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Transcription factors that regulate gene expression under drought

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ABSTRACT

Plants recognize the condition of water stress through their roots and they are sending a signal to their leaf to synthesize ABA. The ABA is a major key regulating phyto hormone for drought stress-responsive factors such as gene expression for stress proteins, stomatal closure, osmoprotectants accumulation, and stomatal closure for preventing water loss. The protein kinases SNRK2s and MAPK are detecting the ABA influx in guard cells that regulate the stomatal closure. The transcription factor ABREs and DREBs are regulating wide ranges of gene expression machinery under ABA mediation to drought stress, focusing on intracellular and cellular gene networks that are responsible for drought stress. The wax synthesis gene GLY shows high cuticular wax storage in leaf surface under drought conditions in rice it may play an important role in drought tolerance in rice.

Keywords: Transcription, gene expression, drought and rice

INTRODUCTION

The transcription factor of group AbZIP plays an important role in the ABA signaling pathway. The bZIP transcription factor of OsABF2 was expressed in various tissue in rice under abiotic stress treatment. Compare to the wild type the T-DNA insertional mutant of OsABF2 shows more sensitivity to drought stress these results conclude OsABF2 function as a transcriptional regulator and modulates the expression under drought through ABA dependent pathway [1]. In Arabidopsis nine subfamily of AREBs/ ABF shares a bZIP domain containing Ser/Thr phosphorylation sites that shows drought stress inducibility with three member ABRE1/ABF2, AREBe/ABF12 and ABF3 [1].

Kinases responses ABA treatment and drought stress

The Arabidopsis subclass III SnRK2 are phosphorylate a wide variety of proteins to respond to ABA [3]. In ABA signaling The SnRKs and Ca+2 dependent protein kinases CDPKs/CPKs shares some substrate The PYL, PYR, RCAR, SnRK, and PP2Cs.
The mitogen-activated protein kinase (MAPK/MPK) mediated stress responses such as ABA and jasmonic acid signaling [29-30], ROS signaling [4]. The MAPK regulates drought-induced or ABA-induced gene expression, stomatal closure, and drought stress tolerance. Also, the MAPK cascade components MAPKKK18 interact with ABA insensitive 1 (ABI1) encoded PP2C to regulate kinase activity [5].
Abscisic acid (ABA) plays an important role in plant adaptation under abiotic stress. The pyrabactin resistance-like (PYL) gene family OsPYL3 ABA receptor from drought tolerance Japonica rice Nagina 22. Under drought, cold and high temperatures found the induced level of expression of PYL3 transcript, and the drought susceptible rice IR64 showed a down-regulated expression level of PYL3. The translational fusion of PYL3 with the GFP C-terminal was localized in the cytosol and the nucleus shows functional conservation of PLA protein as a ABA receptor. The OsPLA3 overexpressed Arabidopsis transgenic were hypersensitive to ABA suggest the ABA-dependent molecular responsive of the OsPLA3 and they are improve drought tolerance [6]. The histidine kinases (HK) involve environmental and osmotic stresses in plants they found eight histidine kinases in Arabidopsis one of the HK, AHK1 (initially known ATHK1) involves as aosmo sensor and positive regulator for osmatic stress. The over-expression Arabidopsis plant of AHK1 shows increased osmotic stress tolerance, the knocked-out mutant of ahk1shows stress-sensitive phenotype. This experiment shows that AHK1 is a positive regulator of stress tolerance and an osmotic sensor [7].

Stomatal closure under drought stress

The Maize phytochrome interacting factor (ZMPF2) plays an important role in the regulation of plant growth and development the transgenic rice of Maize PIF family gene ZMPIF3 improves drought resistance in rice without yield penalty. The ZmPFI1 transgenic rice shows drought stress through water-saving mode association with reduced stomatal aperture and transpiration rate with increased panicle and tillers numbers in transgenic rice [8-9]. The H_2O_2 is essential for stomatal closure it was dependent on ABA concentration overexpression of OsASR5 in rice showing higher accumulation of H_2O_2 along with increased ABA level, simultaneously increased stomatal closure and reduced water loss under drought stress conditions [10]. The MAPK member MPK4 and 12 interacted with high leaf temperature1(HT1) [11-12], this model MPK1/MPK12-HT1 regulating SLAC1 to reduce the stomatal opening under high amount CO2 concentration suggest CO2 induced stomatal closure by regulating SLAC1 activity [13-14].

The wax synthesis under drought stress

Plants activate several defense responses under drought the evidence suggests that accumulation of cuticular wax is also associated to prevent dehydration under drought in Arabidopsis ABA-responsive transcription factor MYB96 promotes transcriptional activation of genes which encodes very-long chain-fatty acids considering enzymes involve cuticular wax biosynthesis by direct binding to the motif in the gene promoter [15]. Under increased drought conditions plants have smaller and thicker cuticular epidermis in leaf. epidermis accumulate lipid to form wax to increase the reflection of sunlight to prevent excessive transpiration [16]. The outermost surface of plants covered with an epicuticular wax layer provides primary waterproof protection against environmental stress. The wax synthesis gene Glossy 1 (GLY1) controlling wax synthesis sequence analysis shows 11 homologous gene of GLY1 in rice. Overexpression of one of these gene OsGL1-2 in rice shows high cuticular wax storage in the leaf surface and the mutant line of this gene shows a reduced amount of cuticular wax simentaniouslysensitivity against drought stress. Concluding the genetic modification of OsGL1-2 may potential option to improve drought resistance in rice plants [17].

Water use efficiency

The over-expression line of Ribosomal protein large (RPL). They have validated the RPL's water use efficiency the RPL subunit RPL23A shows increased quantum efficiency, suitable growth and yield under the condition of limited water availability also shows a significant increase of fresh weight, root length, chlorophyll contents under simulated drought [18]. The cell-membrane ABA transporter AtABCG25 over-expressed Arabidopsis transgenic plant shows enhanced drought tolerance with transportation-reduced phenotype without growth retardation. Finally, the AtABCG25 shows enhanced water use efficiency with greater biomass per amount of water [19].

Regulation of small RNAs during drought stress

The small noncoding RNAs, miRNA (microRNA), and siRNA (small interfering RNA) are works as a negative regulators at posttranscriptional levels by degradation of targeted mRNA [20]. Transcriptome analysis reveals many small RNAs are affected under drought stress condition [21]. The mRNA of nuclear factor Y subunit A5 (NF-YA5) targeted by miR169a and suppress the expression under drought stress [22]. During drought the NF-YA5 mRNA was highly accumulated and the miR169a was downregulated. The over-expression of miR169a and the knockout line of NF-YA5 shows decreased level drought tolerance [23].

Late embryo abundant proteins (LEA)

LEA proteins have been accumulated in the late stage seed development and a typical drought responsive factor in plants. Some studies show this proteins may function like a molecular chaperon for example the LEA protein in wheat prevented protein aggression due to desiccation in vitro [28]. Under drought conditions, the knocked out A group II LEA family gene LTI30 (low temperature- induced 30) shows decreased tolerance in arabidopsis [24].

Reactive oxygen species (ROS)

ROS is a secondary messenger in drought stress signaling [25]. Chloroplast is the essential organ for photosynthesis under drought condition two chloroplast gene is negatively expressed which will be important for thylakoid formation the HCF106 knocked out shows an increased level of ROS in guard cells, increased stomatal closure, and reduced water loss during drought [26]. the overproduction of ROS causes oxidative damage to cellular compounds. the ROS scavenging enzyme APX (ascorbate peroxide) and SOD (superoxide) are induced by drought and they are converting ROS to the nontoxic compound to prevent over-accumulation of ROS in stomata under ABA treatment shows higher water loss and decreased drought stress tolerance [27, 31].

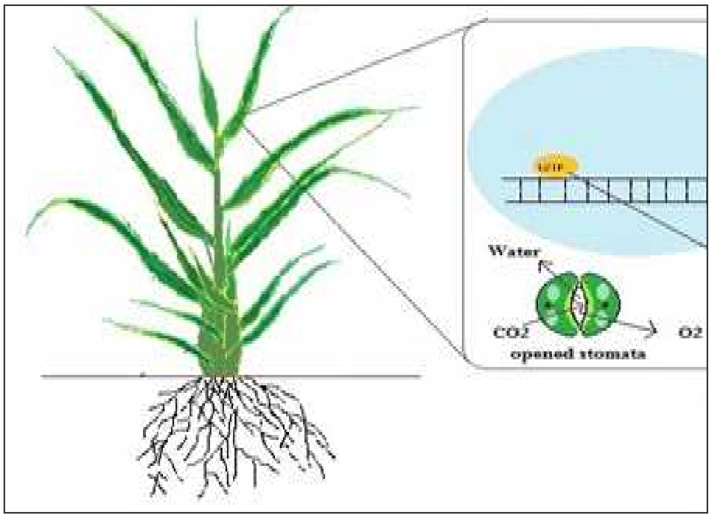

Figure: expression genes under drought or ABA presence condition in Rice.

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