



Transgenic and Molecular Breeding Approaches for Drought Stress Tolerance

*Shubham Khichi and Yudhishtir Bhanwariya

Ph.D. Scholar, Department of Genetics and Plant Breeding, Agriculture University,
Jodhpur, Rajasthan, 342304, India

*Corresponding Author's email: shubhamkhichi32@gmail.com

The world is growing swiftly and will have 9.7 billion people by the year 2050. The rapid development and quick climatic change has led to increasing occurrence of abiotic stressors which have major impact on the crop growth and productivity worldwide. The most acute of these environmental concerns is water deficiency, commonly known as “drought” which affects crops and endangers the livelihoods of farmers, especially in semi-arid areas. For instance, drought causes US\$ 520 million losses in groundnut production each year. Drought stress is a complex phenomenon with many physiological and biochemical effects. Plants develop large levels of harmful reactive oxygen species (ROS), such as H₂O₂ and O₂⁻, under drought stress, which can lead to cell death. ROS adversely affect the synthesis of chlorophyll, photosynthetic capability and general metabolic activities like stability of proteins and lipids. Traditional breeding has improved agricultural yields by selecting for early maturity to “escape” drought, but this strategy has serious drawbacks. Traditional approaches to selection for yield are constrained by substantial genotype by environment (G×E) interactions under stress. Traditional labor intensive procedures are likely to convey undesirable genes together with desired genes. Thus, modern plant biotechnology, including molecular breeding, transgenic techniques, and genome editing, gives options for rapid and accurate genetic changes.

Molecular breeding and QTL mapping of drought resistance

Genetic breeding uses genetic markers to discover specific sections of the genome associated with complex traits, such as drought tolerance, known as Quantitative Trait Loci (QTL). This approach provides the basis for marker assisted selection (MAS) where breeders can select for desirable traits more effectively than phenotypic selection alone.

Important success stories of QTL in cereals

For several of the major mandate crops important progress has been made in discovery and transfer of QTLs for drought tolerance for:

A major QTL for grain yield and Panicle Harvest Index (PNHI) under terminal drought was identified on linkage group 2 (LG2). Marker-assisted backcrossing (MABC) was successfully employed to Introgress the tolerant allele at this QTL into sensitive backgrounds to generate introgression lines with better drought resistance.

Sorghum: The “stay-green” breeding objective permits plants to retain green leaves and continue photosynthesizing when soil moisture levels are low. Key QTLs for this trait (stg1, stg2, stg3 and stg4) have been introgressed into senescent lines using MABC and resulted in improved stover quality and grain yield under terminal stress.

Rice: Drought yield is a complex trait controlled by numerous QTLs; editing of these yield-related QTLs either alone or in multiplex can lead to substantial increases in performance in drought prone locations.

Methods for integrated QTL mapping

Candidate genes were found by combining standard QTL mapping and modern “omics” techniques. In tomato, integration of QTL-seq and RNA-seq led to the identification of candidate genes, SICathB2 and SIGST, in key QTL areas associated with stress tolerance.

Functional and transgenesis approaches of genomics

Transgenic breeding is direct manipulation of the genes to get the desired phenotypes. This allows scientists to break down reproductive barriers between species and to directly target the signaling pathways involved in the perception and response to stress.

Master regulators 3.1.1 Transcription Factors (TFs)

Transcription factors are important to the activation of stress-responsive genes that encode proteins that protect cells. Dehydration-responsive element binding (DREB1) factors are involved in the regulation of expression of genes associated with drought and cold tolerance. NAC members. They are responsible for growth and defence of the plant. OsNAC10 overexpression enhances rice drought tolerance and grain yield. Another study demonstrated OsNAC6 regulated root architecture for tolerance. WRKY and MYB Factors: These TFs are known to be engaged in vast regulatory networks of metabolism and abiotic stress responses. WRKY genes are induced by drought and salinity in oil palm.

Plant hormones and signal transduction pathways

Drought stress perception initiates signaling cascades that are regulated by phytohormones such as Absciscic Acid (ABA). SnRK2 Kinases - phosphorylate specific ion channels that lead to the closure of stomata under drought conditions. ZmPP2C-A and other maize genes confer drought tolerance via regulating ABA production and defense-related genes in PP2C Clade A.

Removing ROS

The main mechanisms of drought tolerance in transgenic plants are linked with the increased antioxidant defense system. Water deficiency results in ROS production which are harmful. Transgenic lines overexpressing enzymes including Superoxide Dismutase (SOD), Catalase (CAT) and Ascorbate Peroxidase (APX) aid to detoxify the ROS.

MiRNAs

MicroRNAs (miRNAs, 21-24 nt) are involved in post-transcriptional regulation of gene expression in response to drought stress. Plants respond to drought by up or down regulation of expression of certain miRNAs targeted on mRNA for destruction or translational inhibition. miR319 Drought responsive, implicated in leaf growth and hormone miR169: A big and conserved family involved in drought and salt tolerance in diverse species miR393: Associated with rice flowering control and early stress response and highly activated in water deficit.

Gene Editing: the future of CRISPR/Cas9

The emergence of CRISPR/Cas9 technology has transformed the crop improvement by delivering a fast, precise and efficient genome editing tool. CRISPR technology can knockout or modify the endogenous genes precisely, instead than introducing foreign DNA as the transgenic approach.

Precision Genome Engineering Strategies for Stress Tolerance

Individual Gene Targeting: The NAC2 Gene Targeting to Improve Water Use Efficiency in Arabidopsis.

Fast breeding approaches: state-of-the-art technologies like IMGE (haploid-inducer mediated genome editing) and Hi-Edit integrate haploid induction with CRISPR/Cas9 to quickly insert drought-tolerant characteristics into elite lines in two generations, skipping years of backcrossing. CRISPR may be used to simultaneously edit several genes or QTLs involved in complicated stress responses, unlike other approaches.

Conclusion

Together molecular breeding and transgenic technologies are projected to produce a “second green revolution” to meet the world’s food needs in the face of climate change. Conventional breeding has paved the way, but current methods like QTL mapping, manipulation of transcription factors and CRISPR/Cas9 enable the accuracy to tackle the intricate genetics of drought tolerance. More research on these bioengineered (BE) crops is needed to avert millions from starving and to provide nutritional security for the growing population.

References

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