Rice (Oryza sativa L.) is widely grown as a major staple food crop providing calories for about half of the world’s human population and is grown on 160 million hectares worldwide. It is being cultivated in India and China for several thousands of years. A significant yield loss in this crop is due to various biotic and abiotic stresses including insect pests, diseases, drought, salinity, adverse temperature and submergence. Development of abiotic stress tolerant rice genotypes with high grain yield is the major objective now in rice breeding and genomic research. Despite many concerted efforts all over the world, conventional breeding approaches are resulting in slow progress in developing abiotic stress tolerant rice genotypes. One of the approaches to rectify this is to introduce genes of interest that confer tolerance to abiotic stress via genetic engineering methods. Besides, with the availability of high quality rice genome sequence (IRGSP, 2005), there has been rapid accumulation of functional genomic resources including many known cloned and characterized genes particularly for abiotic stress tolerance, genes/full-length cDNA from global expression profiles and resequences of the rice genotypes. The identified genes are successfully transferred into rice to produce transgenics with promising traits. Transgenics are now being evaluated under field conditions in different countries. The objective of this review is to provide an overview of recent developments on the production of various transgenic lines in rice that are highly promising for abiotic stress tolerance.

Keywords: Genetic engineering, Rice, Abiotic stress

Introduction

Rice is the most important cereal crop, leading as food crop for more than half of the world population (IRRI, 2006). The global rice area cultivation has increased from about 129 million hectares in 1968 to about 159.4 million hectares in 2010. India has the largest farm area under rice production in 2009 at 44 million hectares. China and India are the largest rice producers followed by Indonesia, Bangladesh, Vietnam, Myanmar and Thailand.

Abiotic stress has a negative impact on plant growth and productivity. It leads to a series of morphological, physiological, biochemical and molecular changes that adversely affect plant growth and productivity (10). Generally, plants are able to cope with moderate levels of stress. However, when the stress exceeds the threshold level, the physiological mechanism imparting tolerance breaks down causing death of the plants. Among abiotic stresses, drought, cold and salinity, are the most pervasive that limit the yields of crop plants including rice. Understanding the mechanism of stress tolerance that involves a plethora of genes involved in stress signaling network is vital for
crop improvement (Fig. 1). Since large portions of rice-growing areas are affected by abiotic stress conditions, it would be difficult to meet the future food demands of ever increasing world population (11). Efforts involving conventional breeding methods for improving traits that confer tolerance to the abiotic stresses have met with limited success (12). Therefore, to meet the food demands of the growing world population, conventional breeding methods need to be combined with tools such as molecular markers and genomics. Several biotechnological approaches are adopted to increase quality and quantity of rice as well as its resistance to pests, diseases and environmental stresses (13). Ye et al. (14) produced transgenic golden rice with high source of provitamin-A (β-carotene) by manipulating the biosynthetic pathway using tissue specific promoters. They introduced three genes, phytoene synthase, lycopene cyclase and phytoene desaturase (2 genes

Fig. 1. Schematic representation of developing abiotic stress tolerant plants

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from Daffodil and 1 gene *Erwinia uredovora* respectively and expressed them in the endosperm. The development of recombinant DNA technology allowed the investigators a deeper understanding of transcriptional regulation of genes and facilitated overproduction of endogenous or foreign proteins in plants, besides unraveling the biochemical and molecular processes. A large body of literature on genetic engineering of rice is now available. An attempt was made here only to review the literature concerned with abiotic stress.

**Genetic engineering for abiotic stress tolerance**

The strategies for plant genetic engineering for abiotic stress tolerance rely on the expression of genes that are involved in signaling and regulatory pathways or genes that encode proteins conferring stress tolerance or enzymes present in pathways leading to the synthesis of functional and structural metabolites. Many genes and gene products have been identified which get induced upon exposure of plants to various abiotic stresses. Therefore, stress inducible genes have been utilized to improve stress tolerance through gene transfer. Although gene transformation in *japonica* rice is performed routinely in several laboratories, transformation in *indica* rice is comparatively difficult. Therefore, relatively large number of transgenic plants must be developed in *indica* species in order to select desirable transformants as well as to study the expression of introduced genes. Since the last two decades, a large number of genes were isolated and cloned which are involved in signal transduction, transcription regulation, ion transporters and metabolic pathways. Recently, some genes of calcium- signal and nucleic acid pathways have been reported to be up-regulated in response to both cold and salinity stresses indicating the presence of cross talk between these pathways. The role of calcium as an important signaling molecule in response to various stress signals has also been reported (16).

**Abiotic Stress Tolerance**

**Genes for abiotic stress tolerance**

**Transcription factors**: Genes that have been utilized for transformation of rice till date are listed in the Table 1. Plant stress response is regulated by multiple signaling pathways that activate gene transcription and its downstream machinery. Transcriptome analyses using microarray technology, together with conventional approaches have revealed that dozens of transcription factors (TFs) are involved in plant response to abiotic stress. *Arabidopsis* dedicates about 5.9% of its genome coding for more than 1,500 TFs (18).

**Osmolyte biosynthetic genes**: Osmolytes are synthesized in response to osmotic stress and do not interfere with normal cellular biochemical reactions. There are several examples of accumulation of osmolytes contributing to the relatively high water content necessary for growth and cellular metabolism (57). Osmolytes include proline, sugars (fructans and trehalose), polyols (mannitol and D-ononitol), quaternary ammonium compounds (glycine betaine) and tertiary sulfonium compounds. Trehalose is a nonreducing disaccharide of glucose that functions as a compatible solute in the stabilization of biological structures under abiotic stress in bacteria, fungi, and invertebrates. These findings demonstrated the feasibility of engineering rice for increased tolerance to abiotic stress and enhanced productivity through tissue specific or stress dependent overproduction of trehalose. OsTPP1 and OsTPP2 are two major trehalose-6-phosphate phosphatase genes over-expressed in vegetative tissues of rice that transiently induced tolerance in transgenic rice in response to chilling and other abiotic stresses (9). Accumulation of trehalose in transgenic *indica* rice using bifunctional fusion enzyme of trehalose-6-phosphate synthase and trehalose-6-phosphate phosphatase of *E. coli* has resulted in osmoregulation, removal of free radicals and stabilization of the hydrated structure of proteins to maintain membrane integrity and protein stability under various stress conditions (39). Trehalose helps in maintaining individual cell structure and functions during severe environmental stress conditions. It affects sugar metabolism and imparts osmoprotection. The enzyme arginine decarboxylase (adc), associated with putrescine biosynthesis is involved in minimal chlorophyll loss under salt stress in *O. sativa*. Accumulation of proline in dehydrated plants is caused both by activation of biosynthetic pathway enzymes and by inhibition of its degradation. It has been
demonstrated that overproduction of proline results in increased tolerance to salinity in transgenic rice (40).

**Heat shock proteins**: Heat shock proteins (Hsps) and molecular chaperones, as well as late embryogenesis abundant (LEA) protein families, are involved in abiotic stress tolerance (41). Hsps and LEA proteins help protect against stress by controlling the proper folding and conformation of both structural (i.e. cell membrane) and functional (i.e. enzymes) proteins. Overexpression of *HSP101* from *Arabidopsis* in rice plants resulted in significant improvement in growth performance during recovery from heat stress (24). Overexpression of LEA proteins was correlated in several cases with desiccation tolerance, although the actual function of these proteins is still unknown (42). Recently, overexpression of *HVA1*, a group 3 LEA protein isolated from barley (*Hordeum vulgare* L.), conferred dehydration tolerance in transgenic rice (43).

**Detoxification genes**: During stress, electrons that have a high energy state are transferred to molecular oxygen (O\(_2\)) to form reactive oxygen species (ROS) (44). ROS, such as singlet oxygen (O\(_2^*\)), superoxide ions (O\(_2^-\)) and peroxides, the most widely distributed being hydrogen peroxide (H\(_2\)O\(_2\)) are toxic molecules (45). ROS target high molecular mass molecules, such as membrane lipids or mitochondrial DNA. The toxic effects of ROS in plants are counteracted by inducing enzymatic as well as non-enzymatic antioxidative system such as: superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione reductase (GR), ascorbic acid (AsA), tocopherol, glutathione, phenolic compounds etc. Chloroplast transformation of tobacco with *E. coli* catalase gene (*kat E* gene) with tomato rbcS3C promoter efficiently improved plant resistance to photo-oxidation caused by drought stress at high light intensity, despite the inactivation of APX in the chloroplast (46). Same gene *kat E* when over expressed under CaMV 35S promoter in *japonica* rice, conferred tolerance to 250 mM NaCl and enhanced the catalase activity to 1.5 to 2.5 times more than non-transgenic plants (47). Overexpression of *glyoxalase I (gly I)* and *glyoxalase II (gly II)* genes together have conferred improved salinity tolerance in transgenic tobacco plants (35) and thus offered another effective strategy for manipulating stress tolerance in crop plants. These findings further have established the potential of manipulation of the *glyoxalase* pathway involving enzymes as a probable candidate gene for increased salinity tolerance (NaCl) without affecting yield in crop plants. The *glyoxalase II* cDNA cloned from rice (*Osgly II*) encoding a polypeptide of 336 amino acids was overexpressed in rice that displayed tolerance to various abiotic stresses (48). Thus, the multi-stress response of *Osgly II* gene documents its future utility in developing tolerance to various stresses in crop plants.

**Engineering transcription factors for abiotic stress tolerance**: Transcription factors (TFs) are proteins that act together with other transcriptional regulators, including chromatin remodeling/modifying proteins, to employ or obstruct RNA polymerases to the DNA template (49). TFs interact with cis-elements in the promoter regions of several stress-related genes and thus up-regulate the expression of many downstream genes resulting in imparting abiotic stress tolerance (50). Transcriptome data in *Arabidopsis* and in numerous other plants suggest that there are several pathways that independently respond to environmental stresses (in both ABA dependent- and independent- manner), suggesting that stress tolerance or susceptibility is controlled at the transcriptional level by an extremely intricate gene regulatory network (Fig. 2) (51, 52). Few of the TFs and their utility in engineering stress tolerance for crop improvement programs are given in Table-2 (53 - 77).

**ABA dependent**: The phytohormone ABA is the central regulator of abiotic stress particularly drought resistance in plants, and coordinates a complex gene regulatory network enabling plants to cope with decreased water availability (78, 79). ABA-dependent signaling systems have been illustrated as pathways that mediate stress adaptation by induction of at least two separate regulons (a group of genes controlled by a certain TF): (1) the AREB/ABF (ABA-responsive element-binding protein/ABA-binding factor) regulon; and (2) the MYC
The AREB or ABFs are bZIP (basic leucine zipper) TFs that bind to the ABRE motif and activate ABA-dependent gene expressions. They were first isolated in a yeast one-hybrid screening (81). A conserved cis-element named as ABA-responsive element (ABRE; PyACGTGG/TC) was identified from the promoters of ABA-inducible genes (82). Subsequently, it was revealed that ABA-responsive gene expression needs multiple ABREs or the combination of an ABRE with a coupling element (CE) as a functional promoter (83). Both in the ABA-deficient aba2 and in ABA-overexpression, improved salinity tolerance was recorded in rice (84). Overexpressing OsbZIP23, a member of AREB/ABF subfamily significantly improved drought and high salinity resistance in transgenic rice at the reproductive stage (47). Enhanced tolerance to drought and heat was observed in 35SOSAREB1 transgenic Arabidopsis plants (55).

**Fig. 2.** A schematic representation of transcriptional regulatory networks of cis-acting elements and transcription factors involved in abiotic-stress-responses. Transcription factors are shown in boxes cis-acting elements are shown in ellipses and target stress inducible genes are shown in long rectangular box at the bottom.
ABA independent regulons: ABA-independent well known regulons are: (1) NAC (NAM, ATAF and CUC) and ZF-HD (zinc-finger homeodomain) regulon and (2) CBF/DREB regulon. However, in addition, several studies have identified the existence of both ABA-dependent and independent pathways of stress response that function through AP2/EREBP (ERF) family members (85).

1. The NAC (NAM, ATAF and CUC) and ZF-HD (zinc-finger homeodomain) regulon: The NAC family of plant-specific TFs is one of the largest in the plant genome, with 106 and 149 members in Arabidopsis and rice, respectively (86, 87). NAC family TFs contains a highly conserved N-terminal DNA-binding domain and a diversified C-terminal domain (88). A rice NAC gene, ONAC045 was induced by drought, high salt, low temperature, and ABA treatment in leaves and roots (106). The SNAC1 overexpressing in rice seedlings showed significantly higher survival rate than wild type under drought treatment and significantly enhanced salinity tolerance as well (70). A rice R2R3-MYB gene (UGS5) containing putative NACRS in the promoter region was also induced in the SNAC1-overexpressing plants (70). Many abiotic and biotic stress responsive genes were upregulated in the OsNAC6 transgenic plants, and the transgensics were tolerant to dehydration, and high salt stresses (71). Similarly, ONAC045 overexpressing rice plants showed enhanced tolerance to drought and salt treatments (72). Hence, NAC TFs play an indispensable role in physiological adaptation for successful plant development under abiotic stress conditions.

2. CBF/DREB regulon: The dehydration responsive element binding proteins (DREBs) are important APETALA type (AP2/ERF) TFs that induce a set of abiotic stress-related genes, thus imparting stress tolerance to plants. These play an important role in the ABA-independent pathways that activate stress responsive genes. OsDREB2A and OsDREB2B were induced early (within 40 min) after cold exposure but not on ABA treatment. OsDREB1A was induced within 5 h of salinity stress whereas OsDREB1C showed constitutive expression (89). A detailed study of all five rice OsDREB2s showed that OsDREB2A expressed to the highest levels under the control condition, and its expression was increased to some extent by high temperature, drought and high salinity, but not by low temperature treatments. Expression of OsDREB2B was markedly increased after 20 min of high and 24 h of low temperature stress. While the transcript levels of OsDREB2C, OsDREB2E and OsABI4 were low under the control condition and were transiently induced by the abiotic stresses (67). Transgenic Arabidopsis and rice plants over expressing OsDREB1A displayed tolerance to low temperatures, high salinity and drought (90). Likewise, the constitutively over expressing CBF3/DREB1A and ABF3 transgenic rice showed better drought and salinity tolerance without any growth inhibition or phenotypic anomalies (59). Overexpression of OsDREB1F greatly enhanced the tolerance of plants to high salinity, drought, and low temperature both in rice and Arabidopsis, thus playing a significant role in plant stress signal transduction (68).

Function of AtDREB1A: AtDREB1A protein consists of its characteristic AP2 domain that binds to DRE/CRT cis acting element present in promoters (Fig. 3). The tertiary structure of AtDREB1A (Fig. 4) consists of a three-stranded â-sheet and one â-helix running almost parallel to it that contacts DNA via Arg and Trp residues located in the â-sheet (91). Two conserved functional amino acids (valine and glutamic acid) at 14th and 19th residues respectively, exist in the DNA binding domain, which are crucial sites for the binding of DREBs and DRE core sequences (92). An alkaline N-terminal amino acid region that serve as a nuclear localization signal (NLS) and a conserved Ser/Thr rich region responsible for phosphorylation near the AP2/ERF DNA binding domain are also mostly present (92, 93). The proteins contain an acidic C terminal region which might be functional in trans-activation activity (94). The activation of these transcripts is organ-specific and comparative to the extent of the stress given. AtDREB1A was induced within 10 min at 4 ºC Liu et al (95). AtDREB1A gene expression in response to abiotic stresses is activated by signal sensing,
perception and transduction through abscisic acid (ABA)-independent manner.

Overexpression of Arabidopsis CBF3/DREB1A and ABF3 in transgenic rice showed tolerance to abiotic stress without stunting growth (59). The Arabidopsis gene CBF3/DREB1A has been used to improve abiotic stress tolerance in *japonica* rice (*Oryza sativa* cv. Nakdong) by constitutive expression (59) and in *indica* rice (*O. sativa* cv. BR29) by inducible expression (96).

**Studies under field conditions**: Plant productivity should be taken into consideration while evaluating the plants for abiotic stress tolerance. Also, drought and heat stresses occur concurrently in the field. Therefore, the results obtained under greenhouse/laboratory conditions are incomparable to that of the observations made under field conditions. Field trials thus play a critical role for the analysis of stress-tolerant transgenic crops. Drought tolerant transgenic rice constitutively overexpressing OsLEA3-1 gene that encodes the proteins which accumulate in high quantity in water-stressed tissues and the plants expressing stress-inducible promoter transgene under field conditions was analyzed by Xiao et al. (97). Xiao et al. (98) also examined drought tolerance of transgenic rice overexpressing seven well-reported stress related genes namely CBF3/DREB1A, an AP2/ERF-type transcription factor; SOS2, a serine/threonine protein kinase; NCED2 and LOS5, enzymes involved in ABA biosynthesis; NPK1, a mitogen activated protein kinase kinase; ZAT10, a C2H2-type zinc finger transcription factor; and NHX1, a vacuolar Na+/H+ antiporter with an actin promoter under field conditions. Drought stress in the field decreased grain yield in these transgenics whereas the same
in LOS5, ZAT10 and NHX1 overexpressors were less affected. Since absolute grain yields under normal growth conditions were less in the transgenic rice over expressing CBF3/DREB1A, SOS2, NPK1, LOS5, ZAT10, and NHX1 with the stress-inducible promoter in comparison with untransformed controls, further improvement is required for practical application.

Field grown transgenic rice plants overexpressing SNAC1, a NAC type transcription factor subjected to two different levels of drought stress treatments of severe stress with 15% soil moisture and moderate stress with 28% soil moisture given at the anthesis stage has resulted in increased spikelet fertility in the transgenic plants whereas agronomic traits like plant height, panicle number, spikelet number, spikelet fertility, and grain yield, were similar between transgenic plants and the controls under non-stressed conditions (70). Exposure to drought stress by draining surface water and halting irrigation until leaves were rolled carried out during the panicle heading stage in the drought resistant transgenic rice overexpressing OsNAC5, OsNAC9/SNAC1 and OsNAC10 under the control of root-specific promoter have shown similar results among all the three transgenic rice lines. The grain yield decreased under drought conditions and the grains were significantly smaller in all three transgenic lines than those observed in their non-transgenic counterparts (99, 100 and 101). You et al. (102) studied the drought tolerance of transgenic rice plants overexpressing OsOAT gene that codes for OsOAT protein, an enzyme that increases proline content and is a direct target gene of the stress-responsive NAC transcription factor SNAC2, under field conditions. In the field, exposure to drought stress in the field at the panicle heading stage by draining the surface water and halting irrigation until leaves were rolled (103). The drought treated transgenic plants showed increase in grain yield which was due to the higher grain-filling rate compared to that of the drought treated non transgenic plants. The field evaluation of transgenic rice plants overexpressing EDT1/HDG11, a homeodomain-leucine zipper transcription factor, has also been performed by Yu et al. (104). The field grown transgenic rice subjected to drought by stopping the irrigation until the seed maturation stage, has shown higher grain yields with larger panicle sizes and higher tiller numbers than those observed in the drought treated non-transgenic rice.

Future prospects in the enhancement of abiotic stress tolerant transgenic rice: Although there are many reports of transgenic rice plants with enhanced abiotic stress tolerance during field trials, further research is required to reveal the regulatory mechanisms of stress response and tolerance under field conditions. The discovery of new genes that elevate stress tolerance without yield loss under abiotic stress is very much needed. Other approaches to new gene investigation is to study stress tolerance mechanisms of stress-adapted extremophiles such as desert plants, halophilic plants, cold water fishes and thermophilic bacteria (105). The functions of 18-38% of total proteins in a well characterized species remain unknown (106) and the explanation of which will be helpful in discovering new genes. Uga et al. (107) reported that the QTL Deeper Rooting 1 (DRO1) enhanced the growth angle of root in rice showing high-yield performance under drought stress conditions. This study shows that the modification of root architecture also plays an important role in the development of abiotic stress-tolerant rice plants. The development of submergence-tolerant rice cultivars and studies of submergence-tolerance mechanisms that have improved considerably (108, 109, 110, 111 and 112) signifies the exceptional properties of drought-tolerant rice plants with submergence-tolerant cultivar backgrounds which can survive under low as well
<table>
<thead>
<tr>
<th>Nature of gene</th>
<th>Gene</th>
<th>Function</th>
<th>Source</th>
<th>Response</th>
<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>Transcription factor</td>
<td>chs1</td>
<td>CRT/DRE binding factor</td>
<td><em>A. thaliana</em></td>
<td>Transformants showed regulation of several <em>cor</em> genes at the same time and showed freezing tolerance.</td>
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</tr>
<tr>
<td>Nitrilase</td>
<td>DREB1A</td>
<td>DRE-binding protein</td>
<td><em>A. thaliana</em></td>
<td>Transformants showed enhanced expression of various stress-induced genes and showed tolerance to freezing and heat stress</td>
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<tr>
<td>Nitrilase</td>
<td>chs3</td>
<td>CRT/DRE binding factor</td>
<td><em>A. thaliana</em></td>
<td>Transformants showed regulation of several <em>cor</em> genes at the same time and showed freezing tolerance.</td>
<td>22</td>
</tr>
<tr>
<td>Nitrilase</td>
<td>Cys2/His2 type STZ (salt-tolerance zinc finger protein)</td>
<td>Zinc-finger transcriptional repressor</td>
<td><em>A. thaliana</em></td>
<td>Transformants exhibited dehydration, high - salt, cold stress and ABA tolerance to drought stress</td>
<td>23</td>
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<tr>
<td>Nitrilase</td>
<td>abi3</td>
<td>Abscisic acid-induced protein</td>
<td><em>A. thaliana</em></td>
<td>Marked increase in expression of low temperature-induce freezing tolerance.</td>
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<td>Nitrilase</td>
<td>czatp1</td>
<td>Transcriptional repressor</td>
<td>yeast</td>
<td>Showed tolerance to drought stress and resistance against bacterial infection in <em>Arabidopsis</em>.</td>
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<tr>
<td>Nitrilase</td>
<td>afl1</td>
<td>Member of Zn finger family proteins</td>
<td><em>Medicago sativa</em></td>
<td>Transformants overexpressing <em>afl1</em> showed salinity tolerance.</td>
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</tr>
<tr>
<td>Nitrilase</td>
<td>s coff1</td>
<td>Soybean cold-inducible factor-1</td>
<td><em>A. thaliana</em></td>
<td>Transformants showed induction of <em>cor</em> genes and enhance cold tolerance.</td>
<td>27</td>
</tr>
</tbody>
</table>

| Saccharide | ts1 | Tobacco stress induced gene 1 | *N. tabacum* | Transformants showed marked tolerance towards salinity and salicylic acid. | 28 |
| Saccharide | sacB | Fructosyl transferase (fructan synthesis) | *Nicotiana tabacum* | Enhanced growth of seedling under osmotic stress. | 29 |
| Osmolytes Trehalose | OsTPP1 & OsTPP2 | Trehalose biosynthesis | Rice | Tolerance towards chilling and other abiotic stress | 30 |
| Osmolytes Betaine | betB | Betaine aldehyde dehydrogenase | *N. tabacum* | Transformed plants showed better growth under osmotic stress conditions. | 31 |
| Osmolytes Betaine | codA | Choline oxidase A (glycine betaine synthesis) | *A. thaliana*, *Oryza sativa* & *Brassica juncea* | Transformed tolerant to salt and cold. Enhanced tolerance to salt and low temperature stress. Enhanced capacity to germinate under salt stress. | 32, 33, 34 |
| Polyamines | adc | Arginine decarboxylase (putrescine biosynthesis) | *O. sativa* | Minimal chlorophyll loss under salt stress. | 35 |
| D-ornitotol | int1 | Myo- -inositol-3-methyl transferase | *N. tabacum*, *Arabidopsis thaliana* | Transformants were better adapted to water and salt stress. Enhance seed germination | 36, 37 |
| Mannitol | mliD | Mannitol-1 phosphate dehydrogenase | *N. tabacum*, *A. thaliana* | Enhanced tolerance to methyl viologen induced oxidative stress. Enhanced salt tolerance. | 38a, 38b, 39 |
| Signal | at-df2 | Cell cycle regulated phosphoprotein | *N. tabacum* | Transformants showed striking tolerance to heat, salt, cold and osmotic stress upon over | 29 |

**Abiotic Stress Tolerance**
as excessive soil water content conditions. Global climate changes may alternately expose crops to abiotic stresses like drought, salinity, flooding etc. Attempts to develop rice cultivars that exhibit abiotic stress tolerance would be of great help to overcome the adverse conditions in the present climatic conditions for increasing the rice crop production so as to meet the growing food demands.

**Conflict of interest** The authors declare that they have no conflict of interest.

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**References**

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### Table 2. Over expression of stress-responsive transcription factors in transgenics

<table>
<thead>
<tr>
<th>Gene</th>
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<td>ZFP</td>
<td>Petunia</td>
<td>Drought</td>
<td>76</td>
</tr>
<tr>
<td>Others</td>
<td>HARDY</td>
<td>Rice</td>
<td>Drought, Salinity</td>
<td>77</td>
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</table>


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