Improvement of drought tolerance in rice (Oryza sativa L.): genetics, genomic tools, and the WRKY gene family

ABSTRACT

Drought tolerance is an important quantitative trait with multipart phenotypes that are often further complicated by plant phenology. Different types of environmental stresses, such as high irradiance, high temperatures, nutrient deficiencies, and toxicities, may challenge crops simultaneously; therefore, breeding for drought tolerance is very complicated. Interdisciplinary researchers have been attempting to dissect and comprehend the mechanisms of plant tolerance to drought stress using various methods; however, the limited success of molecular breeding and physiological approaches suggests that we rethink our strategies. Recent genetic techniques and genomics tools coupled with advances in breeding methodologies and precise phenotyping will likely reveal candidate genes and metabolic pathways underlying drought tolerance in crops. The WRKY transcription factors are involved in different biological processes in plant development. This zinc (Zn) finger protein family, particularly members that respond to and mediate stress responses, is exclusively found in plants. A total of 89 WRKY genes in japonica and 97 WRKY genes in O. nivara (OnWRKY) have been identified and mapped onto individual chromosomes. To increase the drought tolerance of rice (Oryza sativa L.), research programs should address the problem using a multidisciplinary strategy, including the interaction of plant phenology and multiple stresses, and the combination of drought tolerance traits with different genetic and genomics approaches, such as microarrays, quantitative trait loci (QTLs), WRKY gene family members with roles in drought tolerance, and transgenic crops. This review discusses the newest advances in plant physiology for the exact phenotyping of plant responses to drought to update methods of analysing drought tolerance in rice. Finally, based on the physiological/morphological and molecular mechanisms found in resistant parent lines, a strategy is suggested to select a particular environment and adapt suitable germplasm to that environment.