefore represent candidates for translational regulation. In A. thaliana, precise mapping of ribosome footprints (RFs) on mRNAs to investigate translational regulation under control and sublethal hyposia stress conditions, demonstrated nearly 100-fold variation in the efficiency of translation of individual mRNAs under both conditions. These findings therefore provide unique insights into posttranscriptional and translational regulation modulated by lower level of applied stress [41]. Yanguet et al. [42] carried out a genome-wide analysis to monitor the changes in the translation efficiency of individual mRNAs of A. thaliana seedlings after exposure to temperature stress. They demonstrated that, translation exerted a wide regulation on gene expression. While for some mRNAs translation is severely repressed, translation of homeostasis and stress related mRNAs follow a differential pattern. Their study suggested that, mRNAs with special features, such low 5′-UTR G+C content and small cDNA length, are preferentially translated.

Several research groups have extensively explored proteomics tools to solve the maze of heavy metal ion stress responses in plants. Under Cd stress, in Brassica juncea L. roots, over expression of sulfite reductase and 0-acetyl serine sulphydrylase proteins revealed the reduction of sulfate to cysteine [43]. A leaf mesophyll protoplasts studies involving Hordeum vulgare L. reveals a MRP-like ABC transporter and two novel CAX transporters (CAX1a and CAX5), assuring Cd\(^{2+}\) transport into the vacuole [44]. Additionally, in Glycine max L. leaves, abundance of Hsp70 and peroxiredoxin were reported [45], and up-regulation of proteins associated with Cd-chelating pathways were reported in different plant species viz. Linumusistissimum, A. thaliana and G. max [46-48]. Similar research has been carried out to decipher cellular responses towards other heavy metals, such as with B deficiency in Lupinus albus roots, where proteins involved in cell division and metabolic processes were found to be down regulated [49]. Under Cr stress, enhanced expression of proteins involved in ROS detoxification, defense responses, photosynthesis and chloroplast organization were reported in Zea mays [50]. Accumulation of Cr-responsive proteins linked to heavy metal tolerance and senescence pathways were reported in Miscanthus sinensis [51]. Furthermore, in the presence of AI, the stress tolerant genotype of G. max showed accumulation of enzymes which catalyze synthesis of citrate (involved in AI\(^{3+}\) detoxification) whereas, the sensitive genotype showed induction of proteins related to general stress response [52].

Subba et al. [53] studied the nuclear proteome in two contrasting chickpea cultivars under drought stress, to identify the proteins playing key roles in drought stress tolerance. Researchers are also exploiting a2DE (two dimensional gel electrophoresis) approach for generating a comprehensive nuclear [54,55] and cell wall proteome [56,57], which will provide a basis for future comparative studies. In addition, Heidavy and Maali-Amiri [58], studied time course dynamics of physio-biochemical and proteome changes in chickpea under cold stress. With this comparative study of biochemical and molecular events under cold stress, they have provided a more comprehensive view of chickpea stress responses.

Besides differential protein abundance, post-translational modifications (PTMs) also increase protein complexity and dynamics, regulating different cellular events. Advances in proteomics techniques made global identification of PTMs feasible. Patton [59] described the simple and specific methods, suitable for different PTMs, for visualization of modified proteins in a gel. PTM studies are further aided by the sensitivity of mass spectrometry, to help in analyzing the in vivo phosphorylation of proteins at the proteome scale [60]. For example, in salt-treated rice roots, increased relative abundance of 17 phosphoproteins (e.g., dnak-type chaperone HSF70, putative GST, small GTP-binding protein OsRac2, mannose-binding RICE lectin), and a decreased relative abundance of 11 phosphoproteins (e.g., putative protein kinase, ATP synthase β chain) have been reported. Tanou et al. [61], suggested an important role of protein carbonylation and S-nitrosylation patterns in the salinity response of citrus. Their study has shown a strong increase in the level of carbonylated proteins (ADH, chaperonin 60 subunit α, glycolytic enzymes, HSP70, Rubisco LSU, subunits of chloroplast and mitochondrial ATP synthase F1, mitochondrial
Caldana et al. [69], carried out eight environmental conditions. Metabolic response to high light stress response in photosynthesis and accumulation of osmolytes during drought. Verslues and Juenger [68] revealed changes in the levels of metabolites including branched chain amino acids (BCAAs) [66,67]. Wheat, exposed to water stress conditions, suggested common mildly desiccated leaves. Metabolite profiling of maize and accumulated in severely desiccated leaves but decreased in expanding leaves, which correlates with the transcriptional response [65]. In the case of amino acid metabolism, most amino acids were accumulated in severely desiccated leaves but decreased in mildly desiccated leaves. Metabolite profiling of maize and wheat, exposed to water stress conditions, suggested common changes in the levels of metabolites including branched chain amino acids (BCAAs) [66,67]. Verslues and Juenger [68] revealed an important role of metabolic regulation, including regulation of biosynthesis and accumulation of osmolytes during drought stress response in A. thaliana. Caldana et al. [69], carried out transcriptome and metabolome profiling of A. thaliana under eight environmental conditions. Metabolic response to high light showed accumulation of the photo respiratory intermediates, glycine and glycolate in the early phase. Interestingly, they have reported similar responses during the mid-phase of high light stress and low temperature treatments, including accumulation of shikimate, phenylalanine and fructose, and the decrease of succinate; however, the physiological meaning of these overlapped responses is currently not known.

Kusano et al. [70], studied the effect of UV light on A. thaliana metabolism and documented a biphasic response. In the early phase, they reported major changes in the levels of primary metabolites, including ascorbate derivatives. By contrast, mid-to late-term responses were observed in the classically defined UV-B protectants, such as flavonoids and phenolics. Their results suggested cell priming upon early exposure to UV-B, which involves reprogramming of the metabolism for efficient diversion of carbon towards aromatic amino acid precursors of the phenyl propanoid pathway. They have also suggested the importance of ascorbate in the short-term response to UV-B. Furthermore, this group combined transcriptomics with metabolomics to determine the metabolic changes responsible for adaptation to increased exposure to UV-B, and metabolic changes involved in the perception-signaling relay, which alerts the plant cell to respond against the stress [71]. Metabolite profiling of A. thaliana leaves also helped in elucidating the metabolic basis of dark-induced senescence and function of the mitochondrial alternative electron transport pathway during dark treatment [72]. In other metabolite profiling studies, an increase in BCAAs, i.e.,valine, leucine, isoleucine, and other amino acids sharing synthetic pathways with BCAAs i.e. lysine, threonine and methionine were reported under abiotic stress conditions [72,73]. The authors have suggested that BCAAs function as compatible osmolytes, since drought stress led to increased accumulation of BCAAs in various plant tissues. Interestingly, protein degradation serves as an alternative respiratory substrate for stressed plants [74].

Although, all of these approaches greatly increased our knowledge with regards to candidate genes, proteins and pathways playing crucial roles in plant stress responses, there is still a long avenue to explore. Recently, researchers have combined either two or all three omics approaches to obtain a holistic view of stress responses [35,75-79]. Mehmeti et al. [80], reported discrepancies between transcriptomic, proteomic and metabolite data of lactic acid bacteria, suggesting regulation beyond the level of transcription. These discrepancies are either because of noise/poor statistics for the microarray data or due to varying efficiency of transcription and translation. They have indicated additional posttranscriptional or translational regulation in these bacterial cells. Complementary analysis of the proteome and metabolome combined with a comprehensive transcriptome provided an important validation tool for the expression of key genes in Macleaya sp. [79]. Combinations of transcriptome, proteome and metabolite profiling helps in revealing the correlation between the expression of stress related biosynthetic genes and corresponding metabolic products, which further increases our understanding of plant stress responses [75,78]. Zeng et al. [79] also combined these.
Omics approaches to reveal alkaloid biosynthesis in Macleaya sp. While studying phosphate-deficient *A. thaliana* roots, Lan et al. [81], revealed multiple levels of gene regulation, and suggested integrated measurement and interpretation of changes in protein and transcript abundance for generating a complete inventory of the components that are critical for stress responses. Colmsee et al. [82] established a data warehouse for maize, OPTIMAS-DW. It can handle different data domains, integrates data from different data domains, such as transcriptomics, metabolomics, ionomics, proteomics, phenomics, and enables the user to find answers to different systems biology questions. Amiour et al. [83] discussed the potential use of ‘omics’ studies to improve understanding of whole plant nitrogen economics in maize.

Srivastava et al. [84], proposed a data evaluation strategy to provide an efficient way of compiling complex, multi-platform datasets to obtain significant biological information. This study of transgenic populus plants harboring superoxide dismutase gene, provided system-level information on ROS metabolism and responses to oxidative stress. Yang et al. [85] also reviewed applications of omics approaches for understanding secondary metabolism, including the discovery of novel genes, the identification of gene function, and the detection of novel pathways of the metabolic network. All of these studies accelerate our understanding of plants interaction with their environment, and their performance under prevailing stress conditions.

### Summary

Plants are the primary producers on earth and abiotic stresses affect their growth, development and final yield potential. Under stress conditions, plants modulate themselves to transiently adapt to the existing circumstances by changing the expression pattern of genes, proteins and metabolites. To identify those changes, various tools and techniques, such as genomics, transcriptomics, metabolomics, ionomics and phenomics, have been devised to allow us to better understand the genetic makeup of plants and their adaptability potential under stress conditions. Recent omics studies have accumulated a great deal of information at transcript, protein and metabolite levels to perceive the survival potential of plants under stress. However, a highly coordinated approach, such as system biology, is needed for the full comprehension of the complex regulatory nature of plants so that master stress regulators can be identified.

### References

1. Boyer JS (1982) Plant Productivity and Environment. Science 218(4571): 443-448.
2. Larkindale J, Vierling E (2008) Core genome responses involved in acclimation to high temperature. Plant Physiol 146(2): 748-761.
3. Oshino T, Abe, M, Saito R, Ichishi E, Endo M, et al. (2007) Premature progression of anther early developmental programs accompanied by comprehensive alterations in transcription during high temperature injury in barley plants. Mol Genet Genomics 278(1): 31-42.
4. Qin D, Wu H, Feng H, Yao Y, Ni Z, et al. (2008) Heat stress-responsive transcriptome analysis in heat susceptible and tolerant wheat (*Triticum aestivum* L.) by using wheat genome array. BMC Genomics 9: 432.
5. Rizhsky L, Liang H, Shuman J, Shulaev V, Davletova S, et al. (2004) When defense pathways collide. The response of *Arabidopsis* to a combination of drought and heat stress. Plant Physiol 134(4): 1683-1696.
6. Molina C, Rotter B, Horres R, Udupa SM, Besser B, et al. (2008) SuperSAGE: the drought stress responsive transcriptome of chickpea roots. BMC Genomics 9: 553.
7. Molina C, Zaman-Allah M, Khan F, Fatnassi N, Horres R, et al. (2011) The salt-responsive transcriptome of chickpea roots and nodules via deepSuperSAGE. BMC Plant Biol 11: 31.
8. De Sousa Abreu R, Penalva LO, Marcotte E, Vogel C (2009) Global signatures of protein and mRNA expression levels. Mol Biosyst 5(12): 1512-1526.
9. Maier T, Gueli M, Serrano I. (2009) Correlation of mRNA and protein in complex biological samples. FEBS Lett 583(24): 3966-3973.
10. Foss EJ, Radulovic D, Shaffer SA, Goodlett DR, Kruglyak L, et al. (2011) Genetic variation shapes protein networks mainly through non-transcriptional mechanisms. PLoS Biol 9(9): e100144.
11. Ghazalpour A, Bennett B, Petyku VA, Orozco L, Hapogian R, et al. (2011) Comparative analysis of proteome and transcriptome variation in mouse. PLoS Genet 7(6): e1001139.
12. Vogel C, Marcotte EM (2012) Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. Nat Rev Ge 13(4): 227-232.
13. Liu MJ, Wu SH, Chen HM (2012) Widespread transcriptional control contributes to the regulation of *Arabidopsis* photomorphogenesis. Mol Syst Biol 8: 566.
14. Juntawong P, Bailey-Serres J (2012) Dynamic light regulation of translation status in *Arabidopsis thaliana*. Front Plant Sci 3: 66.
15. Sormani R, Delanoe R, Lagois S, Bitton F, Lanet E, et al. (2011) Sublethal cadmium intoxication in *Arabidopsis thaliana* impacts translation at multiple levels. Plant Cell Physiol 52(2): 436-447.
16. Kawaguchi R, Girke T, Bray EA, Bailey-Serres J (2004) Differential mRNA translation contributes to gene regulation under non-stress and dehydration stress conditions in *Arabidopsis thaliana*. Plant J 38(5): 823-839.
17. Kawaguchi R, Bailey-Serres J (2005) mRNA sequence features that contribute to translational regulation in *Arabidopsis*. Nucleic Acids Res 33(3): 995-965.
18. Matsuura H, Ishibashi Y, Shimmyo A, Kanaya S, Kato K (2010) Genome-wide analyses of early translational responses to elevated temperature and high salinity in *Arabidopsis thaliana*. Plant Cell Physiol 51(3): 448-462.
19. Kogenara S, Qing Y, Guo Y, Wang N (2012) RNA-seq and microarray complement each other in transcriptome profiling. BMC Genomics 13: 629.
20. Azam S, Thakur V, Ruperao P, Shah T, Balaji I, et al. (2012) Coverage-based consensus calling (CBCC) of short sequence reads and comparison of CBCC results to identify SNPs in chickpea (*Cicer arietinum*; Fabaceae), a crop species without a reference genome. Am J Bot 99(2): 186-192.
21. Gaur R, Azam S, Jeena G, Khan AW, Choudhary S, et al. (2012) High-throughput SNP discovery and genotyping for constructing a saturated linkage map of chickpea (*Cicer arietinum*). DNA Res 19(5): 357-373.
22. Hiremath PJ, Kumar A, Pennetsa R, Farmer A, Schlueter JA, et al. (2015) Omics Study for Abiotic Stress Responses in Plants. Adv Plants Agric Res 2(1): 00037. DOI: 10.15406/apar.2015.02.00037
al. (2012) Large-scale development of cost-effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. Plant Biotechnol J 10(6): 716-732.

23. Hiremath PJ, Farmer A, Cannon SB, Woodward, J, Kudapa H, et al. (2011) Large-scale transcriptome analysis in chickpea (Cicer arietinum L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. Plant Biotechnol J 9(8): 922-931.

24. Thudi M, Bohra A, Nayak SN, Varghese N, Shah TM, et al. (2011) Novel SSR markers from BAC-end sequences, DArT arrays and a comprehensive genetic map with 1,291 marker loci for chickpea (Cicer arietinum L.). PlJ 6(11): e27275.

25. Varshney RK, Nayak SN, May GD, Jackson SA (2009) Next-generation sequencing technologies and their implications for crop genetics and breeding. Trends Biotechnol 27(9): 522-530.

26. Li YF, Wang Y, Tang Y, Kakani VG, Mahalingam R (2013) Transcriptome analysis of heat stress response in switchgrass ( Panicum virgatum L.). BMC Plant Biol 13: 153.

27. Wakasa Y, Oono Y, Yasawara T, Hayashi S, Ozawa K, et al. (2014) RNA sequencing-mediated transcriptome analysis of rice plants in endoplasmic reticulum stress conditions. BMC Plant Biol 14: 101.

28. Rasmussen S, Barath P, Suarez-Rodriguez MC, Bressendorff S, Friis P, et al. (2013) Transcriptome responses to combinations of stresses in Arabidopsis. Plant Physiol 161(4): 1785-1794.

29. Raney I, Reynolds D, Elztiga D, Page J, Udall JA, et al. (2014) Transcriptome analysis of drought induced stress in switchgrass ( Panicum virgatum L.). BMC Plant Biol 13: 55.

30. Kudapa H, Azam S, Sharpe AG, Taran B, Li R, Deonovic B, et al. (2013) Comprehensive transcriptome assembly of chickpea (Cicer arietinum L.) using sanger and next generation sequencing platforms: development and applications. PlJ One 9(8): e86039.

31. Jain D, Chattopadhyay D (2010) Analysis of gene expression in response to water deficit of chickpea (Cicer arietinum L.) varieties differing in drought tolerance. BMC Plant Biol 10: 24.

32. Xu Y, Gao S, Yang Y, Huang M, Cheng L, et al. (2013) Transcriptome sequencing and whole genome expression profiling of chrysanthemum under dehydration stress. BMC Genomics 14: 662.

33. Zhu YN1, Shi DQ, Ruan MB, Zhang LL, Meng ZH, et al. (2013) Transcriptome analysis reveals crosstalk of responsive genes to multiple abiotic stresses in cotton ( Gossypium hirsutum L.). PlJ One 8(11): e80218.

34. Trujillo LE, Sotolongo M, Menendez C, Ochagavia ME, Coll Y, et al. (2008) SodERF3, a novel sugarcane ethylene responsive factor (ERF), enhances salt and drought tolerance when overexpressed in tobacco plants. Plant Cell Physiol 49(4): 512-525.

35. Gygi SP, Rochon Y, Franza BR, Aebersold R (1999) Correlation between protein and mRNA abundance in yeast. Mol Cell Biol 19(3): 170-1730.

36. Hakeem KR, Chandra R, Ahmad P, Jibral M, Ozturk M (2012) Relevance of proteomic investigations in plant abiotic stress physiology. OMICS 16(11): 621-635.

37. Hossain Z, Komatsu S (2013) Contribution of proteomic studies towards understanding plant heavy metal stress response. Front Plant Sci 3: 310.

38. Anderson L, Seilhamer J (1997) A comparison of selected mRNA and protein abundances in human liver. Electrophoresis 18(3-4): 533-537.

39. Komili S, Silver PA (2008) Coupling and coordination in gene expression processes: a systems biology view. Nat Rev Genet 9(1): 38-48.

40. Halbeisen RE, Gerber AP (2012) Correction: stress-dependent coordination of transcriptome and proteome in yeast. PlJ Biol 10(1): 10.1371/annotation/7462bca2-5358-43c8-be2e-94e8a8f6159.

41. Juntawong P, Girke T, Bazin J, Bailey-Serres J (2014) Translational dynamics revealed by genome-wide profiling of ribosome footprints in Arabidopsis. Proc Natl Acad Sci U S A 111(1): E203-E212.

42. Yanzuge E, Castro-Sanz AB, Fernandez-Bautista N, Oliveros JC, Castellano MM (2013) Analysis of genome-wide changes in the transcriptome of Arabidopsis seedlings subjected to heat stress. PlJ One 8(8): e7425.

43. Alvarez S, Berla BM, Sheffield J, Cahoon RE, Jez JM, et al. (2009) Comprehensive analysis of the Brassica juncea root proteome in response to cadmium exposure by complementary proteomic approaches. Proteomics 9(9): 2419-2431.

44. Hossain Z, Hajika M, Komatsu S (2012a) Comparative proteome analysis of high and low cadmium accumulating soybeans under cadmium stress. Amino Acids 43(6): 2393-2416.

45. Hossain Z, Makino T, Komatsu S (2012b) Proteomic study of β-a-aminothiobutyric acid-mediated cadmium stress alleviation in soybean. J Proteomics 75(13): 4151-4164.

46. Hradilova J, Rehulka P, Rehulkova H, Vrbova M, Griga M, et al. (2010) Comparative analysis of proteome changes in contrasting flax cultivars upon cadmium exposure. Electrophoresis 31(2): 421-431.

47. Semane B, Dupae J, Guypers A, Noben JP, Tuomainen M, et al. (2010) Leaf proteome responses of Arabidopsis thaliana exposed to mild cadmium stress. J Plant Physiol 167(4): 247-254.

48. Ahsan N, Nakamura T, Komatsu S (2012) Differential responses of microsomal proteins and metabolites in two contrasting cadmium (Cd) accumulating soybean cultivars under Cd stress. Amino Acids 42(1): 317-327.

49. Alves M, Moes S, Jeno P, Pinheiro C, Passarinho J, et al. (2011) The analysis of Lupinus albus root proteome revealed cytoskeleton altered features due to long-term boron deficiency. J Proteomics 74(8): 1351-1363.

50. Wang R, Gao F, Guo BQ, Huang JC, Wang L, et al. (2013) Short-term chromium-stress-induced alterations in the maize leaf proteome. Int J Mol Sci 14(6): 11125-11144.

51. Sharmin SA, Alam I, Kim KH, Kim YG, Kim PJ, et al. (2012) Chromium-induced physiological and proteomic alterations in roots of Miscanthus sinensis. Plant Sci 187: 113-126.

52. Daressa D, Soliman K, Taylor R, Senwo Z (2011) Proteomic analysis of soybean roots under aluminum stress international. Int J Plant Genomes 2(1): 1-28.

53. Subba P, Kumar R, Gayali S, Shekhar S, Parveen S (2013) Characterization of the nuclear proteome of a dehydration-sensitive cultivar of chickpea and comparative proteomic analysis with a tolerant cultivar. Proteomics 13(12-13): 1973-1992.

54. Pandey A, Choudhary MK, Bhushan D, Chattopadhyay A, Chakraborty S (2006) The nuclear proteome of chickpea (Cicer arietinum L.) reveals predicted and unexpected proteins. J Proteome Res 5(12): 3301-3311.

55. Jaiswal DK, Mishra P, Subba P, Rathi D, Chakraborty S, et al. (2014) Membrane-associated proteomics of chickpea identifies Sad1/
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UNCC-84 protein (CaSUN1), a novel component of dehydration signaling. Sci Rep 4: 4177.

Bhushan D, Pandey A, Chattopadhyay A, Choudhary MK, Chakraborty S, et al. (2006) Extracellular matrix proteome of chickpea (Cicer arietinum L.) illustrates pathway abundance, novel protein functions and evolutionary perspective. J Proteome Res 5(7): 1711-1720.

Bhushan D, Pandey A, Choudhary MK, Datta A, Chakraborty S, et al. (2007) Comparative proteomics analysis of differentially expressed proteins in chickpea extracellular matrix during dehydration stress. Mol Cell Proteomics 6(11): 1868-1884.

Heidari L, Amiri MR (2013) Physio-biochemical and proteome analysis of chickpea in early phases of cold stress. J Plant Physiol 170(5): 459-469.

Patton WF (2002) Detection technologies in proteome analysis. J Chromatogr B Analyt Technol Biomed Life Sci 771(1-2): 3-31.

Kwon SJ, Choi EY, Choi YJ, Ahn JH, Park OK (2006) Proteome studies of post-translational modifications in plants. J Exp Bot 57(7): 1547-1551.

Tanou G, Job C, Rajlou L, Arc E, Belghazi M, et al. (2009) Proteomics reveals the over-lapping roles of hydrogen peroxide and nitric oxide in the acclimation of citrus plants to salinity. Plant J 60(5): 795-804.

Kosova K, Prasil IT, Vitamvas PP (2013) Protein contribution to plant salinity response and tolerance acquisition. Int J Mol Sci 14(4): 6757-6789.

Weckwerth W, Kahl G (2013) The handbook of plant metabolomics. Wiley-Blackwell, Weinheim, USA.

Urano K, Maruyama K, Ogata Y, Morishita Y, Takoda M, et al. (2009) Characterization of the ABA-regulated global responses to dehydration in Arabidopsis by metabolomics. Plant J 57(6): 1065-1078.

Skirycz A, De Bodt S, Obata T, De Clercq I, Cleys H, et al. (2010) Developmental stage specificity and the role of mitochondrial metabolism in the response of Arabidopsis leaves to prolonged mild osmotic stress. Plant J 65(2): 226-244.

Witt S, Galicia L, Lisec J, Cairne J, Tiessen A, et al. (2012) Metabolic and phenotypic responses of greenhouse-grown maize hybrids to experimentally controlled drought stress. Mol Plant 5(2): 401-417.

Bowen JB, Erwin TA, Juttner J, Schnurbusch T, Langridge P, et al. (2012) Drought responses of leaf tissues from wheat cultivars of differing drought tolerance at the metabolite level. Mol Plant 5(2): 418-429.

Vershues PE, Juenger TE (2011) Drought, metabolites, and Arabidopsis natural variation: a promising combination for understanding adaptation to water-limited environments. Cur Currin Plant Biol 14(3): 240-245.

Caldana C, Degenkolbe T, Inostroza AC, Klie S, Sulpiice R, et al. (2011) High-density kinetic analysis of the metabolic and transcriptomic response of Arabidopsis to eight environmental conditions. Plant J 67(5): 869-884.

Kusano M, Tohge T, Fukushima A, Kobayashi M, Hayashi N, et al. (2011) Metabolomics reveals comprehensive reprogramming involving two independent metabolic responses of Arabidopsis to UV-B light. Plant J 67(2): 354-369.

Tohge T, Kusano M, Fukushima A, Saito K, Fernie AR (2011) Transcriptional and metabolic programs following exposure of plants to UV-B irradiation. Plant Signal Behav 6(12): 1987-1992.

Araujo WL, Ishizaki K, Nesi AN, Tohge T, Larson TR, et al. (2011) Analysis of a range of catabolic mutants provides evidence that phytanoyl-coenzyme A does not act as a substrate of the electron-transfer flavoprotein/electron-transfer flavoprotein:ubiquinone-oxidoreductase complex in Arabidopsis during dark-induced senescence. Plant Physiol 157(1): 55-69.

Joshi V, Jong JG, Fei Z, Jander G (2010) Interdependence of threonine, methionine and isoleucine metabolism in plants: accumulation and transcriptional regulation under abiotic stress. Amino Acids 39(4): 933-947.

Araujo WL, Tohge T, Ishizaki K, Leaver CJ, Fernie AR (2011) Protein degradation-an alternative respiratory substrate for stressed plants. Trends Plant Sci 16(9): 489-498.

Wochniak BJ, Luedemann A, Kopka J, Selbig J, Tunali UR, et al. (2003) Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. EMBO Rep 4(10): 989-993.

Baginsky S, Kleffmann T, von Zychlinski A, Gruissem W (2005) Analysis of shotgun proteomics and RNA profiling data from Arabidopsis thaliana chloroplasts. J Proteome Res 4(2): 637-640.

Zulak KG, Carnish A, Daskachuk DE, Deyholos MK, Goodenow DB, et al. (2007) Gene transcript and metabolite profiling of elicitor-induced opium poppy cell cultures reveals the coordinate regulation of primary and secondary metabolism. Planta 225(5): 1085-1106.

Desgagne-Penix I, Khan MF, Schriemer DC, Cram D, Nowak J, et al. (2010) Integration of deep transcriptome and proteome analyses reveals the components of alkaloid metabolism in opium poppy cell cultures. BMC Plant Biol 10: 252.

Zeng J, Liu Y, Liu W, Liu X, Liu F, et al. (2013) Integration of transcriptome, proteome and metabolism data reveals the alkaloids biosynthesis in Macleayacordata and Macleayamicrocarpa. PLos One 8(1): e53409.

Mehmeti I, Jonsson M, Fergestad EM, Mathiesen G, Nes IF, et al. (2011) Transcriptome, proteome, and metabolite analyses of a lactate dehydrogenase-negative mutant of Enterococcus faecalis V583. Appl Environ Microbio 77(7): 2406-2413.

Lang P, Li W, Schmidt W (2012) Complementary proteome and transcriptome profiling in phosphate-deficient Arabidopsis roots reveals multiple levels of gene regulation. Mol Cell Proteomics 11(11): 1156-1166.

Golmsee C, Mascher M, Czauderna T, Hartmann A, Schluter U, et al. (2012) OPTIMAS-DW: A comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. BMC Plant Biol 12: 245.

Amour N, Imbaud S, Clement G, Agier N, Zhvy M, et al. (2012) The use of metabolomics integrated with transcriptomic and proteomic studies for identifying key steps involved in the control of nitrogen metabolism in crops such as maize. J Exp Bot 63(14): 5017-5033.

Srivastava V, Obudula O, Bygdell J, Loestedt T, Ryden P, et al. (2013) OnPLS integration of transcriptomic, proteomic and metabolomic data shows multi-level oxidative stress responses in the cambium of transgenic hpl-superoxide dismutase Populus plants. BMC Genomics 14: 893.

Yang D, Du X, Yang Z, Liang Z, Guo Z, et al. (2014) Transcriptomics, proteomics, and metabolomics to reveal mechanisms underlying plant secondary metabolism. Engineering in Life Sciences 14(5): 456-466.

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