Common Components, Networks, and Pathways of Cross-Tolerance to Stress. The Central Role of "Redox" and Abscisic Acid-Mediated Controls[1]

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The vigor and responsiveness of plants to environmental stress result from the constant re-adjustment of physiology and metabolism throughout the life cycle within the framework of the genetic background. Plants have developed unique strategies for responding to ever-changing environmental conditions, exhaustively monitoring their surroundings and adjusting their metabolic systems to maintain homeostasis. The severity of stress, the genetic background of the plant, and its individual history determine everyday survival or death. These factors dictate the destiny of any individual. The genome-environment interaction is, therefore, an essential focus for the elucidation of the nature of the phenotypic variation leading to the successful response of plants to environmental cues.

Plants acclimate to biotic and abiotic stresses by triggering a cascade or network of events that starts with stress perception and ends with the expression of a battery of target genes. The key components of the stress-response relationship are illustrated in Fig. 1. These are stress stimulus, signals, transducers, transcription regulators, target genes, and stress responses, including morphological, biochemical, and physiological changes. In evolutionary terms, components that are near to the end of the stress-response cascade are not predicted to be the ones whose actions significantly affect the operation of other genes. However, factors that act at early stages are critical for other cell functions. Plants make use of common pathways and components in the stress-response relationship. This phenomenon, which is known as cross-tolerance, allows plants to adapt/acclimate to a range of different stresses after exposure to one specific stress. The major focus of this review, therefore, concerns the basic features of signaling that underpin cross-tolerance and result from the action of common elements, which are likely to occur early in the stress response cascade. First, using drought and chilling as examples, we explore the evidence for common signals and elements that confer cross-tolerance. Second, we highlight the importance of "redox signals" in such networks and discuss the evidence to date for the existence of such pathways in plants. The elucidation of common components has enormous potential and has, therefore, become a priority in research and breeding programs aimed at improving plant stress tolerance.

REGULATION OF TRANSCRIPTION DURING STRESS

Gene expression is mainly regulated at the initiation of transcription. The proportion of the plant genome dedicated to genes encoding transcription factors reflects this important feature. Approximately 25% of the 25,498 genes encoding proteins from 11,000 families in the Arabidopsis genome are involved in transcription, signal transduction, and the control of cell destiny and survival. Moreover, about 15% of the genes sequenced in chromosome 4 alone participate in the regulation and mechanics of transcription (Bevan et al., 1998). Although an increasing number of the regulatory proteins involved in transcription have been identified in plants, our current knowledge of transcription factors mediating the stress response and their regulation is still limited compared with the vast amount of information available for animals and yeast.

Gene expression is mediated by one or more interacting transcription factors. Multiple protein-protein and/or protein-DNA interactions frequently dictate the rate of transcription by activation/repression of a given promoter under given environmental conditions. A good example is the interaction between the bZIP and Dof transcription factors in the expression of Arabidopsis glutathione-S-transferase-6 (*GST6*). The *GST6* promoter contains Dof-binding sites closely linked to a 20-bp octopine synthase (ocs) element. The ocs element is not only the binding site for bZIP proteins, but it is also responsive to H_2O_2 and pathogens. The *GST6* promoter is induced in roots after treatment with salicylic acid or H_2O_2 (Chen and Singh, 1999). However, mutation of the ocs element does not abolish expression suggesting

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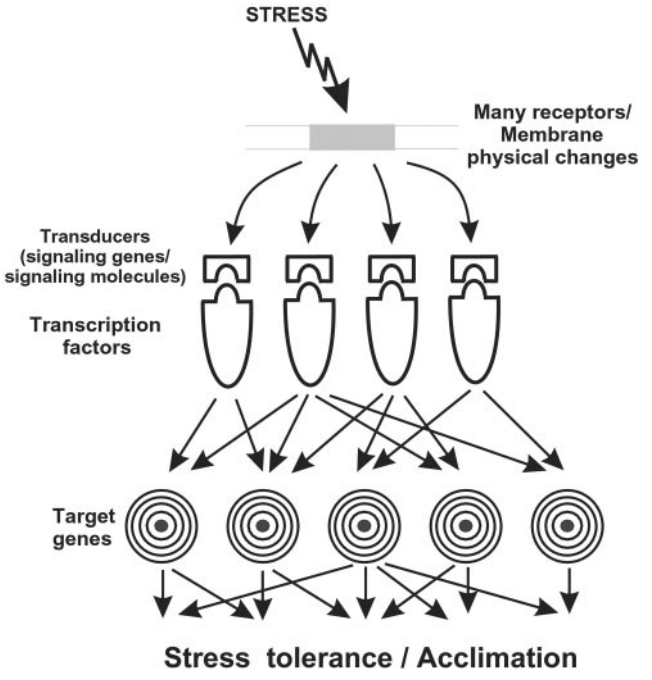

Figure 1. Schematic diagram of the components of the stress-response relationship. Receptors present on any membrane can respond to changes in the immediate environment (physical, chemical, or metabolite) and trigger signal transduction. Transducers are essential components in this process. They may participate at all levels: production, perception, and transmission of primary and secondary messengers. Transcription factors (regulators) are genes, which bind either directly or indirectly to cis-regulatory elements. These can act as activators or repressors of transcription or have other related functions. Target genes are denoted by the bulls-eyes, because these are the endpoints of each cascade of events.

that other promoter elements are also important in the regulation of *GST6*.

CIS-ELEMENTS AND BINDING FACTORS INVOLVED IN DROUGHT AND COLD

Drought and low growth temperatures cause major limitations on crop productivity. These stresses are complex environmental phenomena. Plant breeding for improved stress tolerance has consistently demonstrated that plant vigor over a range of environmental conditions is governed by multiple loci. Hence, stress tolerance is inherently multigenic in nature. Although the vast majority of these genes remain to be identified, some transcription factors and regulatory sequences in plant promoters have been described. *Cis*-elements and corresponding binding proteins have been implicated in both drought and low temperature tolerance in Arabidopsis as discussed below. This may be explained by the common requirement for stability during dehydration, a component inherent to both of these stresses and also to other environmental extremes such as high salt. The cis-acting element identified in the promoter region of the *RD29A* gene, for example, is responsive to both drought and low temperatures. This dehydration-responsive element (DRE) is essential for the regulation of expression of dehydration-responsive genes. It is also found in the promoter regions of other dehydration- and cold-inducible genes, such as *rd17*, *kin1*, and *cor6.6* (Wang et al., 1995; Iwasaki et al., 1997). The cDNAs encoding the DRE-binding proteins DREB1A and DREB2A were isolated using the yeast two-hybrid screening system. When DREB1A was expressed in transformed plants, under the control of *35S* cauliflower mosaic virus (CaMV) promoter, deregulated expression of stress-inducible genes was observed leading to increased freezing, salt, and drought tolerance (Liu et al., 1998). Moreover, even greater stress tolerance and improved growth was observed in other transformed plants where the stress-inducible *rd29A* promoter was used to drive DREB1A expression, compared with the growth retardation observed in CaMV promoter-DREB1A expressing plants under similar conditions (Kasuga et al., 1999).

CBF genes encode transcriptional activators that control the expression of a suite of genes containing C-repeat/DRE sequences in their promoters (Jaglo-Ottosen et al., 1998). Constitutive expression of CBF1 or CBF3 (equivalent to DREB1B and DREB1A) enhanced freezing tolerance and induced the expression of the cold-regulated (*COR*) genes. Moreover, overexpression of CBF3 resulted in the activation of multiple components in response to chilling. Transgenic plants overexpressing CBF3 had enhanced levels of Pro and total soluble sugars, including Suc, raffinose, Fru, and Glc (Gilmour et al., 2000).

Other transcriptional regulators, such as the MYC and MYB proteins, are activators in the dehydration- and abscisic acid (ABA)-inducible expression of the *rd22* gene (Abe et al., 1997). The promoter of *rd22* gene contains a 67-bp fragment with two closely situated recognition sites for the basic helix-loop-helix protein MYC. There is also a putative recognition site for MYB in the promoter of the *rd22* gene. All three recognition sites function as cis-acting elements in the dehydration-induced expression of *rd22*.

DRE-related motifs have been reported in the promoter region of the cold-inducible *wcs120* gene from wheat (*Triticum aestivum*; Ouellet et al., 1998). The copy number and organization of *wcs120* are identical in wheat cultivars with different degrees of freezing tolerance, and expression is regulated mainly at the transcriptional level. Homologs of *wcs120* are not expressed in other chilling-sensitive monocotyledonous (monocot) species, such as rice (*Oryza sativa*) and maize (*Zea mays*). The lack of expression may be due to inefficient cis-acting elements or to the absence of transcription factors regulating these genes. This could explain, at least in part, the inability of these chilling sensitive species to acclimate to cold temperatures. Moreover, these observations emphasize the

importance of identifying the specific responses of monocot and dicotyledonous species to stress.

Overexpression of the transcription factor Alfin1 was found to improve tolerance to salt stress in alfalfa (*Medicago sativa*) enhancing root growth under normal and saline conditions (Winicov and Bastola, 1999). Alfin1 binds to promoter fragments of the NaCl-inducible *MsPRP2* gene regulating its expression in a tissue-specific manner.

Analysis of the expression of dehydration-inducible genes in Arabidopsis suggests that there are at least four independent signal transduction pathways for the induction of genes in response to dehydration (Shinozaki and Yamaguchi-Shinozaki, 1997). Two of these are ABA-dependent and two are ABA-independent. ABA has been implicated in the regulation of many processes in plants, particularly those that involve metabolic arrest and cell survival. These include specific expression patterns during seed development and drought, cold, and salt responses. The mechanism of ABA-mediated regulation of transcription has been elucidated by analysis of the cis-acting sequences required for ABA-induced gene expression. ABA-inducible genes, such as *Em* from wheat and *rab16A* from rice, were used in expression studies. Analysis of protein binding in vitro revealed the presence of an ABA-responsive element (ABRE) in the promoters of these genes (Marcotte et al., 1989; Mundy et al., 1990). The ABRE family is similar to the G-box sequence group that is present in many promoters responsive to environmental stimuli such as UV, wounding, and anaerobiosis (Merkens et al., 1995). Analysis of the promoter of the chalcone synthase (*chs*) gene revealed two types of cis-elements, G-box and H-box, which seem to act differentially in tissue-specific and stress-induced expression (Faktor et al., 1997). Mutation of the G- and H-boxes decreased the response of the *chs* promoter to the abiotic elicitor $HgCl_2$ and TMV infection, the impairment being stronger in the case of the H-box mutation, which also affected the response of the promoter to wounding.

In summary, a single transcription factor can orchestrate the expression of many genes to improve stress tolerance. However, acclimation to complex stresses such as cold and drought must involve the simultaneous operation of many signaling pathways/networks. It is worth noting that, in many cases, plants survive stress by metabolic arrest, in which growth and development essentially stop. Such dramatic changes may be enhanced as a result of activation or de-regulated expression of transcription factors in transformed plants. Unpredictable performance is an important outcome of such manipulations and is a crucial limiting factor in terms of crop quality and yield. Agriculturally important parameters, such as yield and biomass, are critical points in any consideration of manipulations in the major food crops, particularly wheat and maize.

It is, therefore, not only essential to identify stress-regulated transcription factors, but it is also vital to characterize the proteins and the signaling mechanisms that control their function. The cis-responsive elements in the promoters of these signaling genes may hold the key with which to unravel the underlying mechanisms conferring tolerance to cold and drought. Because oxidative stress is a common signaling event in all stress situations, the elucidation of "redox"-mediated networks and pathways for the control of transcription is an essential step to understanding plant stress responses.

OXIDATIVE STRESS-RELATED CIS-ELEMENTS AND TRANS-ACTING FACTORS

The most important and best documented common response of plants to different abiotic and biotic stresses, such as heat, cold, high-light intensities, drought, osmotic shock, wounding, UV-B radiation, ozone, and pathogens is the accelerated production of active oxygen species (AOS) such as superoxide, hydrogen peroxide, and the hydroxyl radical. It is, therefore, surprising that little information is available on the cis-responsive elements and trans-acting factors related to oxidative stress responses in plants, particularly in comparison with that reported for other kingdoms.

A range of trans-acting factors has been identified in *Escherichia coli* and higher eukaryotes that regulate the expression of genes induced by oxidative stress (Table I). In *E. coli*, the transcription factor SoxR/SoxS mediates responses to superoxide ($O^{\cdot}_2{}^-$), whereas OxyR activates genes responsive to H_2O_2 (Christman et al., 1985; Greenberg et al., 1990; Tsaneva and Weiss, 1990). In mammalian systems, the transcription factors NF-κB and AP-1 are central to the regulation of the oxidative stress response. NF-κB is a multiunit transcription factor that is post-translationally activated by low H_2O_2 concentrations, causing the rapid induction of genes encoding defense and signaling proteins (Schreck et al., 1991). The activator protein-1 (AP-1) family comprises both Fos and Jun related proteins, which are post-transcriptionally regulated by complex mechanisms (Meyer et al., 1993; Bergelson et al., 1994). The yeast YAP-1 protein is homologous to the AP-1 family of eukaryotic transcription factors. *YAP*-deleted strains are sensitive to $O^{\cdot}_2{}^-$, H_2O_2, and compounds that generate these oxidants (Moye-Rowley et al., 1989). An antioxidant-responsive element (ARE) or electrophile-responsive element (EpRE), consisting of two non-overlapping core sequences GTGACA(A/T)(A/T) GC, is the binding site for the AP-1 transcription factor complex (Daniel, 1993). ARE is present in animal *GST* genes but not in plant *GST*s. To date, apart from AP-1 and ARE, no homologs of other major animal or microbial redox-sensitive elements and factors have been reported in plants.

Table I. *Control of gene expression under oxidative stress*
AOS, Active oxygen species.

Organism	AOS	cis-Element	Transcription Factor	Gene/s	Reference
E. coli	H_2O_2	–	OxyR	Catalase Glutathione reductase Alkyl hydroperoxide reductase	Greenberg et al. (1990)
	$O_2^{\cdot-}$	SOXS	SOXR/SOXS	MnSOD Endonuclease IV G6PDH	Tsaneva and Weiss (1990) Christman et al. (1985)
Yeast	H_2O_2, $O_2^{\cdot-}$	TPA/TRE	AP-1		Moye-Rowley et al. (1989)
Higher eukaryotes (mammals)	AOS	5′-GGGRNN(YYC)C-3′ TPA/TRE	NF-κB AP-1	Defense, signaling kinases	Schreck et al. (1991) Meyer et al. (1993) Bergelson et al. (1994)
Animals	H_2O_2	ARE	AP-1	GST NADPH-QR γ-ECS Metallothionein I MnSOD	Daniel (1993) Reviewed by Kahl (1997)
Plants	H_2O_2	ARE	–	CAT1 CAT2 CAT3	Polidoros and Scandalios (1999)
	Oligopeptide elicitor	W-box	WRKY	PR-1	Rushton et al. (1996)
			AP-1	GST	Reviewed by Marrs (1996)
	Ozone	inverse ERE	–	Stilbene synthase PR-1	Sandermann et al. (1998) Eckey-Kaltenbach et al. (1997)

Only recently have oxidative stress-responsive elements been identified in the promoters of plant genes, and these are relatively few. Signaling pathways for ozone and pathogen responses seem to involve the activation of the same cis-element. An ozone-responsive region was found in the promoter of the grapevine stilbene synthase gene (Sandermann et al., 1998). The promoter sequence contains an inverse elicitor-responsive element, also found in the promoters of defense-related genes, such as pathogenesis-related 1 protein. Pathogenesis-related 1 and related proteins are induced by both ozone and a fungal elicitor (Eckey-Kaltenbach et al., 1997). Plant *GST* promoters often contain ocs elements, which are similar to EpREs. Both ocs and EpREs have tandem binding sites, and both are binding sites for dimeric bZIP transcription factors (Zhang and Singh, 1994).

The action of H_2O_2 as a signal in the induction of the expression of the catalase (*Cat*) genes (*Cat1*, *Cat2*) and of *GST1* has recently been demonstrated (Polidoros and Scandalios, 1999). The ARE is present in all three maize *Cat* promoters having a role in the induction of gene expression in response to oxidative stress. Gel retardation analyses revealed that ARE interacts strongly with an unidentified transcription factor at late stages of germination in maize seeds, when the scutellum is undergoing senescence. *Cat1* and *Cat3* transcripts increase dramatically in wounded leaves, the response being independent of jasmonic acid and ABA (Guan and Scandalios, 2000). *Cat2* is specifically induced during drought in wheat leaves (C. Luna, G.M. Pastori, and C.H. Foyer, unpublished data). The sequence motif responsible for *Cat1* up-regulation during wounding was found to overlap with ABRE (G-box) in the *Cat1* promoter. This suggests that H_2O_2 may be the signal in wounding-regulated *CAT* expression.

Together with catalase, ascorbate peroxidase (APX) controls the amount of H_2O_2 present within the plant cell (but not the apoplast) so that it rarely approaches the concentrations that inhibit metabolism and trigger cell death. Several sequence motifs, characteristic of the heat shock element, are present in the promoters of pea (*Pisum sativum*) and Arabidopsis *APX1* genes (Storozhenko et al., 1998). In addition, sequences similar to the cis-elements as-1 from the CaMV promoter, ocs from ocs promoter, and the H-box recognized by proteins of the MYB family were found in the promoter of the *APX1* gene. The heat shock cis-element contributes to the induction of the gene by heat shock in vivo and only partially to the induction mediated by methyl viologen, a superoxide generating herbicide.

The Arabidopsis binding protein, CEO1, was found not only to confer tolerance to oxidative stress caused by tert-butylhydroperoxide, but also to give cross-tolerance to H_2O_2 and the superoxide generator, diamide, in a Yap-1 yeast mutant (Belles-Boix et al., 2000). CEO1 interacts physically with two DNA-binding-like proteins, and this suggests that CEO1 is a cofactor interacting with transcription factors involved in responses to stress. It is interesting to note that no CEO1 homologs have been reported to date in animals or microbes.

REDOX (OXIDANT AND ANTIOXIDANT)-MEDIATED SIGNALING

The concept that redox signals are key regulators of plant metabolism, morphology, and development is widely accepted. Key electron transport components, particularly plastoquinone and ubiquinone, have recently been shown to play a major role in local and systemic acquired resistance responses. Moreover, the importance of AOS in such responses has been repeatedly demonstrated (Levine et al., 1994; Alvarez et al., 1998; Chamnongpol et al., 1998). For example, H_2O_2 is considered to be a local and systemic signal involved in the adaptation of leaves to high light (Karpinski et al., 1999). Similarly, H_2O_2 induces synthesis of heat shock proteins and tolerance to heat shock as well as to low temperatures (Prasad et al., 1994; Foyer et al., 1997). H_2O_2 has now also been shown to be a crucial component of movement and growth responses, particularly those induced by environmental stimuli (Table II). H_2O_2 is, therefore, central to cross-tolerance phenomena and a key component in the stress survival network. In response to any stress, the flux of H_2O_2 generation is increased. Moreover, the plant cell is able to monitor the extent of flux enhancement or accumulation. Relatively small increases or localized bursts of H_2O_2 influence only part of the network and modify gene expression in such a way as to strengthen plant defense responses. We conclude that changes in H_2O_2 homeostasis are a pivotal signaling event allowing the general enhancement of stress tolerance. In contrast, large increases in H_2O_2 trigger a distinct local sequence of events in gene expression that leads inevitably to programmed cell death. This effective strategy allows rapid, appropriate, and flexible responses to changing environmental threats.

Much remains to be resolved concerning the components of the H_2O_2-induced signaling cascade and the mechanism(s) by which information on redox status is used to modify gene expression. The role of mitogen-activated protein kinases (MAPKs) in oxidative stress signaling has been recently demonstrated in Arabidopsis. A MAPKKK, ANP1, that activates a specific class of stress-induced MAPKs, was found to be induced by H_2O_2 (Kovtun et al., 2000). Evidence for intensive cross-talk between oxidative stress and plant growth, mediated by the MAPK signaling cascade, was provided by the observed strong effect of H_2O_2 on MAPKs activation together with the repressive action of MAPKs on auxin-inducible promoters. Oxidants such as H_2O_2 interact with other signaling systems, particularly hormones (Table II). They also influence and modify the action of other secondary messengers such as Ca^{2+} and NO. To date, however, unlike animals, the formation of peroxynitrite has not been found to be critical in NO action. Similarly, H_2O_2 has a strong regulatory influence on fluxes through Ca^{2+} channels and on Ca^{2+} concentrations in different cellular compartments. Most importantly, the recent observation that H_2O_2 is transported from the apoplast to the cytosol through water channels (aquaporins; Fig. 2) suggests other possibilities for regulation of signal transduction via modulation of transport systems.

The evidence discussed above supports the view that H_2O_2 acts as a signal transducing molecule in optimal and stress conditions. The life-time of H_2O_2 in planta is determined by the capacity of the two major antioxidant buffers of the plant cell, ascorbate and glutathione, together with the antioxidant enzymes that use these antioxidants (Noctor and Foyer, 1998). Most plant cells contain very large quantities of ascorbate (10–100 mM) and glutathione (1–10 mM), and most intracellular compartments, hence, have the capacity to deal with very high fluxes of H_2O_2 production (Noctor et al., 2002). Here, we define the compartment outside the plasma membrane, including the cell wall, as the apoplasm and everything inside the plasma membrane as the cytoplasm. In comparison with the cytoplasm, the apoplasm has relatively little antioxidant defense and, hence, H_2O_2 accumulates when H_2O_2 synthesis (in the plasmalemma or cell wall) is increased. This causes oxidation of the apoplast as observed during the hypersensitive response to pathogens or upon exposure to ozone. A strong oxidative signal can persist on the apoplastic face of the plasmalemma causing modifications in calcium transport and other ion fluxes as well as modifying plasmalemma-based electron transport systems (Fig. 2). In contrast, H_2O_2 transported into the cytoplasm via the aquaporins is immediately neutralized, and the redox state of the cytoplasm can, hence, be maintained at a very different level than that of the apoplasm. Moreover, rapid compartment-specific differences in redox state (and, hence, signaling) that influence the operation of many fundamental processes in plant cells can be achieved by modifying AOS (H_2O_2) production or by repression or activation of the antioxidant defenses or by both. Rapid cell death responses, such as occur

Table II. *Ascorbate, glutathione, and H_2O_2 function as upstream/downstream components of hormone-mediated signal transduction*

Hormones	Tissue	Agent	Function	Reference
Auxin	Root	H_2O_2	Gravitropism	Joo et al. (2001)
Abscisic acid	Leaves	H_2O_2	Stomatal closure	Murata et al. (2001)
Ca^{2+}	Leaves	H_2O_2	Stomatal closure	Pei et al. (2000)
Abscisic acid	Aleurone	Antioxidants	Cell survival	Bethke and Jones (2001)
Gibberelic acid	Aleurone	H_2O_2	Programmed cell death	Bethke and Jones (2001)

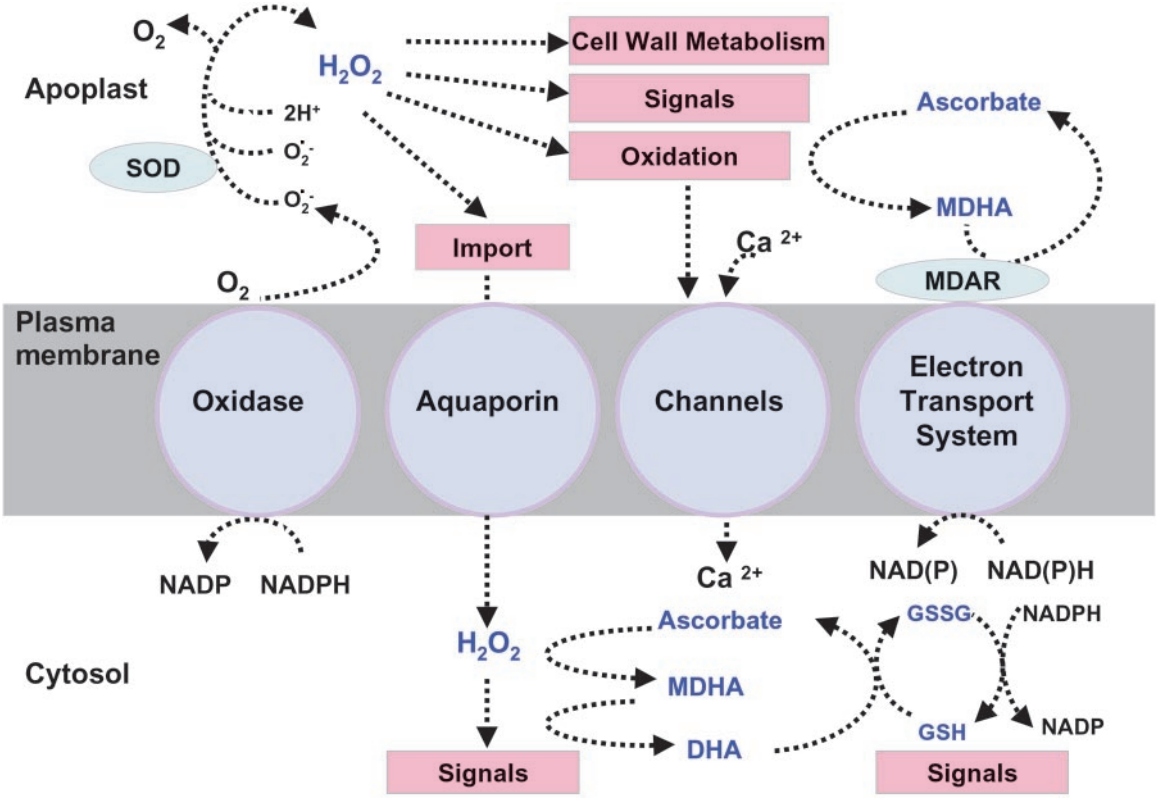

Figure 2. Mechanisms of H_2O_2/antioxidant signaling across the plasma membrane. Upon elicitation, H_2O_2 is produced in the apoplasm by several processes, including activation of NADPH oxidases, cell wall peroxidases, or other related enzymes (Bolwell et al., 1995). For simplicity, we have chosen to show only the pathway that we find most convincing in terms of a high velocity H_2O_2 production. This route involves production of H_2O_2 by the combined action of NADPH oxidase and superoxide dismutase (SOD). In the apoplasm, H_2O_2 has several possible fates. H_2O_2 can be used directly in cell wall metabolism, it can be oxidized by ascorbate, or it can act directly as a local or systemic signal. Most importantly, it can trigger at least three different routes of signal transduction simultaneously. The three possible pathways of H_2O_2 signal transduction are as follows: (a) Transport through the aquaporins allows rapid entry of H_2O_2 in the "sensing" cell, where it can directly trigger local signal transduction events. (b) H_2O_2 modifies calcium flux into the cells and, hence, changes calcium-induced signaling pathways. Other transport systems may also be modified if they are subject to redox-mediated regulation. (c) For regeneration, the oxidized forms of ascorbate have to interact with the plasma membrane or return to the cytosol because the apoplast has little or no reducing power. The reduced and oxidized forms of ascorbate can themselves act as signal-transducing molecules; for example, monodehydroascorbate (MDHA) is involved in cell cycle regulation, whereas dehydroascorbate (DHA) regulates cell growth. Moreover, by interaction with the glutathione pool in the cell, DHA can trigger other signaling sequences because the reduced (GSH) and oxidized (GSSG) forms of glutathione also have effects on gene expression. A plasma membrane associated monodehydroascorbate reductase (MDAR) could be involved in signal transduction perhaps via a plasma membrane electron transport chain. Superoxide itself could trigger an independent series of signaling events, but most will be converted to H_2O_2 by the action of an apoplastic superoxide dismutase (SOD).

in the aleurone cells of cereal grains, incorporate both of these events (Bethke and Jones, 2001).

Specific compartment-based signaling can also be achieved via differential changes in the amounts and relative reduction states of the ascorbate and glutathione pools (Noctor et al., 2000). GSH and ascorbate are key components of redox signaling. The ascorbate/dehydroascorbate and GSH/oxidized glutathione redox couples have been shown to modulate gene expression (Baier et al., 2000; Noctor et al., 2000).

Although glutathione has long been considered as a transcriptional regulator, ascorbate-mediated regulation of gene expression has only recently been demonstrated (Baier et al., 2000; Veljovic-Jovanovic et al., 2001). Thiols such as thioredoxin, dithiothreitol, Cys, and GSH enhance NF-κB DNA binding activity in animal systems (Galter et al., 1994; Arnér and Holmgren, 2000). GSH-responsive elements are present in the promoters of *GST* genes and in genes involved in the synthesis of phytoalexins (Dron et al., 1988; Levine et al., 1994). We have also previously suggested that the low availability of reducing power in the bundle sheath compared with the mesophyll cells of maize leaves may control the intercellular distribution of antioxidant enzymes such as glutathione reductase (GR). The GR enzyme protein is localized exclusively in the maize leaf mesophyll cells, but GR transcripts are found in both bundle sheath and

mesophyll cells of maize leaves (Pastori et al., 2000). This suggests that redox control of translation is a key determinant of protein abundance in maize.

CONCLUSIONS

The ways that plants respond to stress in the physical environment is crucial for productivity. From an agricultural perspective, environmental stresses constitute the most significant factors leading to substantial and unpredictable decreases in crop yield at the present time. The genome-environment interaction is also a key determinant to plant tissue composition (quality factors), anatomy, morphology, and development. Plants have to integrate a diversity of environmental and metabolic signals; they do this via a network of interacting signal transduction pathways that together regulate gene expression during stress. It is not surprising that a common "alarm" signaling system has evolved to provide pre-emptive defenses and protection against the many challenges of a harmful environment. In our view, this alarm signal is oxidative in nature, employing H_2O_2 and other AOS as key signals and messengers. These components are also clearly involved in the regulation of development and differentiation. Agriculture requires fast growth and high yield particularly in cereals. The interaction of signals conferring cross-tolerance and developmental traits and its influence on crop growth and yield is, therefore, a priority in programs for improving plant stress tolerance.

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