Recent Advances in the Drought Stress Tolerance in Rice

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Abstract

Many studies were done in the development of drought stress-tolerant transgenic plants, including crop plants. Rice is considered to be a vital crop target for improving drought stress tolerance. Much transgenic rice showed improved drought stress tolerance was reported to date. They are genetically engineered plants that are developed by using genes that encode proteins involved in drought stress regulatory networks. These proteins include protein kinases, transcription factors, enzymes related to osmoprotectant or plant hormone synthesis, receptor-like kinase. Of the drought stress-tolerant transgenic rice plants described in this review, most of them display retarded plant growth. In crop crops, plant health is a fundamental agronomic trait that can directly affect yield. By understanding the regulatory mechanisms of retarded plant growth under drought stress, conditions are necessary precursors to developing genetically modified plants that result in high yields.

Introduction

A twenty-first-century challenge is the production of sufficient food to meet population demands despite reductions in the quantity and quality of arable land and water and increasingly variable weather patterns that are associated with climate change (FAO). Crop losses due to extremes environment have risen steadily over the past several decades, and climate models predict an increased incidence of floods, droughts and extreme temperatures, salt stress, and cold temperature (Kumar, Kumar, et al., 2013, Kumar, 2013, Kumar, Gho, et al., 2017, Kumar and Kesawat, 2018, Thornton, Ericksen, et al., 2014). Integrated climate change and crop production models project declines in the yields of major crops such as corn, wheat and rice with severe ramifications for global food production this century (Birch, 2014, Iizumi, Sakuma, et al., 2013, Ray, West, et al., 2019, Rosenzweig, Elliott, et al., 2016). Despite the progressive increase in the production of significant crops through germplasm development and agronomic practices since the 1960s, susceptibility to climate variability has risen owing to higher sowing densities, which increase competition for water and nutrients (Lobell, Roberts, et al., 2014). The rapid development and adoption of climate-resilient crop genotypes are imperative to ensure global food security.

Rice is the world's most essential cereals crop, with production comparable to that of other crops. In this Review, we cover different recent advances in drought stress tolerance (Figure 1).

1. Genetic engineering approach

1.1. Signaling

Plants activate three main categories of genes in response to drought stress (Dash, Cao, et al., 2014). They are (1) genes involved in ion transport (2) regulatory genes involved in controlling transcriptional activities, and (3) novel downstream genes of unknown function reported to be involved in drought tolerance. The Cascades of molecules are involved in the perceiving of environmental signal transfer. These groups of molecules trigger the expression of specific downstream genes leading to appropriate biochemical/physiological responses (Golldack, Li, et al., 2014, Hu and Xiong, 2014, Shinozaki and Yamaguchi-Shinozaki, 2007). Many drought-related differential expressed genes have been identified in plants (Joshi, Wani, et al., 2016, Kumar, Choi, et al., 2017, Yamaguchi-Shinozaki and Shinozaki, 2006). These drought-responsive genes are known for their involvement in cellular responses such as "transcriptional regulation and stress perception (Lata, Muthamilarasan, et al., 2015). These genes code for "phytohormones, Protein kinases, transcription factors, late embryogenesis abundant (LEA), and osmoprotectants proteins (Golldack, Li, et al., 2014, Kumar, Lee, et al., 2014, Lata, Muthamilarasan, et al., 2015, Sah, Reddy, et al., 2016, Todaka, Shinozaki, et al., 2015, Varshney, Bansal, et al., 2011) that are involved in drought tolerance.

1.2. Stomatal Regulation

Plant's response to drought stress is generally via ABA-dependent or ABA-independent manner. In rice, ABA-Responsive cis-Elements (ABRE;PyACGTGG/TC) is abundant compared to soybean and Arabidopsis (Maruyama, Todaka, et al., 2011), and ABA concentration dramatically increases in response to drought stress. Increased ABA reportedly involved in (i) H_2O_2 accumulation in guard cells due to reduction in loss of water from the plant, (Iizumi, Sakuma, et al.) stomatal closure, and (iii) metabolites accumulation and stress proteins (protect cells during stress) (Kwak, Mori, et al., 2003, Mustilli, Merlot, et al., 2002, Wang and Song, 2008). The H_2O_2 mediated stomatal closure in rice involved in the ABA independent pathway (Huang, Chao, et al., 2009).

1.3. Kinases

During drought stress tolerance, the signaling mechanism involves sensing and transferring of dehydration signals from the plasma membrane to the nucleus (Ramanjulu and Bartels, 2002, Sanders, Brownlee, et al., 1999). Several protein phosphorylation mechanisms such as receptor-like kinases (RLKs) and mitogen-activated protein kinases (MAPKs) (Das and Pandey, 2010, Seybold, Trempel, et al., 2014, Tena, Boudsocq, et al., 2011). "*DROUGHT-HYPERSENSITIVE MUTANT1* (*DSM1*)"—a protein kinase in rice—scavenges the reactive oxygen species (ROS) produced by drought stress. The *dsm1* mutants are hypersensitive to drought during the panicle development and seedling stage (Ning, Li, et al., 2010). The RLK genes such as *stress-induced protein kinase 1* (*OsSIK1*), induced by drought stress in rice. While *OsSIK1*-Ox rice plants were drought stress-tolerant (Ouyang, Liu, et al., 2010).

1.3.Transcription factors

Many, transcription factors (TFs) regulating drought stress signaling in rice have also been studied. Many of these TFs bind to cis-regulatory elements of "bZIP, AP2/ERF, MYB, NAC, WRKY, NF-Y, CAMTA, and bHLH" families (Castilhos, Lazzarotto, et al., 2014, Licausi, Ohme-Takagi, et al., 2013, Shao, Wang, et al., 2015, Umezawa, Fujita, et al., 2006). These TFs over-expression lines displayed drought tolerance. In ABA independent pathway for drought tolerance, DREB (dehydration-responsive element-binding protein) transcription factors involved as a key player. Among DREBs TFs, DREB1/CBF, and DREB2 are involved in drought stress tolerance (Nakashima, Yamaguchi-Shinozaki, et al., 2014, Srivasta, Mehta, et al., 2010). *DREB1A*-Ox lines were more drought tolerant than rice plants (Datta, Baisakh, et al., 2012). Similarly, Overexpression of a stress-responsive NAC transcription factor gene *ONAC022* improves drought and salt tolerance in rice (Hong, Zhang, et al., 2016).

1.4.Other Aspect.

Along with drought-responsive elements, proteins such as LEA have been identified for drought stress tolerance (Goyal, Walton, et al., 2005). LEA can be accumulated in vegetative tissues as well as in seeds (He, Tan, et al., 2012, Ingram and Bartels, 1996, Liu, Wang, et al., 2013). Over-expression of LEA protein genes, *OsEM1*, and *OsLEA3*-1 make rice drought stress-tolerant (Xiao, Huang, et al., 2007, Yu, Lai, et al., 2016). Similarly, high cuticular wax in many crops imparts tolerance to drought (Xue et al., 2017). Crops with high cuticular wax display more drought-tolerance (Guo, Xu, et al., 2016, Zhou, Ni, et al., 2013, Zhu and Xiong, 2013). Under drought stress conditions, *DEEPER ROOTING 1* increases rice yield and control of root system architecture (Uga, Sugimoto, et al., 2013). Overexpressing heat-shock protein OsHSP50. 2 improves drought tolerance in rice (Xiang, Chen, et al., 2018). Natural variation in *OsLG3* increases drought tolerance in rice by inducing ROS scavenging (Xiong, Yu, et al., 2018). Overexpression of an MYB family gene, *OsMYB6*, increases drought and salinity stress tolerance in transgenic rice (Tang, Bao, et al., 2019). A stress-responsive bZIP transcription factor *OsbZIP62* improves drought and oxidative tolerance in rice (Yang, Xu, et al., 2019). Characterization of transcription factor gene *OsDRAP1* conferring drought tolerance in rice (Huang, Wang, et al., 2018). Overexpression of *OsNAC14* improves drought stress tolerance in rice (Shim, Oh, et al., 2018). Rice *WRKY11* plays a role in drought tolerance (Lee, Cha, et al., 2018).

2. Molecular breeding approach

The complex drought tolerance mechanism is controlled by multiple quantitative trait loci (QTLs) (Fleury, Jefferies, et al., 2010). Advances in plant physiology, and plant genomics, and phenotyping lead to new drought-tolerant varieties. By using the latest tools and gene network information, crop breeders will be able to increase crop yields (Tuberosa, 2012). Traditional molecular breeding methods can be used to explore QTLs for crop drought improvement, and later the candidate genes within drought associated QTL can be the primary targets for raising drought-tolerant transgenic lines (Varshney, Bansal, et al., 2011).

The QTLs are part of the chromosome with specific positioned marker and contain several genes (Chamarthi, Kumar, et al., 2011). In rice, many drought-related QTLs have been identified (Table 2). qDTY1.1, a major QTL with an additive effect on grain yield under drought stress at the reproductive stage in three populations: N22/MTU1010, N22/IR64, and, N22/Swarna, was situated on rice chromosome 1. It is flanked by RM431 and RM11943 marker (Vikram, Swamy, et al., 2011).

3. Conclusions and perspectives

In plants, drought stress signaling is very complicated process because of the many gene families and the complex molecular interactions between TFs with the cis-elements on the promoters of target genes. Also, one transcription factor can regulate many candidate genes with the corresponding cis-elements, whereas different families of TFs can regulate a single gene. Thus, the stress-responsive TFs not only work individually but also cross-talk with each other during drought stress response, which adds more complexity to the signaling networks that are involved in the plant stress responses. For future research work, we should first focus on multiple stress-responsive TF genes that can be regulated commonly by drought stress and have important role in the drought stress signaling cross-talk (Prasch and Sonnewald, 2015). Genetic engineering of these identified stress-responsive genes should give us powerfull platform for improving plant drought stress tolerance. Furthermore, the vital drought stress field trials are required to evaluate the transgenetic plants, primarily focusing on their yield, growth under the drought stress. It will be one of the necessary steps in many strategies to develop drought stress-tolerant rice. Taken together, we still need to work hard for a complete understanding the precise drought stress responses regulatory mechanisms in rice. It will help us to obtain the candidate TF genes for breeding multiple drought stress-tolerant rice crops with better quality and yields.

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Figure 1. Overview of regulatory network of Drought stress signaling in Rice.