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Improving Water Use Efficiency to Sustain Crop Production under Climate Change Scenario

Mehboob B. Sheikh
Florida A&M University, Tallahassee, Florida 32317, USA

Water deficit, caused by lack of water has been a great problem for agriculture worldwide affecting virtually every aspect of plant physiology and metabolism impacting food production. This is especially serious considering other adverse factors such as the high levels of atmospheric CO_2, climate change scenarios and predictions of future global warming, all of which increase drought incidence, frequency and severity. To cope with these stresses plants execute various physiological and metabolic responses to sustain with water stress, which is reflected by the synthesis of specific transcripts and proteins. One way to overcome this adversity is to generate new stress tolerant varieties by identification of specific genes involved in given metabolic processes. Most of the stress-response traits are complex and are influenced by multiple genes and extensive genotype-environment interactions. The expression of genes in response to water deficit stress involves not only transcription of genes but its translation into a protein that must be targeted to a specific cellular location to perform its designated function. To understand the effect of gene regulation, a comprehensive study of gene expression accompanied by metabolic processes within a cell is needed. An in depth proteogenomics study would elevate our knowledge of the biological phenomenon involved with the development of resistance to water stress. In this regard our research is aimed at identifying genes and proteins associated with WS tolerance to develop cultivars with high water use efficiency to reduce water use without yield reduction.

Our studies on grape have shown that water stress impacts stomatal osmotic pressure and expression of CER 5 gene involved in encoding ABC transporter which is required for wax export to the cuticle genes involved in transportation. We have found that several genes associated with cell permeability, transportation and maintenance of osmotic potential such as sucrose synthase, actin, AP2 transcriptional activator, cytochrome b gene, WRK transcription factor, protein kinase, isoprene synthase, cell division protein, rab1, ABF3, ASR2 gene, AP2, xyloglucan endotransglucoxylase and glyoxalase I are suppressed due to water stress. In peanut, we have found over-expression, suppression, and appearance of new proteins in water-stressed seed compared to irrigated control. These data revealed that seed polypeptide composition of drought-tolerant peanut genotypes (Vemana and K-1375) was least affected while that of drought-susceptible genotypes (M-13 and JL-22) significantly altered due to water stress (WS). We have also found that in peanut leaf, ninety-six proteins were differentially expressed in response to water stress. Three proteins, glutamine ammonia ligase, chitinclass II and actin isoform B were found to be unique to tolerant cultivars. We have also discovered that four proteins, serine/threonine protein phosphate PP1, choline monooxygenase, peroxidase 43, and SNF1-related protein kinase regulatory subunit beta-2 which play a role as cryoprotectant through signal transduction and defense were induced in drought-tolerant (DT) cultivar following WS. Several of the leaf proteins that were overexpressed in DT cultivar followingWS were suppressed in susceptible cultivar. The comparative proteome analysis also revealed that inDT cultivar (Vemana)several enzymes involved in cell wall lignification such as methyl transferases, methionine synthases and peroxisome which function as a constitutive physical barrier to minimize the water loss were upregulated while in susceptible cultivar (Florunner)they were down-regulated resulting in weakening of cell wall during progressive dehydration. Further, in DT cultivar (Vemana), the photosynthesis mechanism seems to be least affected as is evident from the abundance of photosynthetic proteins of photosystem Iand II. These data suggest that an integrated approach using conventional as well as genetic engineering approaches are necessary to develop water stress-tolerant genotypes to increase water use efficiency of crop plants to improve productivity.