

A Report on Drought Tolerance in Rice **Tong Wang ***

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Perspective

Rice is one of the world's most important cereal crops, feeding more than half of the world's population. However, as the human population has continued to grow for several decades, a rice shortage has become an urgent threat to breeders. Rapid climate change has further reduced rice yield. As a result, breeders must act quickly to implement advanced breeding methods that will not only increase rice yield but also make rice more environmentally adaptable.

Rice (*Oryza sativa* L.) is a staple food crop that feeds more than half of the world's population and has two subspecies, indica and japonica that are native to tropical or subtropical regions. Rice is a cold-sensitive crop, so cultivation in cold environments is limited. In comparison to indica, japonica is primarily planted at higher altitudes and latitudes. As a result, japonica rice is more cold tolerant than indica rice.

Drought tolerance is a significant quantitative trait with multifaceted phenotypes that are frequently complicated by plant phenology. Different types of environmental stresses, such as high irradiance, high temperatures, nutrient deficiencies, and toxicities, can all challenge crops at the same time, making drought tolerance breeding extremely difficult. Interdisciplinary researchers have been using various methods to dissect and comprehend the mechanisms of plant tolerance to drought stress; however, the limited success of molecular breeding and physiological approaches suggests that we reconsider our strategies. Recent genetic techniques and genomics tools, combined with advances in breeding methodologies and precise phenotyping, will almost certainly reveal candidate genes and metabolic pathways underlying crop drought tolerance. The WRKY transcription factors are involved in a variety of biological processes that occur during plant development. This zinc (Zn) finger protein family is found only in plants, particularly members that respond to and mediate stress responses. There are 89 WRKY genes in japonica and 97 WRKY genes in *O. nivara* (OnWRKY) that have been identified and mapped to individual chromosomes.

To improve rice (*Oryza sativa* L.) drought tolerance, research programmes should use a multidisciplinary approach that includes the interaction of plant phenology and multiple stresses, as well as the combination of drought tolerance traits with various genetic and genomics approaches, such as microarrays,

quantitative trait loci (QTLs), WRKY gene family members with drought tolerance roles, and transgenic crops. This review discusses the most recent advances in plant physiology for precise phenotyping of plant responses to drought, as well as methods for updating drought tolerance analysis in rice. Finally, a strategy for selecting a specific environment and adapting suitable germplasm to that environment is proposed based on the physiological/morphological and molecular mechanisms found in resistant parent lines.

Drought tolerance is a complex mechanism that is influenced by plant phenology and controlled by several quantitative trait loci (QTLs). The plant response is complex and difficult to comprehend unless the genetic and physiological bases of these responses are thoroughly investigated. If the molecular mechanisms correlated with seed yield stability are not well understood, neither modern genetics nor traditional breeding can effectively improve crop plant drought tolerance. Advances in systematic plant genomics, phenotyping, and plant physiology result in new crop drought tolerance discoveries. As a result, crop breeders will be able to increase crop yields by utilising the most recent gene network information and plant improvement tools. As we gain a better understanding of the complex drought tolerance network and its relationships with various traits, successful genomics and molecular biology approaches, as well as increased selection efficiency, will lead to the identification of candidate QTLs and genes associated with these traits. To exploit QTLs for crop improvement, molecular breeding approaches can be used; thus, candidate genes are the main targets for genetic engineering and the production of transgenic lines.

The identification of candidate genes responsible for plant

tolerance under various abiotic stresses, as well as the use of the most appropriate promoters associated with these events is critical for developing transgenic crops with enhanced drought stress tolerance. Despite the fact that genetic engineering approaches are expensive and have a negative public perception of biosafety, "molecular breeding" and "Induced Local Lesions in Genome" (TILLING) products are widely accepted. QTLs are typically found as part of linkage mapping or linkage analysis-based QTL mapping. Traditional QTL mapping entails mapping populations with traits correlated with drought tolerance; identifying polymorphic markers; genotyping the mapping populations with polymorphic markers; constructing genetic maps; accurately phenotyping based on drought tolerance-

correlated traits; and finally, QTL mapping based on genotypic and phenotypic data.

Several drought tolerance linkage mapping studies on various crops have been conducted. Due to the inherent limitations of mapping populations, linkage analysis-based QTL mapping cannot provide detailed information about QTLs. Among these limitations are the following: Due to insufficient time for recombination, insufficient phenotypic variation related to existing traits in the mapping population, and segregation of different QTLs linked to the same traits in diverse mapping populations, the identified QTLs are commonly associated with large chromosomal segments or genomic regions.