

# Efforts in improving drought stress tolerance biology essay

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Efforts in improving drought stress tolerance in the past through selective breeding and genetic engineering have had limited success because stress responses exhibit genetic complexity (Cushman and Bohnert, 2000). The susceptibility of crops to biotic and abiotic stress has increased due to drastic narrowing of genetic variation in plants resulting from domestication and selection (Forster et al, 2000). Humans naturally select for best yield in crops and neglect other characteristics which have resulted in the loss of many of the genes involved in drought stress tolerance. The primary response of plants to a state of water deprivation is the inhibition of shoot growth to allow essential cellular solutes to be diverted to stress related functions instead of promoting growth (Yang et al, 2010). By so doing, the plant ensures that it survives the drought period and can resume growth when the water deficit has been resolved. Through physiological and morphological change, plants have naturally evolved to adapt to environmental stress in their environments. These changes include how effectively the plant draws water from the soil, the cell and tissue water retaining capacity and control of water loss by transpiration and developmental adaptations to avoid water shortage during flowering (Yang et al, 2010). Tuberosa and Salvi (2006) noted that breeding programmes aimed at improving drought tolerance have had limited success in the past because of its quantitative genetic basis and the poor understanding of the physiological basis of yield in drought conditions. Plants utilize a number of signalling molecules such as abscisic acid (ABA) to regulate stress responsive genes that initiate the synthesis of transcription factors, chaperones and enzymes which enhance plant tolerance by vegetative growth attenuation,

osmoprotectant accumulation and reducing the rate of transcription (Yang et al, 2010). As reported by Yang et al (2010), de novo synthesized regulatory proteins such as transcription factors which are associated with drought response in Arabidopsis. In particular, the transcription factors from basic leucine zipper (such as ABA responsive element binding protein/ AREB binding factor), No apical meristem (NAM), cup-shaped cotyledon (CUC2), ATAF1-2, NAC (and stress responsive NAC), CCAAT-binding (such as nuclear factor Y) and zinc finger families (such as C2H2 zinc finger protein) have all been identified to be involved in regulating drought responses and the expression of transcription factors responsible for drought tolerance. Mitra (2001) reported that the mechanism of drought resistance can be categorized into drought escape, drought tolerance and drought avoidance although at any given time, plants initiate more than one of these mechanisms at any time, to become drought tolerant or resistant. Drought escape is the ability of the plant to hasten its phenological development to complete its life cycle before the water deficit develops. Drought avoidance is the ability of the plant to maintain high tissue water potential during a period of low soil moisture and involves increasing water uptake and storage and also reducing water loss. Drought avoidance involves increasing root depth and hydraulic conductance and also reducing water loss by decreasing epidermal conductance and leaf area. By employing these mechanisms, plants are able to balance turgor and reduce water loss. Serraj and Sinclair (2002) stated that osmolyte accumulation (OA) is a putative mechanism for survival and increased in crops under drought conditions. Osmotic adjustment (sometimes called osmoregulation) is the accumulation of

osmolyte compounds within plant cells and tissues and has been proposed to be an adaptive measure taken by plants subjected to drought. OA results in decreased osmotic potential and maintains water absorption and turgor pressure which contributes to physiological processes and has been a selection criterion in crop breeding to improve yield in dry or water shortage environments. A number of genes and cDNAs encoding osmolyte biosynthesis have been identified and introduced into the genome of transgenic plants. Molecular markers and quantitative trait locus (QTLs) associated with osmolyte accumulation have been already been investigated in wheat, rice, barley and sunflower. The most emphasised regulatory factor associated with drought tolerance is ABA which is synthesised de novo in response to drought conditions and high salinity. It has been demonstrated that overexpressing the gene encoding 9-cisepoxycarotenoid dioxygenase (NCED) (an enzyme in ABA biosynthesis) improves drought tolerance in transgenic *Arabidopsis* plants (Shinozaki and Yamaguchi-Shinozaki, 2007). An important mechanism that has been reported in drought response is the closure of the stomata and increased synthesis of abscisic acid (ABA) and the activation of ABA responsive genes (Xiong et al, 2006) and induces the expression of genes such as *rab18*, *rd298* and *kin1*. Mutant *ABA* *Arabidopsis* plants show that drought signalling is mediated by ABA dependent and ABA independent pathways and results in the activation of various drought induced genes (Luchi et al, 2001). ABA is a plant hormone that accumulates in many plant species when exposed to drought conditions. 75 AREB/ARF homologous have already been identified in the *Arabidopsis* genome. Overexpression of AREB1/ABF2, ABF3 or AREB2/ABF4 in transgenic

Arabidopsis plants resulted in an increased ABA response and reduced transpiration (Yang et al, 2010). Full-size image (93 K)Figure 1: The complexity of plant response to abiotic stress. Primary stresses, such as drought, salinity, cold, heat and chemical pollution, are often interconnected and cause cellular damage. The initial stress signals trigger the downstream signalling process and transcription controls, which activate stress-responsive mechanisms to re-establish homeostasis and to protect and repair damaged proteins and membranes. Inadequate responses at one or more steps in the signalling and gene activation process might ultimately result in irreversible changes in cellular homeostasis and in the destruction of functional and structural proteins and membranes, leading to cell death (Vinocur and Altman, 2005). During water deficit periods, maize plants reduce the rate of photosynthesis per plant (Bruce et al, 2002) due to a reduction in light interception and carbon fixation per unit leaf area. A major area of research remains understanding the molecular mechanisms involved in drought tolerance in plants because a better knowledge of these underlying mechanisms will provide the information required to engineer transgenic lines (Umezawa et al, 2006). Various responses to drought conditions such as gene expression alterations, accumulation of ABA and phytohormone and protein synthesis have been identified in plants. The strategy for genetic engineering to enhance drought tolerance in plants involves the introduction of functional genes that are involved in these mechanisms (Umezawa et al, 2006). Xiong et al (2006), investigated the inhibition of lateral root development as a response to drought stress. Drought inhibition of lateral root growth (DIG) loci was identified through

genetic analysis of transgenic *Arabidopsis* plants. They reported that the *DIG3* locus was required for ABA inhibition of lateral root growth is a possible target pathway for improving drought tolerance. Accelerated leaf senescence and leaf abscission, closing of the stomata to minimize water loss and shedding of older leaves are all methods undertaken by plants naturally in drought conditions (Rivero et al, 2007). Rivero et al (2009) reported that leaf senescence in transgenic plants can be delayed by inducing the expression of isopentenyltransferase (IPT) which catalyzes the rate limiting step in cytokinin (CK) synthesis. CK maintains stomata opening and increases stomatal conductance and transpiration and its accumulation is decreased during drought stress conditions. Gaxiola et al (2001) reported that transgenic plants overexpressing the vacuolar proton pumping pyrophosphate, *AVP1*, showed greater drought resistance than the wild type. In their study, they proposed that this increased resistance results from the accumulation of solutes by the plants. An external file that holds a picture, illustration, etc. Object name is pq1913893003. jpg Object name is pq1913893003. jpg

Figure 2: Wild-type and *AVP1* (*AVP1-1* and *AVP1-2*) transgenic plants deprived of water. Plants were watered with a diluted nutrient solution every 4 days for 4 weeks. At week 5, the plants were watered. The photograph corresponds to plants at day 10 of water-deficit stress (A) and the same plants 24 h after rewatering (Gaxiola et al, 2001). As reported by Shinozaki and Yamaguchi-Shinozaki (2007), the introduction of stress induced genes which code for amino acids, amines and various sugars and alcohols as well as LEA proteins and heat shock proteins has enhanced abiotic stress tolerance in transgenic plants. A gene encoding a key enzyme

in biosynthesis of the raffinose family oligosaccharide, called galactinol synthase (GolS), has been used to improve drought tolerance in transgenic *Arabidopsis* plants. Another transcription factor identified in *Arabidopsis* that has been implicated in drought tolerance is AtNF-YB1, a subunit of nuclear factor Y of the NF-Y complex which controls transcription through CCAAT DNA elements (Nelson et al, 2005). In their study, Nelson et al (2005) identified that the NF-YB protein in *Arabidopsis* and the NF-YB protein in *Zea mays* are orthologous so the phenomenon observed in *Arabidopsis* could be translated into maize as well. Figure 3: Expression of AtNF-YB1 confers drought tolerance in *Arabidopsis*. Pots of transgenic plants (Left) and controls (Right) are shown at the end of a dry-down period (Upper) and at 5 days after rewatering (Lower) (Nelson et al, 2005). Conventional breeding methods have had some success in producing varieties that have improved yield in drought conditions, particularly in cereals (Morison et al, 2008). Traditional breeding marker assisted selections have had very limited success unlike genetic engineering which has been proven to be the most effective method of inducing drought tolerance. The genes introduced into the plant genome directly or indirectly protect against environmental stress such as the over expression of biosynthetic enzymes for osmoprotectants (Holmberg and Bulow, 1998) and scavengers of reactive oxygen species (Cushman and Bohnert, 2000). Compared to conventional breeding approaches, genomics allow the opportunity for dissecting quantitative traits into genetic determinants called quantitative trait loci thus allowing marker assisted selection (MAS) (Tuberosa and Salvi, 2006). Genetic engineering has successfully been applied to various plant species such as rice, maize,

wheat, soybean and canola to produce drought resistant phenotypes modelled after results from analysis of transgenic Arabidopsis lines (Yang et al, 2010). There are currently 3 breeding approaches for drought resistance in plants. First is to breed under optimum conditions for high yield which ensures that the plants are at their optimum genetic potential. The second is to breed under drought conditions although this method encounters the problem that drought patterns are not constant every year. The final strategy is to improve drought resistance in high yielding genotypes (Mitra, 2001). Advances in biotechnology, bioinformatics, genomics and proteomics will aid the identification of other genes and pathways involved in biotic and abiotic stress in the future. Drought stress results in the loss of millions of tons of crops annually with equally devastating effect on the economy. The need for drought resistant crops is essential to keep up with the growing global population. Climate models have reported that global warming will lead to more frequent drought episodes around the world and thereby, new and more adaptive crop productive techniques need to be introduced to withstand the environmental changes (Rivero et al, 2007). Increasing crop resistance to drought would be of great economic value and would improve crop productivity and reduce agricultural demand on fresh water resources and as a result, screening for drought resistant crops has been a major goal for crop breeders (Xiong et al, 2006). The most effective approach to producing drought resistance crops is genetic mutation although it faces the problem of acceptance into the global market. A plethora of information has been documented on the genes, transcription factors, enzymes, hormones



and regulatory factors involved in drought tolerance and with further research, a possible solution could be in the very near future.