

Drought tolerant rice: metabolic engineering and dissecting proteomics in understanding the system

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Abiotic stress is a complex phenomenon which is less understood but causes severe yield losses in major crops globally. Since decades, work is in progress on developing climate-resilient crops using conventional breeding, molecular breeding, and genetic engineering to come up with designer crops suitably adapted across the ecosystems. With advancement of new tools including CRISPER-genome editing, new insights on better crop development might be gained in the near future. Earlier we developed *DREB1A*-based engineered rice driven by the drought/salinity responsive promoter rd29, and showed enhanced drought-tolerant rice (Datta et al 2012). It is well known that plant tolerance to drought is mediated by a number of physiological and biochemical processes, which means that it is a multi-gene trait. The activation of such genes must involve a distinc-

tive set of transcription factors. By over-expressing transcription factor gene(s), it may be possible to change or to increase the level of expression of several downstream target genes responsible for drought (Varshney et al., 2011). Based on drought-tolerant rice plants by over-expressing *Arabidopsis DREB1A*, the metabolic network regulated in the drought-tolerant transgenic rice has been studied. We have demonstrated the comparative proteome analysis between the roots of wild type and transgenic *DREB1A* plants under drought stress condition. The study identified that stress- and defense-related proteins are especially up-accumulated under drought stress in both the plants (Paul et al 2016). A novel protein, R40C1, was reported to be significantly up-accumulated in roots of transgenic plants, which is likely to play a significant role in generation of drought-tolerant plants.

Genetic engineering approaches for drought tolerance in grain legumes: progress and prospects

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Inadequate water resources and the ensuing climate change over the recent years are posing major challenges for food production. Drought in various forms is responsible for major losses to global crop production, affecting millions of resource-poor farmers in the semi-arid tropics. While developing drought-tolerant cultivars could alleviate such economical strains, genetic improvement of grain legumes is difficult to achieve through conventional means due to their highly self-pollinating characteristics and conserved genomes with very little variability. To generate additional genetic diversity, we attempted to enhance drought tolerance in chickpea and peanut through genetic engineering approaches. Independent transgenic events with high transpiration efficiencies (TE) and desirable root and shoot traits were selected for further evaluation under a series of environments under glasshouse and confined field tri-

als to comprehensively study the component traits of drought, and understand the stress adaptive mechanisms. Relationship between TE and its surrogate traits were explored, besides studying the role of biochemical changes in the anti-oxidative machinery under water-limiting conditions. Evaluations were based on water capture, effective use of captured water for producing biomass via photosynthesis, and converting assimilates into harvestable yield. Accordingly, critical assessment of drought tolerance and yield under contained field conditions proved the effectiveness of several events that showed substantial yield improvement under drought stress, without any accompanying yield penalty under irrigation. Details of various strategies to develop drought tolerant transgenic plants, and the results and scope of our own studies will be discussed.