

Experimentation in Biology of Plant Abiotic Stress Responses

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During the course of growth under natural field conditions, crop plants are exposed to a number of different abiotic stresses (such as water stress, temperature stress, salt stress, flooding stress, chemical stress and oxidative stress). These stresses exert adverse effects on metabolism, growth and yield of the crops. The intensity of the abiotic stresses is on the rise, implying that various possible solutions for mitigating the damage caused by such stresses must be combined for future increase in crop production. At the level of plant genetics, there are indications that it may be possible to improve plants against such stress factors. However, the practical success in this regard depends on how well we understand the biochemistry, physiology and molecular biology of the plant abiotic stress responses. The cellular response of plants to abiotic stresses is of complex nature involving simultaneous interplay of several mechanisms. Although there is a great deal of progress in cataloguing the biochemical reactions that are associated with plant abiotic stress responses, precise understanding of the defense reactions leading to acquisition of stress tolerance remains a challenge. A number of different experimental systems including lower and higher plants as well as microbes have been analyzed for examining the plant abiotic stress responses. The molecular analysis of the stress response has been carried out at the level of stress proteins, stress genes, stress promoters, trans-acting factors that bind to stress promoters and signal transduction components involved in mediation of stress responses. The functional relevance of the stress-associated genes is being tested in different trans-systems including yeast as well as higher plant species. In this article, we discuss selective features of experimentation in biology of plant abiotic stress responses.

Key Words: Abiotic stress response, Biotechnology, Experimentation, Molecular biology

Introduction

Green revolution nearly doubled food production. However, world population will touch the 8 billion mark in about 25 years from now. As per predictions, by 2020 we will need 40% more grains than what we produce today (Chrispeels 2000). That too from the agricultural land that is shrinking every passing day due to increased urbanization and excessive use and abuse. This means it is not just production but production per unit area that must increase. Will we be able to increase the genetic capacity of the crops to yield the desired increased output? But before we ask for the increased future agricultural output, it is rather an uneasy feeling to learn that we harvest only a small proportion of the present-day genetic capacity. Detailed studies have shown that we lose between 10 to 90% of the existing genetic capacity in most of the crops (Boyer 1982, Widawsky & O'Toole 1990).

The tapping of the genetic potential in crops is determined to a large extent on the prevailing environmental factors. The genotype x environment interaction (G x E) is thus a key factor controlling the growth performance of the crops. The term environmental factors in this context includes both the climatic and the soil attributes. The irregularity in circadian and seasonal perturbations of these factors is often a rule and not an exception. When environmental perturbations are rapid and unpredicted, there is hardly an opportunity for plants to adjust to the changed conditions. This causes onset of stress regimes. The abiotic stresses (such as drought stress, water stress or desiccation stress caused by paucity of water for long periods; flooding, water-logging or hypoxia/anoxia stress caused by excess water; salt stress caused by increased level of salts in the soils; temperature stress which is both due to low

and high ranges of the ambient temperatures caused due to sudden atmospheric heating or cooling; metal stress caused by excessive levels of heavy metals such as arsenic and cadmium and finally, oxidative stress caused by combination of different stress conditions with high light stress) cause appreciable reduction in biomass production and grain yield in most crops (readers may kindly refer Grime et al. 1989, Jones et al. 1989, Bohnert et al. 1995, Nilsen & Orcutt 1996, Busk & Pages 1998, Khanna-Chopra & Sinha 1998, Lerner 1999 for details on general aspects of plant abiotic stress biology).

Different crop ecosystems are affected by different abiotic stress factors and to a differential extent. Let us consider here an example of rice. This crop species constitutes the most important food crop in the world (Widawsky & O'Toole 1990, Khush & Toenniessen 1991, Khush & Baenziger 1998, Shimomoto 1999). Globally speaking, India is the second largest producer of rice and ranks first in terms of area under rice cultivation (IRRI Rice Almanac 1993). The world rice-growing areas are divided in four different ecosystems namely irrigated rice, upland rice, lowland rice and deep-water rice. These ecosystems differ appreciably with respect to the grain production levels. The abiotic stresses that prevail in different rice ecosystems are shown in figure 1. These stresses have a large bearing on differential production levels of the different rice ecosystems (Widawsky & O'Toole 1990, Khush & Toenniessen 1991, Khush & Baenziger 1998). The assessment of rice economists is that abiotic stresses affect rice more than the biotic stresses (Hossain 1995). Any improvement made for the tolerance to abiotic stresses in rice would therefore have large economic gains. The abiotic stresses have been reported to cause significant losses in almost all crops including wheat, maize, barley, sorghum, chickpea, pigeonpea and cotton.

The conventional breeding methods such as those based on genetic variations, inter-specific or inter-generic hybridization, induced mutations and somaclonal variations have played a major role in increasing crop production. Systematic screening of plant germplasm has shown that there are excellent stress tolerant types locally available. For instance, rice types "FR13A" and "FR43B" of India, "Kurkaruppan" of Sri Lanka and "Goda Heenati" of Indonesia have notably higher level of flooding

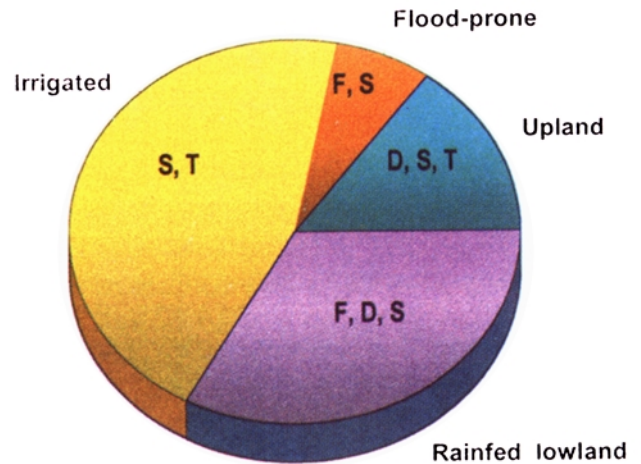


Figure 1 Different world rice ecosystems. The percentage-wise harvested rice area for different ecosystems is as follows: Irrigated-45%, Rainfed lowland-33%, Upland-15% and Flood prone-7%. The major abiotic stress factors that prevail in different rice ecosystems are shown. *D*, drought stress; *F*, flooding stress; *S*, salt stress and *T*, temperature stress.

tolerance (see Mohanty et al. 2000). The genetically-superior collection of germplasm has been made for several other abiotic stresses in rice (i.e. "Pokkali" and "Nona bokra" for salt stress response) as well as for different crops (i.e. "Kharchiya" for salt stress in wheat and "*Alyosa albicans*" for salt stress in pigeonpea). In recent years, the conventional breeding methods have been fortified with the addition of molecular breeding approach which banks on the application of different molecular markers for assisting in the genetic selection process (Mohan et al. 1997, Knapp 1998). Apart from the conventional and molecular breeding methods, production of transgenics has emerged as a powerful approach for altering genetics of crops. Research on production of transgenic plants has made great strides during the past 15 years (Hiatt 1993, Galun & Breiman 1997, Geneve et al. 1997). Tools and techniques for improvement of different crops through genetic engineering approach have been perfected to a great extent in several international as well as national laboratories. There are umpteen reports showing that crops tolerant/ resistant to herbicides, insect pests and viral and bacterial and fungal pathogens have been produced by employing transgenic technology.

In spite of the above progress, stress-tolerant, high-yielding crop cultivars are yet to find place in a common usage in the farmer's field. The success in generation of abiotic stress tolerant crops through the

conventional breeding methods has only been partial (refer Mohanty et al. 2000 for discussion on production of flooding tolerant rice by conventional and unconventional approaches). The application of molecular markers for mapping abiotic stress tolerance is far from fruition. The transgenic approach is yet to produce abiotic stress tolerant plant with high level tolerance that combines well with increased yield (Grover & Minhas 2000). Considering the wide-reaching implications of producing abiotic stress tolerant crops particularly for developing countries which have far-less organized agriculture than the West, incessant research on interactions of abiotic stresses and crops is a must. Our group has discussed the diverse issues that are involved in production of abiotic stress tolerant crops in several recent reviews (Grover et al. 1993, Grover et al. 1995, Singla et al. 1997, Pareek et al. 1997, Grover et al. 1998a, Grover et al. 1998b, Grover 1999, Grover et al. 1999, Minhas & Grover 1999, Katiyar-Agarwal et al. 1999, Grover & Minhas 2000, Grover et al. 2000, Grover 2000, Grover et al. 2001, Katiyar-Agarwal et al. 2001, Dubey & Grover 2001). From these as well as host of other reports published on this theme (Khanna-Chopra & Sinha 1998, Dhaliwal et al. 1998, Bajaj et al. 1999), it can be noted that a number of different biological systems are being employed for the study of abiotic stress responses in crops. These include microbial systems, fish as well as several lower and higher plants for the isolation of requisite genes and yeast and several higher plant systems for testing the relevance of the candidate genes (Grover et al. 1998a, Grover et al. 1999). In this article, we provide details on (i) the experimental systems that have been exploited for understanding the molecular biology and biotechnology of plant abiotic stress responses as well as (ii) the details on molecular parameters that have accrued through the analysis of such systems. It is important to debate on these aspects for making further in-roads into the science of producing abiotic stress tolerant transgenics.

Experimental Systems for Analyzing Molecular Responses of Plants to Different Abiotic Stresses

The experimental work on responses of crops to stress has been carried out using stress conditions that prevail in field as well as induced stress conditions in the laboratory set-up. The most favoured approach has been to experimentally subject the control plants to stress conditions simulated in the laboratory (or

greenhouse). This simplified route is practiced to minimize the experimental variations invariably involved in field-conditions. However, the responses of plant to the stress conditions mimicked in the laboratory may not entirely match with those in the field conditions. In natural habitats, onset of stress is often a gradual process. On the other hand, stress imposition is relatively rapid in laboratory-based experiments where small petri dishes or pots are often used. With respect to salt stress, constantly fluctuating positive as well as negative interactions amongst different salts can potentially alter the cell response in natural habitats as against in laboratory-media that have defined and fixed salt compositions. The plant response to stress conditions also shows variations with respect to the degree of stress. Against lethal levels of stress, the metabolic responses mostly represent the events associated with cell senescence or death. On the other hand, the imposition of sub-lethal stress provides certain beneficial effects in adapting the system to stressful regimes (however, under certain circumstances, even the cell senescence or death associated with lethal or sub-lethal stress levels is the component of the adaptive strategy). Notably, plants exposed to sub-lethal stress prior to lethal stress are often more tolerant to lethal stress than the plants which are directly transferred from control to lethal stress regimes (Lin et al. 1984, Singla et al. 1997). The sub-lethal stress level has therefore emerged as the choicest approach for the analysis of adaptive stress responses. Apart from the sub-lethal stressed systems, there are strong indications that changes that follow in the recovery phase are directly correlated with tolerance mechanisms. The samples harvested at various intervals during recovery from stress have served as useful materials for understanding the tolerance mechanism.

The stress effects have been examined at canopy level, whole-plant level and at the level of organs, tissues and individual cells. At all these levels, plant-abiotic stress interactions have been scored using morphological (such as change in growth pattern of the roots etc.), physiological (such as root-shoot partitioning, photosynthesis and nitrogen metabolism) and biochemical (such as enzyme activities and macromolecular changes) parameters (Pareek et al. 1997, Singla et al. 1997, Grover 1999). As the basis of all plant metabolic adaptations are the events that take place at the molecular level (i.e. gene

expression changes in terms of altered patterns of RNA and protein synthesis), molecular events are the targets when aim is to alter the genetics of crops for improved stress tolerance. The understanding of the RNA and protein alterations induced by different stresses has thus turned out to be a key objective in stress-related studies.

The research work on plant-abiotic stress interactive responses has been carried out employing a number of different plant species. This selection is often made on the basis of relative sensitivity/ tolerance as well as economic importance. *Rumex* has been exploited as a model system to study the relationship between flooding resistance and plant distribution (Arteca 1997). Detailed studies using this genus have provided valuable information on the role of root physiology in determining flooding tolerance. Upon exposure to dehydration stress, *Craterostigma plantagineum*, a resurrecting moss, is noted to lose almost up to 99% of its total water content and yet upon rehydration revives and turns to the normal growth patterns (Bartels et al. 1990). This system has been intensively analyzed for examining water stress responses. *Tortula ruralis* has been much-analyzed system for understanding the reasons underlying stability of ribosomes under extreme water stress conditions (Dhindsa & Bewley 1978). *Mesembryanthemum crystallinum*, the common ice plant, has been studied to a great detail for examining salt stress responses (Cushman et al. 1990). When stressed by addition of salt to the medium, or by drought or cold, *Mesembryanthemum* plants reproducibly change their primary mode of carbon assimilation from C₃ to CAM (Cushman et al. 1990). The weedy dicotyledonous species *Arabidopsis thaliana* has been extensively employed for the studies on abiotic stress responses. A large number of mutants have been generated in this species which have proven to be of enormous help in characterization of stress responses (Liu & Zhu 1997, Liu & Zhu 1998, Hong & Vierling 2000). The complete genome of *Arabidopsis* has recently been sequenced (The *Arabidopsis* Genome Initiative 2000) and currently there is a great deal of emphasis on the functional genomics of this species (for further details on structural and functional genomics, refer Somerville & Somerville 1999, Walbot 1999, Maheshwari et al. 2001, Dubey & Grover 2001). The understanding of the fundamentals of the stress responses from this species will possibly be more

elaborate than any other plant species in times to come. Amongst the crop plants, a great deal of experimental work on flooding stress response has been undertaken on *Oryza sativa* (Hossain et al. 1994, Hossain et al. 1996, Rivoal et al. 1997) and *Zea mays* (Wignarajah & Greenway 1976, Laszlo & Lawrence 1983, Kelley 1989, Kelly et al. 1991). *Z. mays* is a highly-sensitive crop to flooding stress while *O. sativa* is relatively a flooding-tolerant cereal (Perata & Alpi 1993). *Hordeum vulgare* has turned out to be a favourite material for studies on salt stress. This species is considered to be the most salt-tolerant cereal (Suhayda et al. 1992). *O. sativa* and *Triticum aestivum* are reported to be highly-sensitive to salt stress (Maas & Hoffman 1976, Rawson 1986, Maas & Grieve 1990, Bhushan & Grover 1993, Barlow et al. 1977). The effects of water stress have been extensively analyzed using *O. sativa* and *T. aestivum* (Mundy & Chua 1988, Claes et al. 1990, Bostock & Quatrano 1992, Kusano et al. 1992, Pareek et al. 1995, Nakagawa et al. 1996, Pareek et al. 1997, Singla et al. 1997). The experimentation in abiotic stresses responses utilizing the above as well as other species have involved high-yielding stress sensitive cultivars, moderately-yielding stress tolerant cultivars and low-yielding stress tolerant wild relatives of the specific plants (figure 2). The wild relatives of crop species are

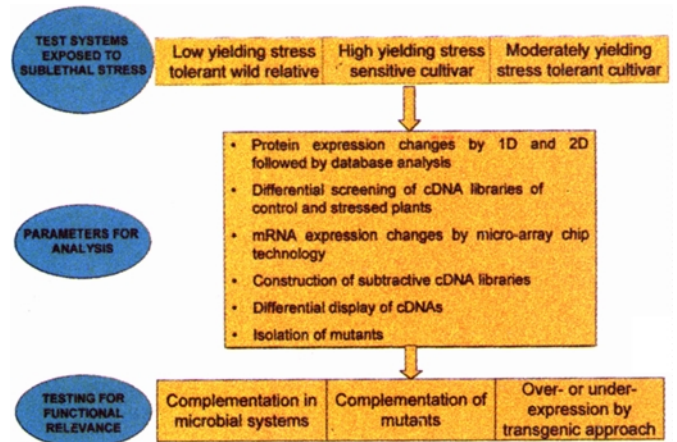


Figure 2 Experimental systems and techniques that have often been employed for the analysis of abiotic stress responses. The experimentation in abiotic stress responses have been undertaken employing highly sensitive and the highly tolerant types as well as the contrasting germplasm. These systems are subjected to sub-lethal stresses in order to evoke the stress responses. The induced responses have subsequently been examined at various hierarchical levels which include molecular, biochemical and physiological changes examined at tissue-, organ- as well as organism-based expression. The relevance of the candidate stress responsive genes and proteins towards conferring stress tolerance is examined using different microbial and higher plant systems (see text for details).

extremely useful source for agronomically-important genes. As mentioned above, "Nona bokra" and "Pokkali" are the low-yielding local selections of rice that have proven useful for studying mechanism(s) of salt tolerance in rice (Akbar et al. 1986, Moons et al. 1995). The halophytic wild relative of rice *Porteresia coarctata* is noted for its salt tolerance (Raychaudhuri & Majumdar 1996). Another wild rice type *O. granulata* has notable sensitivity to water-logging. The use of breeding lines that have a contrast in their stress responses has also been followed in many instances. In *H. vulgare*, CM72 and Prato cultivars have a notable contrast with respect to their salt stress responses (Epstein et al. 1980). These contrasting types have been analyzed for RNA and protein expression studies (Ramagopal 1987a, b, c). On the same line, FR13A and FR 43B rice types have been exploited for studies on flooding response (Mohanty et al. 2000). Several national and international breeding programs have been initiated to introgress flooding tolerance from the above sources into high-yielding modern rice cultivars resulting in production of selected tolerant lines which are presently at different stages of testing (Mohanty et al. 2000).

While the use of specific plant species is emphasized in the above account, it must also be appreciated that plant-abiotic stress responses are, by and large, conserved. For instance, the nucleotide sequences of different *hsp* (heat shock protein) genes is nearly identical in different biological systems (Singla et al. 1997, Katiyar-Agarwal et al. 2001). Therefore, any conclusion made with regard to stress response of a specific plant would be applicable to a wide range of different plant species. This conclusion is further supported by the observed synteny in the genomes of different plant species (Gale & Devos 1998). The use of different species in varied studies is thus hardly a handicap in stress-related literature.

The microbial systems can provide genes for bringing in high-level plant abiotic stress tolerance as well. These organisms are uniquely empowered with the capacities to grow and reproduce under conditions in which the life of higher plants is difficult to even imagine. These organisms are present in snow-capped glaciers, volcanoes, deserts or springs. The natural thermophilic habitats such as sulphur or iron-rich hot springs and geothermal vents allow growth and survival of several microbial populations. Several classes of osmo-tolerant microorganisms are

found in a wide range of environments such as bacteria and algae in salt lakes, several kinds of yeast in syrups and filamentous fungi in saline soils of low water content and stored food. In their natural habitats, microorganisms are frequently exposed to osmotic changes that are not only sensed but converted into an activity change of specific enzymes and transport proteins and/ or their synthesis *de novo* such that the osmotic imbalance is rapidly restored (Edwards 1990). Selected examples of osmo-compatible solutes include glycerol, arabitol, erythritol, mannitol, glycosyl glycerol, sucrose, trehalose, proline, glutamate, glycinebetaine and proline-betaine (Edwards 1990). *Bacillus* responds to osmotic stress by initially taking up K^+ ions followed by large amounts of proline by *de novo* synthesis (Measures 1975, Whatmore et al. 1990, Whatmore & Reed 1990). This bacterium also uses compatible glycinebetaine solute which is accumulated either due to *de novo* synthesis or direct uptake from the environment. Multiple transport systems are noted to be involved in the uptake of glycinebetaine in *Bacillus*. It has been observed that the most prominent physiological effect in osmotically-stressed yeast cells is the enhanced production of glycerol to counterbalance the osmotic pressure (Pavlik et al. 1993). Obligate thermophiles are represented by a wide range of species, the best studied of which are *Bacillus* and *Thermus* genera. The thermotolerant species of *Bacillus* such as *B. licheniformis* and *B. subtilis* are able to tolerate a temperature of 20-50°C, facultative thermophiles such as *B. coagulans* tolerate a range of 30-60°C and obligate thermophiles such as *B. sterothermophilus* and *B. acidocaldarius* tolerate a range of 40-80°C. *Bacillus* population is shown to possess well-formed mechanisms for tolerating severe heat stress (Visick & Clarke 1995). Examples of selected genes of microbial origin proven useful for enhancing abiotic stress tolerance of higher plants are mentioned in the subsequent account.

Molecular Parameters for Analyzing Abiotic Stress Responses

Detailed characterization of stress responses has shown that specific proteins accumulate in response to imposition of stress conditions. These proteins are commonly referred to as stress proteins. The classical example of such proteins is the heat shock proteins

(HSPs) that are induced primarily in response to high temperature stress (Vierling 1991, Singla et al. 1997, Katiyar-Agarwal et al. 2001). Specific stress proteins have also been noted to accumulate in response to low temperature stress, water stress, salt stress and oxidative stress (Grover et al. 1998a, Grover et al. 1999, Chang et al. 2000, Grover et al. 2001). The amino acid sequence of the stress proteins has enabled isolation of the specific gene clones (Claes et al. 1990, Moons et al. 1998). The stress genes have also been isolated by differential screening of cDNA libraries constructed from control and stressed tissue mRNAs as well as through use of subtractive cDNA libraries. In recent years, the technique of differential display of cDNA clones has also been successfully employed for isolation of stress-specific clones (Liang & Pardee 1992, Huq & Hodges 1999). Selective examples of genes and proteins induced by heat shock, cold stress, water stress and salt stress are presented in table 1. The stress genes isolated and cloned from microbial systems include mannitol phosphate dehydrogenase gene from *E. coli*, genes encoding betainealdehyde dehydrogenase, choline dehydrogenase and levan sucrase isolated from *B. subtilis* and gene encoding choline oxidase from *Arthobacter globiformis*. The recent progress made in isolation, cloning and characterization of anaerobiosis, low temperature and high temperature-induced stress promoters is among the major developments which have taken place in stress biology in recent years (table 2). Most of the stress promoters contain an array of stress-specific cis-acting elements that are recognized by the requisite transcription factors. Importantly, the knowledge generated from stress promoters is proving useful not only with respect to the fundamental studies on stress-inducibility but also for the regulated expression of stress gene in transgenic systems (for further details see Katiyar-Agarwal et al. 1999). The studies on the mechanisms behind switching on and off of the stress genes have placed a great deal of emphasis on transcription factors for the regulation of stress promoters (table 3). The generation of stress tolerance through engineering for over-expression of transcription factor genes is emerging as an attractive possibility in recent years. More details on stress proteins, genes, promoters, transcription factors and signal transduction components can be seen in the recent paper by Grover et al. (2001).

Experimental Systems for Analyzing Functional Relevance of the Stress Genes

The foremost goal of the abiotic stress biology research is to seek understanding of the plant responses at the fundamental level. The question being addressed is how plants sense stresses and how is the defense mounted? The other equally-important goal of stress biology research is to produce plants that have genetically-enhanced capacity to tolerate abiotic stresses. As the output from the first objective is an essential input for the second objective, both basic and applied aspects of abiotic stress molecular biology science have an interwoven relevance.

The term stress genes that includes genes which are up-regulated in response to application of stress treatments is a misnomer. It is possible that a given stress gene may not be primarily related to the events of stress tolerance. Therefore, it is prudent to experimentally work out how the specific stress gene is related to stress tolerance. The methods for genetically introducing the desired gene in the trans-host have fortunately been optimized to a great deal, enabling the use of reverse genetics approach for the same. Further, it is possible now to not only overexpress the gene but to under-express it as well (through antisense technology) so that the consequences of the gene action are proved either way.

In several studies, plant stress genes have been over-expressed in yeast. Yeast is a unique eukaryotic system in terms of its genotypic organization and yet has many of the advantages which are normally seen in the prokaryotes in terms of growth cycle (Bassham & Raikhel 2000). The complete genome of yeast has been sequenced and is noted to encode for nearly 6000 functional proteins (Goffeau et al. 1996). Importantly, attempts are being made to raise knockout mutants of each one of the yeast genes. The availability of this kind of flexibility in the yeast system is of paramount importance. The functional complementation of the higher plant genes with the yeast system has proven a fertile approach. In recent years, a number of different plant genes have been introduced in yeast with this objective. The plant *hsp100* genes have been shown to functionally complement *hsp104* mutation in yeast (Schirmer et al. 1994, Lee et al. 1994, Wells et al. 1998). On the note of caution, there are several plant

Table 1 Selective examples of genes/ proteins induced by abiotic stresses

Plant Species	Genes/ Proteins	Characteristic Feature(S)	Reference
Heat shock responsive gene/ proteins			
<i>Arabidopsis thaliana</i>	HSP81-1	Expression occurs at low level in absence of heat shock (HS) and at high level at 35°C	Takahashi et al. 1992
	HSP81-2	Constitutively expressed at higher level and is moderately enhanced by elevated temperature; analysis of HSP81-2 genomic and partial cDNA sequence suggests that the coding region is interrupted by two introns of 304 and 106 base pairs	Takahashi et al. 1992
	<i>hsp70-1</i>	Constitutively expressed, 4-5 fold increase in mRNA levels after HS	Wu et al. 1988
	<i>AtHSP17.6</i>	Induced by HS; gene encodes 17.6 kDa protein having 157 amino acids	Helm and Vierling 1989
	HSP18.2 and HSP17.4	Transcript undetectable in control tissues but induced by HS	Takahashi & Komeda 1989
	<i>AtHSP101</i>	Induced by HS, partially substitutes the function of yeast <i>hsp104</i>	Schirmer et al. 1994
	<i>AtHSP22</i>	Induced by HS, encodes 22 kDa protein and is localized in the ER during HS	Helm et al. 1995
<i>Brassica oleracea</i>	90, 88, 86, 74, 69, 66, 47, 43, 42, 27, 23, 21, 19 and 18 kDa proteins	HSPs induced by HS	Fabijanski et al. 1987
<i>Catharanthus roseus</i>	cDNA for <i>hsp90</i> homologue	Protein constitutively expressed in cell cultures grown at 25°C; not detected in young plants at room temperature but seen after a HS at 37°C for several hours	Schroder et al. 1993
<i>Cucurbita</i> sp.	76 and 73 kDa proteins	HSPs induced by HS	Strzalka et al. 1994
<i>Daucus carota</i>	<i>pMON 9508</i>	<i>hsp70</i> genomic clone encoding HSP 70	Rochester et al. 1986
	<i>Dchsp70</i>	Accumulation of mRNA is heat- inducible and reaches maximum levels at 37°C	Lin et al. 1991
<i>Glycine max</i>	LMW classI proteins	15-18 kDa, responsible for thermotolerance	Hsieh et al. 1992
	<i>hsp17.6-L</i> , <i>hsp17.5-M</i> and <i>hsp17.5-E</i>	Code for proteins in molecular weight range of 17.3-17.5 kDa	Nagao et al. 1985
	<i>hsp22</i>	Induced by HS, encodes 22 kDa protein	Helm et al. 1993
	<i>hsp101</i>	Induced by HS, encodes 101 kDa protein	Lee et al. 1994
<i>Helianthus annuus</i>	Tetraubiquitin mRNA known as <i>haUbiS</i>	Induced by HS	Almoguera et al. 1995

Table 1 (Contd..)

	HSP17.6 and HSP17.9	Induced by HS as well as water stress	Almoguera et al. 1993
<i>Hordeum vulgare</i>	94,85,76,71,39, 32 and 24 kDa proteins	Proteins accumulated in response to HS	Clarke & Critchley 1992
	<i>hsp90</i> mRNA	Induced by pathogen infection and HS	Walther-Larsen et al. 1993
<i>Lycopersicon peruvianum</i>	Seven LMW HSPs (15-20 kDa)	Proteins induced by heat stress	Kato et al. 1993
	Polyubiquitin (Ubq1-1)	Induced by HS, 7 ubiquitin units with two additional amino acids	Rollfinke & Pfitzner 1994
	25-91 kDa HSPs	Metal ion responsive proteins	Kapoor 1986
<i>Nicotiana tabacum</i>	<i>pTC B48</i> cDNA clone	Encodes calmodulin-binding HSP	Lu et al. 1995
<i>Oryza sativa</i>	<i>hsp82B</i>	Encodes 82 kDa protein, mRNA accumulates to high levels within 120 min after plants are shifted to 42°C	Breusegem et al. 1994
	33 kDa HSP	Synthesis occurs at high temperature	Fourre & Lhoest 1989
	<i>Oshsp16.9 A</i> and <i>Oshsp16.9 B</i>	16.9 kDa HSPs	Tzeng et al. 1992
	110 kDa HSP	Heat and ABA-inducible	Singla & Grover 1993
	<i>pTS1</i> and <i>pTS3</i>	Encode 16-20 kDa HSPs; also synthesized in response to heavy metal stress	Tseng et al. 1993
	104 kDa HSP	Heat-inducible	Singla & Grover 1994, Pareek et al. 1995
	90 kDa HSP	Heat-inducible	Pareek et al. 1995
<i>Pharbitis nil</i>	<i>hsp83A</i>	DNA sequence homology to members of 83 to 90 kDa <i>hsp</i> gene family; increase in mRNA levels found 2 h after end-of-day dark treatment; encodes a protein that exhibits 70% amino acid identity with <i>Drosophila</i> HSP83	Felsheim & Das 1992
<i>Phaseolus aureus</i>	HSP70	70 kDa protein induced under heat stress, also induced due to low temperature	Wu et al. 1993
<i>Phaseolus vulgaris</i>	<i>hsp70</i>	68 kDa protein loosely associated with the mitochondrial envelope	Vidal et al. 1993
<i>Pisum sativum</i>	HSP18.1	18.1 kDa class I protein	Neumann et al. 1989
	HSP62	Etioplast-encoded protein	Necchi et al. 1987
	HSP21	21 kDa nuclear encoded chloroplast-localized HSP	Vierling et al. 1988
	sHSPs	Class I and class II cytoplasmic HSPs, accumulate in embryo without HS at levels similar as that present in heat-stressed leaves	DeRocher & Vierling 1994

Table 1 (Contd..)

<i>Vigna radiata</i>	114, 79, 73, 70, 60, 56, 51, 46 and 18 kDa proteins	HSPs induced by HS	Collins et al. 1995
<i>Zea mays</i>	60 kDa protein	Protein induced under high temperature	Sinibaldi & Turpen 1985
	108, 89, 84, 76, 73, 30, 23 and 18 kDa proteins	HSPs induced by HS	Atkinson et al. 1989
	<i>hsp70</i>	Low level of expression at normal temperature and it increases 40-60 fold at 42°C, 68% homologous to <i>hsp70</i> of <i>Drosophila</i>	Rochester et al. 1986
Cold responsive genes/ proteins			
<i>A. thaliana</i>	<i>cor pHH 7.2, 28, 29, 67</i>	Induced by ABA and water stress	Hajela et al. 1990
	<i>skin1</i>	Identical to <i>cor 6.6</i> ; ABA and low temperature inducible	Kurkela & Franck 1990
	<i>lti40</i>	Induced by water stress, low temperature and by fluridone treatment	Nordin et al. 1991
	<i>rab18</i>	18.5 kDa glycine rich protein induced by low temperature, water stress and ABA	Lang & Palva 1992
	<i>cor15</i>	Induced by low temperature and drought	Lin & Thomashow 1992
	<i>lti78</i>	Induced by low temperature	Nordin et al. 1993
	<i>lti65</i>	Induced by low temperature, drought and ABA	Nordin et al. 1993
	<i>cor15b</i>	Homologue of <i>cor15a</i> , responsive to low temperature stress and ABA but not to drought stress	Wilhem & Thomashow 1993
	<i>lti30</i>	Belongs to <i>dhn/lea/rab</i> gene family, expressed during cold stress	Welin et al. 1994
	<i>lti45</i>	ABA independent expression	Welin et al. 1994
	<i>cor47</i>	Drought responsive but not responsive to ABA	Welin et al. 1994
<i>Bromus inermis</i>	22 kDa protein	Inhibited by low temperature	Robertson et al. 1987
	<i>pBGA12, 56, 85 and 25</i>	ABA inducible cold responsive genes; implicated in freezing tolerance	Lee & Chen 1993
<i>Brassica napus</i>	22-23 kDa protein	Inhibited by cold stress	Meza-Basso et al. 1986
<i>Cucumis sativus</i>	25, 38, 50, 70 and 80 kDa proteins	HSPs, also induced by chilling	Lafuente et al. 1991
<i>G. max</i>	HSP70 related protein	HSC protein, increased synthesis at low temperature	Cabane et al. 1993
<i>H. vulgare</i>	75 kDa protein	Most abundant cold stress protein	Cattivelli & Bartels 1989

Table 1 (Contd..)

	<i>pAF93, pT59, pAO86 and pAO29</i>	Cold regulated cDNA clones	Cattivelli & Bartels 1990
	45 kDa protein	Protein synthesis in response to cold, drought and ABA	Grossi et al. 1992
	<i>hva1</i>	Group 3 <i>lea</i> gene	Sutton et al. 1992
	<i>bH101</i>	Induced by low temperature, ABA and drought	Goddard et al. 1993
<i>Lycopersicon esculentum</i>	27 and 35 kDa proteins	35 kDa protein is synthesized and 27 kDa protein is inhibited by chilling	Cooper & Ort 1988
<i>Medicago sativa</i>	<i>MsaciA</i> clone	Encodes for glycine-rich protein	Laberge et al. 1993
	15 kDa protein	Low temperature responsive protein	Monroy et al. 1993
<i>Nicotiana plumbaginifolia</i>	SOD cDNAs	Transgenic plants overexpressing these cDNAs show freezing tolerance	Bowler et al. 1991
<i>O. sativa</i>	95, 75, 25 and 21 kDa protein	Induced at low temperature	Hahn & Walbot 1989
	<i>rab16A</i>	Induced by low temperature, water stress and ABA	Hahn & Walbot 1989
	<i>psaB, psbB, rbcL and atpE</i>	Chloroplast encoded genes inhibited at low temperature	Hahn & Walbot 1989
	<i>rbcS and cab</i>	Nucleus-encoded genes, reduced expression in response to low temperature	Hahn & Walbot 1989
	<i>lip5, lip9 and lip19</i>	Induced by low temperature; <i>lip5</i> and <i>lip19</i> also stimulated by ABA	Aguan et al. 1991
<i>Spinacia oleracea</i>	85 and 160 kDa proteins	Synthesized in response to low temperature and water stress	Guy et al. 1992
	<i>cor85 and cor140</i>	Heat-stable proteins; responsive to low temperature, ABA, drought and wounding	Kazuoka & Oeda 1992
	<i>cap79</i>	79 kDa protein, plays role in renaturation of denatured proteins during cold stress	Neven et al. 1992
<i>Solanum tuberosum</i>	<i>ci13, ci19, ci7 and ci21</i>	Transcript transiently expressed in response to low temperature	Berkel et al. 1994
<i>Triticum aestivum</i>	<i>wcs120</i>	Strongly induced by cold	Houde et al. 1992
	<i>wcs19</i>	Leaf-specific gene stimulated by light during low temperature stress	Chauvin et al. 1993
<i>Z. mays</i>	<i>adh1</i>	Cold inducibility shown; primarily induced by anaerobiosis	Christie et al. 1991

Table 1 (Contd..)

Water stress responsive genes/ proteins			
<i>A. thaliana</i>	<i>lti78</i> and <i>lti64</i>	<i>lti78</i> (77.8 kDa protein) mainly responsive to low temperature while <i>lti64</i> (64.5 kDa protein) responsive to drought and ABA	Nordin et al. 1993
	<i>rd22</i>	ABA mediates the drought induced expression but not the seed-specific expression of <i>rd22</i>	Yamaguchi-Shinozaki & Shinozaki 1993b
	<i>ERD5</i> cDNA clone	Encodes a precursor of proline dehydrogenase (oxidase) which is regulated at the level of mRNA accumulation during both hydrated and dehydrated plants - homologous to yeast <i>put1</i> and <i>Drosophila sluggish A</i> genes	Kiyosue et al. 1996
	<i>rd29A</i> and <i>rd29B</i>	Induced by exogenous ABA following 3 h of application	Yamaguchi-Shinozaki & Shinozaki 1993a, 1994
<i>B. napus</i>	<i>bnd22</i>	Increased by progressive or rapid water stress and salinity and disappeared on rehydration	Reviron et al. 1992
<i>Craterostigma plantagineum</i>	Several <i>in vitro</i> synthesized polypeptides	Synthesized after treatment with ABA; cDNA clones corresponding to mRNA expressed only in desiccation tolerant tissues	Bartels et al. 1990
	Desiccation specific major <i>pcC</i> gene families	Desiccation-related cDNA clones	Piatkowski et al. 1990
	<i>cdeT27-45</i>	Induced by ABA in leaves and callus, promoter active in developing embryos and mature pollen grains in transformed tobacco	Michel et al. 1993
<i>Gossypium hirsutum</i>	6 LEA proteins and genes	Expressed during the maturation and desiccation phases of seed development	Baker et al. 1988
	<i>lea5</i> and <i>lea14</i> (27-45 homologue genes)	Highly induced in vegetative tissues; induced in post-abscission stage of embryogenesis and environmentally induced in embryo by desiccation or treatment with ABA or high osmoticum	Galau et al. 1993
<i>D. carota</i>	DC8	ABA regulated	Franz et al. 1989
<i>H. annuus</i>	<i>hsp17.6</i> and <i>hsp17.9</i> mRNAs	Expressed in response to HS or water stress	Almoguera et al. 1993
<i>L. esculentum</i>	TAS14 and TSW12	Induced by drought stress, also induced by low temperature stress	Godoy et al. 1990, Torres-Schumann et al. 1991, 1992 Hughes et al. 1992
	Genes for proteases and ubiquitin	Induced by water deficit; gene products may be involved in the degradation of proteins that are denatured during cellular water loss	Bray 1993

Table 1 (Contd..)

	<i>le16</i>	Encodes a 12.7 kDa protein, induced by drought stress and regulated by ABA specifically in aerial vegetative tissues; also induced by salt, heat, cold and water stress	Plant et al. 1991
	<i>plc30-15</i>	ABA and drought induced	Chen & Tabaeziadeh 1992, Chen et al. 1993
<i>Mesembryanthemum crystallinum</i>	<i>imt1</i>	Induced by osmotic stress	Vernon & Bohnert 1992
	Two isogenes for PEP carboxylase <i>ppc1</i> and <i>ppc2</i>	<i>ppc1</i> shows 30 fold increase in transcription rate in leaves and <i>ppc2</i> transcripts decrease slightly in leaf tissues; in roots transcripts for both the genes decrease with time of exposure of stress; induced by salt stress also	Cushman et al. 1989
<i>Nicotiana glauca</i>	MIP1	Down regulated under drought stress	Smart et al. (unpublished report)
<i>O. sativa</i>	<i>rab16B</i> , <i>rab16C</i> and <i>rab16D</i>	ABA regulated	Yamaguchi Shinozaki et al. 1990
	23 kDa polypeptide	ABA responsive, not responsive to NaCl and cold treatment, boiling stable and immunologically related to the RAB 16 family of proteins	Rao et al. 1993
	23 kDa polypeptide	Induced in cell suspensions	Reddy et al. 1993
	<i>rab16A</i>	Osmotic stress and ABA responsive, conserved sequence motifs in the <i>rab 16A</i> promoter specifically bind nuclear protein factors	Mundy et al. 1990
	RAB21	RAB21 mRNA and protein (16.5 kDa) accumulate in rice embryos, root, leaves and callus derived suspension cell upon treatment with NaCl or ABA	Mundy & Chua 1988
<i>P. sativum</i>	<i>pPsB12</i> cDNA clone	Encodes a polypeptide of 20.4 kDa; pea dehydrin lacks a stretch of serine residues which is conserved in other dehydrins, ABA induced expression of dehydrins in the unstressed seedlings	Robertson & Chandler 1992
<i>Sorghum bicolor</i>	<i>BADH1</i> and <i>BADH15</i> cDNA clones	Encode betaine aldehyde dehydrogenase	Wood et al. 1996
	MIP1	Membrane intrinsic protein and induced by drought stress	Whitsitt et al. (unpublished report)
<i>G. max</i>	<i>p5cs</i>	Encodes 28.6 kDa enzyme that is involved in proline biosynthesis	Delauney & Verma 1990
<i>T. aestivum</i>	<i>em</i>	ABA regulated gene	Marcotte et al. 1989

Table 1 (Contd..)

<i>Vigna radiata</i>	<i>Em</i> like protein clone	Synthesized during early germination of axis and ABA extends its synthesis	Manickam et al. 1996
<i>Z. mays</i>	RAB17	Induced during late embryogenesis when ABA levels are high and it is also ABA and water stress inducible in embryo and vegetative tissues	Vilardell et al. 1990
	<i>rab28</i>	ABA-inducible in embryos and vegetative tissues; also induced by water stress in young leaves	Pla et al. 1993
Salt responsive genes/ protein			
<i>A. thaliana</i>	<i>Sal1</i>	Induced by salt stress, over expression in <i>Arabidopsis</i> or yeast overcomes Na ⁺ and Li ⁺ toxicity, homologous to <i>hall1</i> of yeast	Quintero et al. 1996
<i>B. napus</i>	<i>bnd22</i>	22 kDa protein, level increased by progressive or rapid water stress and salinity	Reviron et al. 1992
<i>Citrus sinensis</i>	Salt associated 23-25 kDa protein	Induced by salt stress, ABA and water stress	Ben Hayyim et al. 1993
<i>Dunaliella salina</i>	<i>p150</i>	150 kDa protein, induced by salt stress, <i>de novo</i> synthesized protein	Sadka et al. 1991
<i>H. vulgare</i>	26 kDa and 27 kDa proteins (salt induced poly-peptides SIP S1-S4)	Salt stress induces S ₁ -S ₄ polypeptides but water deficit did not induce S ₂ polypeptides	Hurkman & Tanaka 1988
	<i>hva1</i>	Induced by ABA, drought, NaCl, cold and heat treatment	Hong et al. 1992
<i>L. esculentum</i>	TAS-12	Salt and water stress induced lipid transfer protein	Torres-Schumann et al. 1992
	<i>le-16</i> gene	Induced by drought, PEG, salinity cold and heat stress	Plant et al. 1991
<i>M. crystallinum</i>	<i>ppc-1</i> and <i>ppc-2</i> isogenes	Encodes PEP carboxylase, induced by salt and water stress, exogenous ABA is a poor substitute for NaCl to induce it	Cushman et al. 1989
	<i>lmt1</i>	Encodes myo-inositol o-methyl transferase1; induced by NaCl and osmotic stress	Vernon & Bohnert 1992
	<i>inps1</i>	Encodes myo-inositol 1-phosphate synthase (INPS 1), shows significant homology to corresponding genes in plants and yeast	Ishitani et al. 1996
<i>N. tabacum</i>	26 and 43 kDa polypeptides	Levels increase in both NaCl and PEG induced water stress adapted cells but are not detectable in unadapted cells	Singh et al. 1985
	58, 37, 35.5, 34, 26, 21, 19.5 and 18 kDa polypeptides	Increased levels with increased NaCl tolerance	Singh et al. 1985
	30 kDa polypeptide	Heat shock at 38°C induces cross tolerance to salt stress	Harrington and Alm 1988
	Vitronectin and fibronectin like proteins	Found in membranes and cells wall of NaCl adapted cells	Zhu et al. 1993
	Osmotin	26 kDa protein, protein level enhanced in both NaCl and PEG induced water stress adapted cells but not in unadaptable cells	Singh et al. 1987
<i>O. sativa</i>	RAB21	Induced when plants are subjected to water stress, <i>rab21</i> mRNA and protein accumulate in rice embryos leaves, roots and callus derived suspension cells upon treatment with NaCl and/or ABA	Mundy & Chua 1988
	<i>salT</i>	mRNA accumulates rapidly in shoots and roots of mature seedlings with ABA salts, PEG, NaCl and KCl; no induction in leaf lamina	Claes et al. 1990
	<i>em</i>	Induced by ABA and salt stress, salt interacts synergistically with ABA	Bostock & Quatrano 1992

*The names of various genes and proteins have been by and large reproduced here as per the original publications of the authors.

Table 2 Selective examples on the stress induced promoters involved in up-regulation of stress-related genes.

Gene	Source	Trans-Host, If Any	Inducing Stress Type(S)	Reference
Salt, low temperature and abscisic acid				
<i>bn115</i>	<i>B. napus</i>	-----	Low temperature	Jiang et al. 1996
<i>cat1</i>	<i>Z. mays</i>	<i>Z. mays</i>	ABA and osmotic stress	Guan et al. 2000
<i>cdeT27-45</i>	<i>C. plantagineum</i>	<i>N. tabacum</i>	Desiccation and ABA	Nelson et al. 1994
<i>ci21A</i>	<i>S. tuberosum</i>	<i>S. tuberosum</i>	Low temperature, drought and ABA	Schneider et al. 1997
<i>cor15A</i>	<i>A. thaliana</i>	-----	Low temperature, ABA and drought	Baker et al. 1994
<i>cor6.6</i>	<i>A. thaliana</i>	<i>N. tabacum</i>	Low temperature, osmotic stress and dehydration	Wang et al. 1995
<i>em</i>	<i>T. aestivum</i>	<i>N. tabacum</i> and <i>O. sativa</i>	ABA	Marcotte et al. 1989
<i>hva1</i>	<i>H. vulgare</i>	-----	Drought, low temperature, heat, salinity and ABA	Straub et al. 1994, Shen et al. 1996
<i>kin1</i>	<i>A. thaliana</i>	<i>N. tabacum</i>	Low temperature, osmotic stress and dehydration	Wang et al. 1995
<i>osmotin</i>	<i>N. tabacum</i>	<i>N. tabacum</i>	ABA, C ₂ H ₄ and NaCl.	Liu et al. 1995, Raghobama et al. 1997
<i>pin2</i>	<i>S. tuberosum</i>	<i>O. sativa</i>	Wounding, ABA and methyl jasmonate	Xu et al. 1993
<i>rab16</i>	<i>O. sativa</i>	<i>O. sativa</i>	Osmotic stress, water stress and ABA	Ono et al. 1996
<i>rab17</i>	<i>Z. mays</i>	<i>A. thaliana</i>	Water stress and osmotic stress	Busk et al. 1997, Vilardell et al. 1994
<i>rab21</i>	<i>O. sativa</i>	<i>O. sativa</i>	Water stress, osmotic stress and ABA	Mundy et al. 1998
<i>rab28</i>	<i>Z. mays</i>	<i>O. sativa</i>	Water stress and ABA	Pla et al. 1993
<i>rd22</i>	<i>A. thaliana</i>	<i>N. tabacum</i>	Dehydration, salt stress, water deficit and ABA	Yamaguchi-Shinozaki et al. 1993
<i>rd29</i>	<i>A. thaliana</i>	<i>N. tabacum</i>	Desiccation, cold, high salt conditions and ABA	Yamaguchi-Shinozaki et al. 1993, 1994
<i>β-phaseolin</i>	<i>P. vulgaris</i>	<i>N. tabacum</i>	ABA	Bustos et al. 1998
<i>wcs120</i>	<i>T. aestivum</i>	Several monocots and dicots	Low temperature	Oullet et al. 1998
Anaerobic stress				
<i>adh</i>	<i>A. thaliana</i>	<i>A. thaliana</i>	Dehydration, cold and hypoxia	Dolferus et al. 1994
	<i>Z. mays</i>	<i>O. sativa</i>	Dehydration, cold and hypoxia	Kyozuka et al. 1994
<i>gapC4</i>	<i>Z. mays</i>	<i>N. tabacum</i>	Anoxia, UV and wounding	Kohler et al. 1996, Geffers et al. 2000
<i>gpc4</i>	<i>Z. mays</i>	<i>Z. mays</i>	Anoxia	Manjunath et al. 1997
High temperature				
<i>gmhsp17.3B</i>	<i>G. max</i>	<i>N. tabacum</i>	High temperature	Rieping et al. 1992
<i>gmhsp17.5E</i>	<i>G. max</i>	<i>H. annuus</i>	High temperature	Gurley et al. 1986, Czarnicka et al. 1992
<i>hahsp17.6G1</i>	<i>H. annuus</i>	<i>N. tabacum</i>	Non-responsive to high temperature	Carranco et al. 1999

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Table 3 Selective characteristics of the genes encoding stress-related transcription factors.

Transcription Factor	Plant Species Examined	Binding Site	Characteristics	Reference
<i>alfin1</i>	<i>M. sativa</i>	G- rich triplets	Encodes a novel protein with a Cys4 and His/Cys3 putative zinc-binding domain, may play a role in the regulated expression of MsPRP2 in alfalfa roots contributing to salt tolerance	Bastola et al. 1998
<i>athb-12</i>	<i>A. thaliana</i>	Unknown	These genes contain a conserved sequence motif, the homeobox that encodes a DNA binding domain called as the homeodomain; they also contain a second element that codes for a putative leucine zipper motif; treatment with water stress and ABA resulted in the accumulation of <i>Athb-12</i>	Lee & Chun 1998
<i>athb-7</i>	<i>A. thaliana</i>	Unknown	Homeodomain-leucine zipper proteins; putative transcription factors encoded by a class of homeobox genes and are induced in all the organs by water deficit and osmotic stress	Soderman et al. 1996
AtMYB2	<i>A. thaliana</i>	MYB site	ATMYB2 is drought and ABA inducible and encodes the MYB related protein which functions as transcriptional activator of the <i>rd22</i> gene along with <i>rd22BP1</i>	Urao et al. 1993
CBF1	<i>A. thaliana</i>	CRT/DRE	CBF1 encodes an AP2 binding domain containing the transcriptional activator that binds to the CRT/DRE sequence in the genes; induced by low temperature	Stockinger et al. 1997, Medina et al. 1999
DREB1A and 2A	<i>A. thaliana</i>	DRE/ CRT	Bind to the DRE sequence <i>in vitro</i> and bring about freezing and dehydration tolerance; deduced amino acid sequence shows similarity in the conserved DNA binding domain found in the ERBP and APETALA2 proteins like that of CBF1	Liu et al. 1998
DREB 2A and 2B	<i>A. thaliana</i>	DRE/ CRT	Induced by dehydration and high salt stress; unlike the DREB1A these are not induced in response to low temperature; contain a conserved Ser/Thr rich region adjacent to the EREBP/ AP2 DNA binding domain which is considered to be phosphorylated	Nakashima et al. 2000
EmBP-1	<i>T. aestivum</i>	ABRE	Interacts specifically with the 8 bp sequence CACGTGCG in the ABRE; deduced amino acid sequence of the EmBP-1 contains some conserved basic and leucine zipper domains found in the transcription factors in the plants, yeast and mammals	Guilinan et al. 1990
HSF	<i>A. thaliana</i> , <i>L. peruvianum</i> , <i>Z. mays</i> and <i>G. max.</i>	HSE	Despite a considerable variability in size and sequence, their basic structure is similar; there is a highly conserved DNA binding domain near the N-terminus and the oligomerization domain is connected to the DNA binding domain by a flexible linker	Scharf et al. 1993, 1998, Czarnecka-Verner et al. 2000
Rd22BP1	<i>A. thaliana</i>	MYC site	Encodes a 68kDa protein that has a typical DNA binding domain of basic helix loop helix leucine zipper motifs in the MYC related transcription factors; dehydration stress and ABA induce the transcription of the <i>rd22BP1</i> and its induction precedes that of <i>rd22</i>	Abe et al. 1997.

The names of various genes and proteins have been by and large reproduced here as per the original publications of the authors.

processes that yeast system does not possess and testing relevance of genes associated with such processes in yeast may or may not be a valid approach.

The current success in plant genetic engineering research has been possible due to the development of *in vitro* techniques for the culture and propagation of cells and tissues. The first method used successfully for the introduction of exogenous DNA into plants employed the soil-borne organism *Agrobacterium tumefaciens*. Subsequently, several other methods (such as direct DNA transfer through electroporation into protoplasts, particle gun etc.) have been optimized for transferring genes, and this has enabled transformation of a large number of species. As of now, methods for genetic transformation of more than 150 different plant species have been optimized (Birch 1997, Hansen & Wright 1999). Among the plants, the best transformation frequencies have been noted with tobacco and *Arabidopsis*. Most work on testing of novel transgenes has therefore been carried out using these two species which is fair-enough to make a beginning (Grover & Minhas 2000). However, as the trans-gene for stress tolerance must be introduced in the destined species exhibiting stress sensitivity, optimization of the cultivar-specific methods for the genetic transformation of the crops has emerged as a high-priority objective in recent years (Grover et al. 1999). The production of transgenics involves several steps and techniques such as availability of suitable cloning vectors, promoters and related methods of tissue culture. One of the goals of the future research is to optimize tissue culture and genetic transformation work with more number of crop cultivars so that desired stress genes can be suitably trans-expressed.

Synthesis

Abiotic stresses elicit complex responses. To understand these responses, varied biological parameters have been utilized. From such efforts, we understand that abiotic stress responses are triggered at different levels of hierarchy of the cellular organization. It is shown that a large number of physiological and biochemical attributes of the cell are affected when plants experience abiotic stresses. However, specific biochemical/molecular changes that contribute towards stress

tolerance have only been partially identified thus far. Due to this gap in information, generation of abiotic stress tolerant plants through transgenic technology is proving a handicap. For removing the bottlenecks associated with production of abiotic stress tolerant plants, the detailed understanding of the plant abiotic stress responses is the need of the hour. The plant stress molecular biology and biotechnology research is limited by the non-availability of the stress genes to a large extent. The past attempts on the analysis of stress responses have mostly been made for defining the specific changes in gene expression, biochemical reaction or physiological event. These studies have remained focussed on analysis of single or limited number of genes and proteins at a given time. The present need is to look at stress responses with respect to global changes in different proteins/genes. Fortunately, the current developments in genomics and proteomics have the potential to present this kind of picture of the global changes in RNA and proteins. The genome-wide analysis of mRNA expression by micro-array chip technology is providing important clues about the expression patterns and the function of gene products while proteomics is turning out to be the major subject of research for defining the gene functions. The enormity of analyzing genomics is such that no laboratory can individually answer all the questions. Therefore, it is important that groups specializing in different aspects of plant biology look at genomics with their own viewpoints. Those who work with abiotic stresses using diverse experimental materials across the globe need to come under an elaborate network so that efforts are co-ordinated amongst different institutions.

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