ABSTRACT: One of the main problems of corn cultivation and production is the lack of water resources, especially during periods of low rainfall which affect the vegetative growth rate and the amount of yield. Osmotic adjustment is effected by accumulation of free amino acids, proline and sugars in the roots and shoots. Accumulation of proline is a widespread plant response to environmental stresses, including low water potential. Proline has a clear role as an osmoticum. In particular, because of its high hydrophilic characteristics, proline acts as a compatible solute, one that can accumulate to high concentrations in the cell cytoplasm without interfering with cellular structure or metabolism. Proline is a non-protein amino acid that forms in most tissues subjected to water stress and together with sugar, it is readily metabolized upon recovery from drought. Proline fulfils diverse functions in corn plant. Proline synthesis has been associated with tissues undergoing rapid cell divisions, such as shoot apical meristems, and appears to be involved in floral transition and embryo development. High levels of proline can be found in pollen and seeds, where it serves as compatible solute, protecting cellular structures during dehydration. The proline concentrations of cells, tissues and corn plant organs are regulated by the interplay of biosynthesis, degradation and intercellular transport processes. Proline, which increases proportionately faster than other amino acids in corn plants under water stress, has been suggested as an evaluating parameter for irrigation scheduling and for selecting drought-resistant varieties.

Keywords: Proline, maize, drought stress, osmotic adjustment, regulation, metabolism

INTRODUCTION

Drought is undoubtedly the most important environmental stress for corn production and it is becoming an increasingly severe problem in many regions of the world and maintenance of corn water potential during water deficit is essential for continued growth and can be achieved by osmotic adjustment mechanisms resulting from the accumulation of compatible solutes (such as proline, glycinin betaine, organic acids, sugars as mannitol and sucrose) in the cytoplasm (Azarpanah, 2012; Verbruggen, 2008; Passioura, 2007). To improve corn productivity, it is necessary to understand the mechanism of corn responses to drought conditions with the ultimate goal of improving corn performance in the vast areas of the world where rainfall is limiting or unreliable (Umezawa, 2006; Kishor, 2005). In water deficit conditions corn plant water potential and turgor are reduced enough to interfere with normal functions (Zhang, 2008). Barker (2005) exhibited that shoot elongation was reduced by water stress during vegetative period in maize. Results illustrated that water balance parameters in drought resistant line 1304 and susceptible line 389 in maize exposed to 4 to 7 days of drought at the 5-leaf stage was studied. When influence of drought on water regime was checked, total osmotic potential values were lower in both lines (Barker,
2005). On the other hand, Studies on seed germination and seedling vigor for measuring drought tolerance of some maize genotypes indicated that germination stress, germination rate stress and seedling dry matter stress indices were influenced by both genotype and moisture stress level (Bruce, 2002). Choucan, (2007) showed that effects of soil drought on growth in a greenhouse experiment and reported that in maize the genetic variation in the degree of drought tolerance is better manifested under severe conditions of water deficit in the soil.

Drought stress delayed the silking and anthesis dates and reduced the grain filling period of each hybrid, but had little effect on the date of physiological maturity in maize (Golbashy, 2009). Golbashy, (2010) conducted an experiment to determine the effects of drought on the grain yield and yield components of maize. They reported that cob characteristics deteriorated and the economic yield of maize decreased significantly under drought conditions. The main factors that caused the reduction of yield were the decrease of kernels per ear and 100-kernel weight. For a long time, proline was considered as an inert compatible osmolyte that protects subcellular structures and macromolecules under osmotic stress (Yancey, 1982). However, proline accumulation can influence stress tolerance in multiple ways. Proline has been shown to function as a molecular chaperone able to protect protein integrity and enhance the activities of different enzymes. Examples of such roles include the prevention of protein aggregation and stabilization of 

The osmoprotection mechanism is based on intimate associations of non-toxic compounds with various cellular components. To survive under severe osmotic stresses, certain micro-organisms, algae and plants have evolved a high capacity to synthesize and accumulate non-toxic solutes, called osmoprotectants, osmolytes or compatible solutes. The accumulation of such compounds, mostly in the cytoplasm can protect cell membranes, proteins and metabolic machinery, which would preserve subcellular structure from damage as a result of cell
dehydration (Di Martino, 2006). Unfortunately, many investigations have not clearly differentiated between the osmoprotection and osmotic adjustment mechanisms and their respective roles in water-deficit response. It is often assumed that the increase in cellular osmolarity which results from the accumulation of compatible solutes is accompanied by influx or reduced efflux of water from cells, thus resulting in higher turgor and cell expansion (Hare, 1999). The accumulation of compatible osmoprotectant compounds has been a target for plant genetic engineering for more than 15 years and is still in progress for many crops. Genetic engineering for enhanced synthesis of osmoprotectants, such as proline and glycine betaine, is assumed to contribute to drought tolerance improvement.

**Improved soil water recovery in corn plants**

As discussed previously, corn yield increases must be associated with increases in transpirational water losses. Therefore, any putative benefit of OA under water deficit conditions invariably requires an increased recovery of soil water. Two hypothesis have been presented for OA to allow greater soil water uptake. One is to increase the gradient in water potential between the corn plant and soil and the second is to enhance the volume of soil being exploited for water.

**Drought Avoidance Mechanisms in corn plants**

Drought-avoiding corn plants have the ability to complete their life cycle without severe water deficits developing. Some ephemerals have a very short life cycle that can be completed during a brief rainy season. Other corn plants exhibit adaptations to increase water uptake and reduce water loss and thereby avoid drought (Figuera, 2004). It is an almost universal observation that the root: shoot ratio increases with water stress. Increases in root weight may be due to a greater density or depth of roots. Under water stress, new root growth extends into moist soil zones. As water deficits progress, the upper soil layers usually dry first. Thus shallower roots are common in wetter soils as opposed to deeper roots systems in dryer soils layer. Therefore, greater root growth into moist soil can result in drought avoidance (Arca, 2003). According to (Kim, 2000) reduced leaf area, deeper roots, and higher root: shoot ratios account for drought avoidance in most corn species. Root length, density and diameter help determine the ability of the plant to acquire soil water. Severe drought stress may result in increased levels of ABA and subsequent leaf abscission, thereby reducing transpirational demand. These developmental changes within corn plants during water stress are important morphological drought-avoiding adaptations that maintain water potential (Lawlor, 2002).

**Some Biochemical Drought Tolerance Mechanisms in corn plants**

Corn resort many adaptive strategies in response to abiotic environmental stresses such as dehydration and excessive osmotic pressure. These adaptive mechanisms include changes in physiological and biochemical processes. Among them, the accumulation of compatible solutes according to the metabolic responses has drawn much attention (Cattiveli, 2008). Adaptation to all these stresses is associated with metabolic adjustments that lead to the accumulation of several organic solutes like sugars, polyols, betaines and proline (Passioura, 2007). The compatible solutes may be classified into two categories: one is nitrogen-containing compounds such as proline and other amino acids, quaternary ammonium compounds and polyamines and the other is hydroxy compounds, such as sucrose, polyhydric alcohols and oligosaccharides (Vendruscolo, 2007). The accumulation of the amino acid proline in tissues of several plant species is regarded as a general response to water and other kinds of stresses (Caballero, 2005). In fact, Proline is a proteinogenic amino acid with an exceptional conformational rigidity, and is essential for primary metabolism and A dramatic accumulation of proline due to increased synthesis and decreased degradation under a variety of stress conditions, such as salt, drought and metals, has been documented in different corn plant species (Roberts, 2002). It should be pointed out the first report on proline accumulation in wilting perennial rye grass (Lolium perenne)( Kemble, 1954). Furthermore, This strong accumulation of cellular proline (up to 80% of the amino acid pool under stress compared to 5% under normal conditions) seems to have diverse physiolo- gical roles, such as acting as a compatible osmolyte for osmotic adjustment, stabilization of proteins, membranes and subcellular structures, buffering cellular redox potential and protecting cellular functions by scavenging reactive oxygen species (ROS) (ober, 2003). Water stress in corn plants due to drought can lead to major physiological and biochemical disruptions, such as reduced photosynthesis, and marked changes in gene expression (Tyerman, 2002). Physiological changes under drought stress are often reflected at the transcription level, where the levels of mRNA related to key processes such as photosynthesis are down-regulated (Zhang, 2008). When corn plants experience water deficits, stomatal pores progressively close (Trouverie, 2003). This process is regulated largely by leaf water potential but can be mediated by ABA. Stomatal
Proline biosynthesis responses to drought stress in corn plants

Proline (PRO) acts as a compatible osmolyte since it can accumulate to high concentrations without damaging cellular macromolecules. Proline can also serve as a nitrogen carbon source in the cell (Kishor, 2005). Moreover, PRO has a protective action which prevents membrane damage and protein denaturation during severe drought stress. Thus, proline can be used as a metabolic marker in relation to stress (Umezawa, 2006). In addition to acting as an osmo-protectant, proline also serves as a sink for energy to regulate redox potentials, as a hydroxyl radical scavenger (Heidari, 2006), as a solute that protects macromolecules against denaturation and as a means of reducing acidity in the cell (Raymond, 2002). The oxidation of proline was catalysed by two enzymes, proline oxidase and proline dehydrogenase (Tyerman, 2002). Furthermore, proline accumulation was found to be independent of the levels of ABA, which accumulates more rapidly in stressed leaves (Roberts, 2000). The former is localized in the inner mitochondrial membrane and requires oxygen as the electron acceptor, while the latter is localized in the cytosol and occurs as an active site on a protein which also functions as pyrroline 5 carboxylate (P5C) reductase. P5C reductase and proline dehydrogenase catalyse reactions with the same reactions and coenzymes, but working in opposite directions (Kishor, 2005). Several investigators have proposed the beneficial effects of proline accumulation as a compatible osmotic solute as a protein stabilizing or solubilizing factor under limiting cell water conditions and as a source of reduced nitrogen and carbon (Umezawa, 2006). It has also been proposed that PRO can act as an electron acceptor, avoiding damage of photo- systems due to their photoinhibition by activated oxygen species (Raymond, 2002). The role of proline in response to osmotic stress includes a very important part in the biosynthesis of cell-wall matrix proteins, such as extensins, that have important roles in cell morphology and provide mechanical support for cell under stressed conditions (Caballero, 2005). In corn plants, proline is synthesized from either glutamate or ornithine (Vendruscolo, 2007). The first two steps of proline biosynthesis from glutamate are catalyzed by a single bio functional enzyme, Δ1-pyrroline-5-carboxylate synthetase (P5CS), which produces glutamic g-semialdehyde (GSA). This GSA is spontaneously converted to pyrroline-5-carboxylate (P5C) that is reduced by P5C reductase (P5CR) to proline (Raymond, 2002). Corn Plants also synthesize proline from ornithine, catalyzed by ornithine-d-aminotransferase (OAT). In corn plants, OAT transaminates ornithine directly to GSA, which is subsequently converted to proline via P5C (Ribarits, 2007). Furthermore, the accumulation of proline also depends on its degradation, which is catalyzed by the mitochondrial enzyme proline dehydrogenase (ProDH) (Xue, 2009). The onset of stress-induced proline accumulation is correlated with transcriptional activation of the gene encoding P5CS, which is the key regulatory and rate-limiting enzyme in this biosynthetic pathway (Xue, 2009). In fact, Arginase and OAT are the key enzymes of the ornithine pathway of proline biosynthesis in corn plants (Zhang, 2007; Ashraf, 2007).

Proline in corn plant development

Increasing amounts of data suggest that proline has certain regulatory functions, controls corn plant development and acts as a signal molecule. The level of free proline varies considerably in different corn plant organs and is usually higher in reproductive organs than in vegetative tissues (Aroca, 2003). Proline, glycine betaine, K+, and carbohydrates have been reported to accumulate as stress responses in maize. The source of proline production in maize is reported to be mature chloroplasts (Passioura, 2007) and endosperm of germinating seedlings (Raymond, 2002). According to Roberts (2000) addition of ABA to maize tissues did not result in proline accumulation. However, Kishor (2005) working with maize seedlings grown in vermiculite for stress concluded that increased ABA is required for proline accumulation in the growing region of maize roots. (Ober, 2003) observed that ABA-treated maize had double the amount of proline and increased osmotic adjustment and greater drought tolerance. These findings suggest that, in maize under drought stress, ABA could be required for proline accumulation. Perhaps this might depend on the experimental tissue or its stage of development. Although the importance of proline accumulation in the adaptation of corn plants to environmental stress has been demonstrated, information on signaling mechanisms that regulate proline synthesis and degradation is scarce. Several signaling molecules, including ABA, Ca2+ and phospholipase D, have been suggested (Jafari, 2009). The ornithine pathway has been suggested to be important during seedling development and in corn plants for stress-
induced proline accumulation (Shoa, 2007). A p5cs2-knockout mutant displays embryo lethality and proline-rescued mutant corn plants show aberrant growth, implying that an adequate proline supply is essential for embryo and corn plant development (Rhodes, 1986). P5CS2 and proline were suggested to regulate cell division and embryogenesis (Meier, 1982). Although proline is usually considered to be a metabolite with protective functions, several reports show that, under certain conditions, exogenous proline can be deleterious to plants and can inhibit growth and cell division (Hoekstra, 2001). In yeast, proline can interact with the Put3p transcription factor and convert it from a transcriptionally inactive to an active form. Active Put3p promotes the expression of specific genes, including those that control proline catabolism (Jafari, 2009).

**Regulation of proline metabolism in corn plants**

Proline biosynthesis is activated and its catabolism repressed during dehydration, whereas rehydration triggers the opposite regulation (Voetberg, 1991). Proline biosynthesis is controlled by the activity of two P5CS genes in corn plants, encoding one housekeeping and one stress-specific P5CS isoform. Although the duplicated P5CS genes share a high level of sequence homology in coding regions, their transcriptional regulation is different (Peng, 1996). Under non-stressed conditions, phospholipase D (PLD) functions as a negative regulator of proline accumulation (Bellinger, 1987). As well as transcriptional regulation, P5CS activity is under metabolic control, as seen by feedback inhibition of P5CS by proline (Caballero, 2005). Loss of feedback inhibition of P5CS leads to elevated proline accumulation (Morgan, 1984). Whereas proline biosynthesis is upregulated by light and osmotic stresses, proline catabolism is activated in the dark and during stress relief, and is controlled by PDH and P5CDH (Hoekstra, 2001). PDH transcription is activated by rehydration and proline but repressed by dehydration, thus preventing proline degradation during abiotic stress (Passioura, 2007). PDH1 transcription is repressed during daylight and induced in darkness; therefore illumination has opposite effects on P5CS1 and PDH1 transcription (Aroca, 2003). Promoter analysis of PDH1 identified the proline and hypo-osmolarity-responsive element (PRE) motif ACTCAT, which is necessary for the activation of the PDH gene (Rhodes, 1986). Such a connection between photosynthesis and proline metabolism is supported by light-dependent proline accumulation, which is regulated by the light-controlled reciprocal P5CS and PDH gene activation (Wang, 2003). In mitochondria, proline has distinct protective functions. After stress, proline pools supply a reducing potential for mitochondria through the oxidation of proline by PDH and P5CDH, provide electrons for the respiratory chain and therefore contribute to energy supply for resumed growth (Yancey, 1994). Proline catabolism is, therefore, an important regulator of cellular ROS balance and can influence numerous additional regulatory pathways. The capacity for proline hyperaccumulation therefore accompanies the extremophile character of certain plant species and is likely that it contributes to their stress tolerance; however, it is not an absolute requirement for adaptation to extreme environmental conditions. Although proline has long been considered as a compatible osmolyte, recent results highlight its multiple functions in stress adaptation, recovery and signaling. Compartmentalization of proline biosynthesis and degradation in the cytosol, chloroplast and mitochondria add to the complexity of functional diversification of proline metabolism (Marur, 2007). Stabilization of proteins and protein complexes in the chloroplast and cytosol, protection of the photosynthetic apparatus and enzymes involved in detoxification of ROS are an important, but not the only function of proline accumulation during drought stress (Larher, 1993). The enhanced rate of proline biosynthesis in the chloroplasts can contribute to the stabilization of redox balance and maintenance of cellular homeostasis by dissipating the excess of reducing potential when electron transport is saturated during adverse conditions. Proline catabolism in the mitochondria is connected to oxidative respiration and administers energy to resumed growth after stress. Moreover, proline oxidation can regulate mitochondrial ROS levels and influence programmed cell death (Levitt, 1980). The complexity of the regulation of proline metabolism and multiple functions of proline illustrate the difficulties of improving plants of agronomic interest by the modified expression of genes involved in this metabolism. One option is the enhancement of proline biosynthesis via increased expression of rate-limiting genes in transgenic plants.

**Proline transport in corn plants**

Compartmentalization of proline metabolism implies that extensive intracellular proline transport must occur between the cytosol, chloroplasts and mitochondria (Larher, 1993). Physiological data suggest that proline uptake into mitochondria is an active process, hinting at the existence of specific amino acid transporters (Yancey, 1994). Plasma membrane proline transporters, identified in corn plants mediate proline transport between cells and organs, but are not involved in organellar transport (Wang, 2003). The recently discovered PSC–proline cycle can deliver electrons to mitochondrial electron transport without producing glutamate and, under certain conditions, can generate more ROS in the mitochondria (Marur, 2007). Evidence connecting changes in proline content with
transport processes comes from developmental as well as stress-related studies. The proline deposition in the elongation zone of maize roots at low water potential was not achieved by biosynthesis but by an increase in proline transport (Kishor, 1995). Another study using maize seedlings demonstrated that proline utilization exceeds biosynthesis and that proline, provided by degradation of proline-rich storage proteins of the endosperm, is imported into the seedling (Patel, 1985). Proline has been detected in both phloem and xylem sap in several corn plants species (Zhang, 2008). Girdling experiments revealed increased proline levels in leaves and reduced proline concentrations in sink organs, also suggesting proline translocation from stressed leaves to culms and roots (Kishor, 1995). As proline metabolism is confined to distinct cellular compartments, intracellular transport of proline is required. Proline biosynthesis takes place in the cytosol and probably in chloroplasts under stress conditions (Marur, 2007). Thus, at least in the absence of stress proline import into plastids is necessary. Furthermore, transfer into mitochondria is essential for proline catabolism. Whereas to our knowledge, information on proline transport into or out of plastids is lacking, proline uptake into mitochondria has been demonstrated to be mediated by two transport systems, i.e. a proline unipporter as well as a proline/glutamate antiport system (Zhu, 2000), though a reversible switch of the transport mode as shown for other mitochondrial carriers cannot yet be excluded (Delauney, 1993). However, no genes encoding intracellular transporters have been identified in corn plants so far.

Some Maize-Specific Responses to Drought Stress

Maize is grown all over the world under a wide range of conditions. Wherever it is grown, drought can cause yield reductions (Nayyar, 2003). Genotypic differences have been identified for a range of morphological and physiological characteristics and responses of maize to water stress. An increase in root growth and increased root:shoot ratio by plants growing in conditions of water stress may be an important adaptive feature (Vamerali, 2003). At water potentials that completely inhibited shoot growth, the primary root continued to grow in maize (Lawlor, 2002). In some cases, the roots of drought stressed corn plants were thicker and more cylindrical (Kishor, 2005). Thickened roots could result in lowered resistance to water flow within the roots and between the roots and the shoots (Zhang, 2008). Accumulation of ABA under water stress has been reported to maintain root growth and inhibit shoot growth in maize seedlings (Nayyar, 2003). This observation was supported by (Heidari, 2006), who showed a significant negative relationship between the rate of leaf expansion and concentration of ABA in xylem of maize under drought stress. Lawlor, (2002) reported in maize, which is a C₄ plant, that inhibition of net photosynthesis by water stress was due more to stomatal closure and reduced CO₂ diffusion than to inhibited CO₂ metabolism. This depended on the speed of dehydration, as rapid dehydration led to inhibition of CO₂ metabolism due to down regulation of the Calvin cycle enzymes namely phosphoenolpyruvate, malate dehydrogenase, and malic enzyme (Roberts, 2000). Sucrose is the transported sugar in most higher plants. Sucrose, as it cannot be used directly for most metabolic processes, must be cleaved into hexoses (glucose and fructose) by invertase and sucrose synthase (Aroca, 2003). Maize under water stress has increased invertase activity resulting in hexose accumulation in leaves (Nayyar, 2003). It has also been observed that invertase (Ivr2) gene expression was enhanced by ABA supply in maize leaves (Wei, 2000). Therefore the accumulation of glucose and fructose in maize experiencing drought may be involved in a signal transduction pathway or an increase in osmotic pressure leading to drought stress tolerance. Like other plants, maize under water stress accumulates proteins. Abscisic acid (ABA) was found to increase synthesis of unidentified proteins in both water stressed and non-water stressed maize seedlings (Cattivelli, 2008). In the same study, water stress also caused reduction in overall protein synthesis, which recovered to normal levels upon dewatering if the stress had not been severe. Water stress and ABA induced the RAB17 LEA protein in maize embryogenesis and vegetative growth (Vamerali, 2003). According to Wei, (2000) ABA induced the synthesis of RAB17 mRNA and protein in maize calli and embryos, where protein phosphorylation was found only in the maize embryos. Thus maize under water stress has altered protein synthesis, which in this case is the RAB (Responsive to ABA) protein. The other unidentified proteins that were induced under water stress (Cattivelli, 2008) to be water channel proteins. Water stress in maize has been found to cause oxidative damage and to elicit the counteractive enzymatic and non-enzymatic antioxidant system. When drought-tolerant (PAN 6043) and sensitive (SC 701) hybrids were exposed to water stress (-0.5 MPa), H₂O₂ and MDA levels increased, and their values were higher in the sensitive than the tolerant genotype (Zhang, 2008). Therefore the enzymatic antioxidant system appears to be one of the most important water stress tolerance mechanisms in many plants, including maize. In summary, when maize is experiencing a water deficit, morphological, physiological, and biochemical changes occur. In almost all the cases, the changes are mediated by or appear to be related to changes in ABA levels. Aslam, (2006) made diallel cross of 6 drought tolerant lines of maize with one drought susceptible variety under rain fed condition in which dominance gene action was important.
for stomata number and leaf number. In the maize the root weight increased whereas shoot weight decreased with water stress (Shoa, 2007).

CONCLUSIONS

Maize is a popular crop in the semi-arid regions of the world where periodic droughts are common. Under water stress, maize exhibits most of the responses mentioned, including both developmental (morphological) and biochemical changes: increased root to shoot ratio; accumulation of proline, glycine betaine, and soluble sugars; and increased antioxidant enzyme activities. Genetic modification of maize plants by breeding to allow growth and yield under water deficits is one approach to dealing with drought stress. This strategy has been employed over the years to produce drought-resistant maize varieties. However, this approach is time consuming and demands sustained effort. In conclusion, the results discussed here support the hypothesis that PRO accumulation during drought stress is a part of a physiological response of corn plant to the imposition of an intense drought stress. These results suggest that it might not be the actual proline content, but the enhanced rate of proline biosynthesis that is an important factor for stress adaptation. Engineering strategies could therefore target the proline biosynthetic pathway, and aim to accelerate proline biosynthesis in the chloroplasts.

The information presented above can be summarized as follows:
1. It is important to choose the corn plant organ in which proline and other related substances accumulate more readily, since accumulation was found to vary among corn plant organs. There is strong evidence in cereals that the accumulation is more intense in stems, especially when sheaths are included, than in leaves.
2. Proline is clearly the substance most readily accumulating in water-stressed corn plants. Other amino compounds and sugars, with the exception of betaine for some species, are of minor importance in terms of the sensitivity of the stress-induced concentration although they may exhibit significant correlations with the accumulation of proline.
3. Corn Plant development is a factor which has to be seriously taken into account although its effects may be affected or even confused by those arising from the previous stress history of corn plants. It is suggested to sample and examine corn plants at comparable growth stages, or, at least, not to mix results from contrasting stages early and too late stages, in order to avoid misleading interpretations.
4. The effect of corn genotypes on the accumulation intensity is clear and may arise from their growth habit. It appears that the higher the growth rates at a given stage, the higher the potential for accumulation.
5. The length of the biological cycle may also be another important factor, with the late corn genotypes tending to exhibit higher concentrations than the earlier ones.
6. A possible association of proline accumulation with the drought resistance of Different corn genotypes will obviously have a major practical importance: it would provide an easy screening criterion to corn plant breeders and help agronomists to assess the field performance of corn genotypes.
7. Under drought stress conditions, corn plants activates osmotic adjustment mechanisms not only in leaves, but also in roots, in such a way increasing its capacity to extract water from dry soil.
8. The results obtained in this investigation may be important for a more complete understanding of the behaviour of the vegetative growth of olive tree plants in semi-arid regions.
9. Improvement of drought tolerance of corn plants via engineering proline metabolism is an existing possibility and should be explored more extensively. The fact that proline can act as a signaling molecule and influence defense pathways, regulate complex metabolic and developmental processes, offers additional opportunities for plant improvement.

Further studies are required to study the feasibility to engineer flowering time or to improve defenses against certain pathogens via the targeted engineering of proline metabolism.

REFERENCES


