Interactions between cytokinin signalling and abiotic stress responses

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Abstract

Plants have evolved elaborate mechanisms for sensing and responding to sub-optimal environmental conditions. Abiotic stresses caused by these conditions trigger a wide range of local and long-distance signals which must be coordinated and integrated into whole-plant processes, such as development, in order for the plant to respond properly and survive. Several hormones function as key regulators of stress tolerance, connecting local stimuli to systemic responses. Cytokinin is a hormone well known for its role in numerous aspects of growth and development, although abundant evidence also indicates that cytokinin functions in stress responses as well. At present, a full understanding of the effects of cytokinin on plant resistance to stress is lacking, possibly as a result of the complex interactions between cytokinin and stress signalling. Current knowledge of the physiological relationship between cytokinin and abiotic stress, based on measurements of cytokinin levels under stress conditions and the effects of cytokinin treatment on stress tolerance, has been examined here. A pattern of transcriptional regulation of stress-related genes by cytokinin in different plant species has also been identified. In addition, research regarding the role of specific cytokinin signalling components in a variety of stress responses is presented. We discuss what this body of research collectively implies with regard to cross-talk between cytokinin and abiotic stress tolerance.

Key words: Abiotic stress, cytokinin, hormones, signal transduction, stress tolerance, transcription factor.

Introduction

Cytokinin is a plant hormone that regulates a wide array of processes crucial to plant development (Werner and Schmulling, 2009; Kieber and Schaller, 2014). Cytokinin was first identified as a potent inducer of cell division in tissue culture and is now known to be a key regulator of the cell cycle (Miller et al., 1955, 1956; Schaller et al., 2014). Along with auxin, cytokinin plays an important role in regulating cell divisions and the maintenance of stem cells in apical meristems of both shoots (Gordon et al., 2009; Zhao et al., 2010; Su et al., 2011) and roots (Dello Ioio et al., 2008; Zhang et al., 2013). Functional roles of cytokinin in growth and development at the tissue and organ level include: inhibition of lateral root initiation (Laplaze et al., 2007; Bielach et al., 2012), differentiation of phloem and metaxylem in roots (Mähönen et al., 2000; Bishopp et al., 2011), regulation of cell division and photomorphogenic differentiation in expanding leaves (Chory et al., 1994; Chiang et al., 2012; Efroni et al., 2013) and inhibition of leaf senescence (Gan and Amasino, 1996; Zwack and Rashotte, 2013). By contrast, interactions between cytokinin signalling, environmental stimuli, and stress have only more recently begun to be well characterized (Argueso et al., 2009; Ha et al., 2012; O’Brien and Benkova, 2013).

Several other plant hormones are known to function in abiotic stress responses. Abscisic acid (ABA) has long been recognized as the primary plant ‘stress hormone’, regulating a wide range of mechanisms leading to enhanced stress tolerance (Cutler et al., 2010; Danquah et al., 2014). Ethylene is also involved in the abiotic stress response, in part, by limiting growth in favour of increased stress tolerance (Morgan and Drew, 1997; Wang et al., 2013). Salicylic acid and jasmonic
acid are important in stress responses as well, however, these hormones are primarily linked to biotic stress (Wasterneck, 2007; An and Mou, 2011). In addition, evidence exists in support of the involvement of auxin and gibberellins in stress adaptation, which may occur indirectly through alterations in growth (Achard et al., 2008; Tognetti et al., 2012).

Cytokinin plays an important and complex role in abiotic stress responses

Cytokinin is generally considered to play a negative role in plant adaptation to stress, however, this is not always clearly supported. In fact, evidence exists for cytokinin having both positive and negative effects on stress tolerance. Much of the conflicting evidence has come from physiological investigations examining endogenous cytokinin levels during and after stress treatments and/or the effects that exogenous cytokinin application has on stress tolerance. Numerous studies, conducted in a wide range of plant taxa, have found that cytokinin concentrations decrease in response to extended stress (Itai and Vaadia, 1965; Itai et al., 1973; Walker and Dumbroff, 1981; Caers et al., 1985; Hubick et al., 1986; Hansen and Dörfling, 2003; Kudoyarova et al., 2007; Albacete et al., 2008; Ghanem et al., 2008). By contrast, other investigations have reported both short-term and sustained increases in cytokinin levels, particularly in response to severe stress (Walker and Dumbroff, 1981; Hansen and Dörfling, 2003; Pospisilova et al., 2005; Alvarez et al., 2008). The measurement of cytokinin in xylem sap of stress-treated plants has indicated that cytokinin long-distance transport is reduced in some species under certain conditions, but the physiological relevance of these findings has been questioned (Burrows and Carr, 1969; Bano et al., 1994; Hare et al., 1997). Expression analyses of Arabidopsis cytokinin biosynthesis (IPT) and catabolism (CKX) genes following NaCl treatment showed that IPT5 and IPT7 are up-regulated for 1–2 h before returning to pretreatment levels. Conversely, CKX1, CKX3, and CKX6 are repressed after 1 h followed by a gradual increase with elevated levels sustained for 5–10+ h (Nishiyama et al., 2011). Taken together, analyses of cytokinin levels during the stress response could be interpreted as indicating that cytokinin concentrations first undergo a transient increase upon exposure to stress followed by either an overall decrease under sustained moderate stress or the maintenance of initially increased higher levels when challenged with more severe conditions (Fig. 1).

The effects of an exogenous cytokinin application towards regulating stress tolerance have also been examined using a variety of hormone-treatment strategies. Bean plants treated with cytokinin by foliar spray were more susceptible to salt treatment than control plants (Kirkham et al., 1974). However, wheat seedlings grown on cytokinin-supplemented media and sprouted potato tubers pretreated with cytokinin demonstrated improved salt tolerance (Naqvi et al., 1982; Abdullah and Ahmad, 1990). Pospisilova and Batkova (2004) found irrigation with cytokinin prior to drought increased the tolerance of bean plants, but had no effect and a negative effect on tolerance in maize and sugar beet, respectively. Cytokinin aided the recovery of leaf photosynthetic performance when applied following heat shock in maize and tobacco; however, cytokinin pretreatment exacerbated the negative effects of the stress (Itai et al., 1978; Caers et al., 1985). Arabidopsis plants grown on media supplemented with cytokinin had a higher survival rate than non-supplemented plants when exposed to freezing or dehydrating conditions (Jeon et al., 2010; Kang et al., 2012). While the plants did survive in these studies, the exogenous cytokinin resulted in overall inhibited growth. Together, these studies indicate that multiple factors influence how cytokinin treatment affects stress signalling and that the spatial, temporal, and developmental context may be important factors in the downstream stress response.

More recently a novel approach has been taken to examine the effects of increasing cytokinin levels in relation to stress tolerance. The isopentenyl transferase (IPT) gene from Agrobacterium tumfaciens, which catalyses the rate-limiting step of cytokinin biosynthesis, was inserted into the genome of tobacco plants under the regulation of a stress-inducible promoter. The resulting transgenic plants increase cytokinin levels specifically in response to stress and have enhanced drought tolerance (Rivero et al., 2007). Subsequent work using this same stress-induced cytokinin circuit has replicated these findings in transgenic rice and peanut plants (Peleg et al., 2011; Qin et al., 2011). In apparent contrast to these findings, Arabidopsis ipt mutants, which have reduced cytokinin levels, are also more drought resistant compared with the wild type (WT) (Nishiyama et al., 2011). Decreased cytokinin levels achieved by over-production of the cytokinin-degrading enzyme cytokinin oxidase (CKX) in either a constitutive or root-specific manner, also has a positive effect on drought-stress tolerance (Werner et al., 2010; Nishiyama et al., 2011; Mackova et al., 2013). Importantly, the root-specific (WRKY6)
promoter used in this study is repressed in response to stress so the over-production of CKX does not persist under drought. Therefore the increased tolerance was attributed to the plants having enhanced root systems as a result of diminished cytokinin (which inhibits root growth) during development (Mackova et al., 2013). Collectively, these experiments clearly demonstrate the potential impact of altered cytokinin metabolism on stress responses, and further emphasize the complex role it plays in such responses.

Transcriptional regulation of stress related genes by cytokinin

Transcriptome-wide responses to cytokinin treatment have been examined many times. These have, in turn, recently been used in comprehensive meta-analyses of transcriptional responses to cytokinin (Brenner et al., 2012; Bhargava et al., 2013; Brenner and Schmulling, 2015). Among the processes from GO term/MapMan analyses, implicated as being regulated by cytokinin were abiotic stress responses, particularly response to oxidative stress—with an abundance of redox-associated enzyme activities (such as peroxidase and glutathione transferase) (Brenner et al., 2012; Bhargava et al., 2013). It was also shown that genes that are most highly responsive to cytokinin tend to be repressed in response to external stimuli including stress conditions (Brenner et al., 2012).

To understand the regulation of stress-responsive genes by cytokinin better, induced and repressed genes from two different cytokinin transcriptome profiling experiments were separately examined in Arabidopsis for additional connections to stress (Rashotte et al., 2003; Brenner et al., 2005). Functional clusters of enriched GO biological process terms were generated using tools available at the DAVID bioinformatics resources website (Table 1) (Huang et al., 2009a, b). For both experiments, the most highly enriched cluster of induced genes included the term ‘response to hormone stimulus’ along with other similar terms. From both sets of down-regulated genes the cluster with the greatest degree of enrichment was characterized by oxidative stress-related terms. A similar analysis of individually enriched terms was also conducted with publicly available transcriptome datasets from cytokinin-treated rice (Oryza sativa) and tomato (Solanum lycopersicum) plants to determine if comparable responses occurred in these species (Table 2) (Gupta et al., 2013; Sato et al., 2013; Shi et al., 2013). In the datasets of both species, genes with molecular functions related to the detoxification of reactive oxygen were over-represented among induced genes. Interestingly, the same terms were enriched for the repressed genes, generally at a higher threshold of significance. Tomato and rice genes repressed by cytokinin were also enriched with the GO terms ‘response to stress’ and ‘response to oxidative stress’, respectively. In agreement with this trend, an examination of differentially expressed Arabidopsis genes in cytokinin-deficient (and salt-tolerant) ipt1,3,5,7 mutant plants revealed that genes involved in response to and breakdown of ROS were greatly over-represented among those with increased expression relative to the WT under normal conditions (Nishiyama et al., 2012). This pattern of regulation suggests that cytokinin may act transcriptionally to alter responses to ROS, which are known to be produced as a result of a wide range of abiotic stress conditions.

The cytokinin signalling pathway interacts with multiple abiotic stress responses

Identification of cytokinin receptors and subsequent characterization of the cytokinin signalling pathway began in the late 1990s; it is now known to be a modified version of the bacterial two-component signalling system (Kieber and Schaller, 2014). The two-component cytokinin signalling pathway (TCS) includes membrane-bound (primarily ER) hybrid histidine kinases (HKs) with a cytokinin-binding input domain (CHKs) (Wulfetange et al., 2011). Upon binding of cytokinin, CHK dimers become auto-phosphorylated (Shi and Rashotte, 2012). A subsequent phosphorelay involves histidine phosphotransfer proteins (HPts) that carry the signal into the nucleus where they phosphorylate the receiver domain of two types of response regulator proteins (RRs). Phosphorylation of B-type RRs (RRBs) activates these GARP domain-containing MYB-like transcription factors, which regulate the expression of cytokinin-responsive genes.

Table 1. Most enriched clusters of biological process GO terms from cytokinin transcriptome datasets

Clustering and enrichment analyses performed using DAVID Bioinformatic Resources Functional Annotation Clustering at high stringency.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Representative term from top cluster</th>
<th>Genes in cluster (%)</th>
<th>Enrichment score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rashotte et al., 2003</td>
<td>Response to hormone stimulus</td>
<td>24</td>
<td>9.71</td>
</tr>
<tr>
<td>Induced</td>
<td>Response to oxidative stress</td>
<td>4.5</td>
<td>3.13</td>
</tr>
<tr>
<td>Rashotte et al., 2003</td>
<td>Response to hormone stimulus</td>
<td>13</td>
<td>16.57</td>
</tr>
<tr>
<td>Repressed</td>
<td>Response to oxidative stress</td>
<td>2.3</td>
<td>7.84</td>
</tr>
<tr>
<td>Brenner et al., 2005</td>
<td>Response to hormone stimulus</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Induced</td>
<td>Response to oxidative stress</td>
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<tr>
<td>Brenner et al., 2005</td>
<td>Response to oxidative stress</td>
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a All genes induced or repressed at any time-point ≥1 h were combined.
genes. Among the most highly induced genes are the A-type RRs (RRAs) which are similar to RRBs but lack a DNA-binding GARP domain. As such, these proteins act as negative regulators of the cytokinin signal primarily by competing with RRBs for phosphorylation by HPts (Gupta and Rashotte, 2012). Like the RRAs, C-type RRs (RRCs) lack a DNA-binding domain and are also believed to act as negative regulators of cytokinin signalling. The elucidation of this pathway and identification of its components, particularly in Arabidopsis has enabled researchers to use reverse genetic approaches to examine in greater detail specific roles of, and interactions involving, cytokinin signalling components in response to abiotic stress (summarized in Fig. 2).

Osmotic stress: drought and salt

Loss of water potential as a result of drought or dehydration reduces transpiration and negatively impacts numerous processes including solute transport and photosynthesis (Farooq et al., 2009). Arabidopsis possesses three CHKs (AHK2, AHK3, and AHK4). The expression of two of these receptors, AHK2 and AHK3, is induced by drought and osmotic stress suggesting a state of heightened cytokinin sensitivity under these conditions. Plants lacking either or both of these receptors have enhanced tolerance to drought treatment as well as increased sensitivity to ABA (Tran et al., 2007). This indicates that these receptors (and presumably the downstream output of the cytokinin signal) negatively impact drought tolerance. By contrast with the AHKs, expression of Arabidopsis HPts (AHPs) is repressed by drought stress. ahp2,ahp3,ahp5 triple mutants do, however, demonstrate a drought-tolerance phenotype similar to receptor mutants (Nishiyama et al., 2013). Interestingly, drought induction of Arabidopsis A-type RRs (ARRs) ARR5 and ARR15 and the C-type RR ARR22 is independent of the cytokinin receptors, implying that these downstream components of the TCS may be regulated by other additional signalling pathways (Kang et al., 2012). Moreover, this same work demonstrated a positive effect of cytokinin pretreatment on drought tolerance which was enhanced in ahk2 and ahk3 mutants, indicating that enhancement of survival by cytokinin was not mediated by these receptors. Because loss of AHK4 did not suppress the enhanced survival, this effect of cytokinin may have been independent of TCS signalling.

Salt and drought stress have similar effects on water potential, but salinity has additional cytotoxic effects within the cell; accordingly, regulatory responses to these conditions may also be distinct (Zhu, 2002). The role of cytokinin signalling in salt stress has also been examined. As is the case for drought, AHK2 and AHK3 are induced by saline conditions, and single ahk2, ahk3 and double ahk2,ahk3 mutants are more tolerant of these conditions (Tran et al., 2007). Consistent with this finding implying a negative regulation
of salt responses by cytokinin signalling, the B-type RR double mutant arr1arr12 demonstrates increased salt tolerance (Mason et al., 2010). However, despite greater cytokinin-sensitivity, arr3, arr4, arr5, arr6 quadruple RRA mutants are also more salt tolerant (Mason et al., 2010). This further supports the notion of RRAs interacting with other signalling systems independent of cytokinin.

In addition to the three cytokinin receptor HKs, the Arabidopsis genome encodes eight other HK proteins. Five of these are ethylene receptors that function independently of histidine kinase activity. The remaining three (AHK1, AHK5, and CKI1) are functional HKs, but lack cytokinin-binding capability (Schaller et al., 2008). AHK1 is induced by drought and is a positive regulator of drought tolerance, possibly acting as an osmosensor (Tran et al., 2007; Wohlbach et al., 2008; Kumar et al., 2013). It is unknown whether this regulation is mediated through downstream TCS components. Alternatively, AHK5, a cytoplasmic HK, is a negative regulator of both drought and salt stress, directly interacting with AHP1, AHP2, and AHP5 (Mira-Rodado et al., 2012; Pham et al., 2012). Although these HK proteins are not activated by cytokinin, they may act through shared downstream components, integrating stress signalling with cytokinin responses (Fig. 2).

**Low temperature stress: cold and freezing**

Cold conditions negatively impact membrane fluidity and transpiration rates leading to dysfunctions in primary metabolism. Chilling also initiates an acclimation response that prepares the plant for the more severe stress associated with freezing temperatures (Beck et al., 2007). Exposure to cold, non-freezing temperatures results in transiently induced expression of the RRAs ARR5, 6, 7, and 15, which is dependent upon the function of the receptors AHK2 and AHK3, along with AHP2, 3 or 5, and the RRB ARR1 (Jeon et al., 2010; Jeon and Kim, 2013). Upon extended cold treatment (6 h) EIN3, a positive regulator of ethylene signalling, represses the expression of ARR5, 7, and 15 (Shi et al., 2012b). This repression can be overcome by cytokinin treatment which, in addition to constitutive overexpression of ARR5, 7 or 15, enhances tolerance to freezing conditions (Shi et al., 2012b). Plants overexpressing ARRI also maintain elevated levels of these RRAs during extended cold and when they are pretreated with cytokinin become more freeze-tolerant than WT controls (Jeon and Kim, 2013). These findings indicate that a subset of RRAs positively regulate resistance to freezing temperatures (Fig. 2).

By contrast, arr5, arr6, and arr7 mutants are reported to have enhanced freeze tolerance and the overexpression of ARR7 results in greater susceptibility to freezing (Jeon et al., 2010). In addition, inducible overexpression of the type-C RR ARR22, represses the expression of several RRAs, including ARR5, 6, and 7; and results in increased resistance to cold (and drought) stress (Kang et al., 2013). These conflicting results make it difficult to determine the precise role of cytokinin signalling in cold-acclimation, yet it seems clear that proper expression, particularly of a subset of RRAs, is crucial for optimal tolerance of freezing conditions.

**Photooxidative stress**

Emerging evidence has implicated cytokinin signalling in additional abiotic stresses related to photosynthetic dysfunction leading to the production of reactive oxygen species (ROS) (Fig. 2). Loss of AHK2 and AHK3 resulted in greater photooxidative stress tolerance as indicated by decreased proline accumulation, lipid peroxidation, and chlorophyll loss. This was interpreted as an indication that these receptors negatively regulate tolerance under such conditions (Danilova et al., 2014). A recent report that ahk2,3 and arr1,12 double mutants were hypersensitive to high-light stress, indicates that cytokinin signalling may play a positive role in this response, again illustrating the complex nature of interaction between cytokinin and abiotic stress responses (Cortleven et al., 2014).

It should be noted that clear connections also exist between cytokinin signalling and biotic stress. These important interactions have been reviewed elsewhere and are outside the scope of this review (Argueso et al., 2009; O’Brien and Benkova, 2013).

**Cross-talk between ABA and cytokinin signalling**

Some of the changes in stress tolerance associated with cytokinin signalling and the metabolism mutants described above are also accompanied by alterations in ABA sensitivity (Tran et al., 2007; Jeon et al., 2010; Nishiyama et al., 2011). In addition, cytokinin-deficient plants have decreased levels of ABA, due to a repression of ABA biosynthesis (Nishiyama et al., 2011; Mackova et al., 2013). Treatment of Arabidopsis plants with ABA has been shown to repress the expression of the type-A RRs ARR6 and ARR9, an effect greatly diminished in ahk2,ahk4 and ahk3,ahk4 double mutants. This implies that this ABA repression occurs, at least in part, by direct interaction with the TCS pathway (Yang et al., 2014).

Direct interactions between the cytokinin and ABA signalling pathways have been described in the regulation of other (non-stress) processes. For example, during seed germination ARR4, 5, and 6 proteins interact with and inhibit the function of the transcription factor ABI5, a positive regulator of ABA signalling (Wang et al., 2011). Another component of the ABA signalling pathway, ABI4, which functions in a manner similar to ABI5, induces the expression of ARR5 in lateral root formation (Shkolnik-Inbar and Bar-Zvi, 2010). In addition, cytokinin signalling enhances cotyledon greening by promoting degradation of ABI5 in a manner dependent upon several different parts of the TCS: AHK4, AHP2, AHP3, AHP5, and ARR12 (Guan et al., 2014). Although such interactions have not been demonstrated in the regulation of the abiotic stress response, these findings support the feasibility of similar mechanisms of cross-talk.

Recently, a very different cytokinin–ABA interaction, not involving the TCS, was reported. ABA-mediated stomatal closure in response to drought involves the production of nitric oxide (NO). Cytokinin inhibits this process through direct interaction with and reduction of the NO molecule,
acting as a scavenger of this signalling molecule (Liu et al., 2013a). Thus, in at least this case, cytokinin itself is directly involved in modulating the ABA response.

**Cytokinin Response Factors: integrators of cytokinin and abiotic stress responses**

Cytokinin Response Factors or CRFs comprise a small monophyletic group of AP2/ERF transcription factors that function as a side branch of the TCS pathway (Rashotte et al., 2006). CRF proteins interact with TCS components, primarily HPtS and, to a lesser extent, type-A and type-B RRs, however, the function of these interactions is unclear (Cutelfifle et al., 2011). An evolutionarily conserved subset of CRFs are transcriptionally induced by cytokinin, placing them downstream of the TCS pathway, yet CRFs themselves regulate transcriptional responses to cytokinin in concert with the RRBs (Rashotte et al., 2006; Shi et al., 2012a; Zwack et al., 2012). CRFs have been functionally linked to classical cytokinin-regulated processes (Rashotte et al., 2006; Okazaki et al., 2009; Zwack and Rashotte, 2013), and a large amount of correlative (expression-based) evidence suggests roles in stress response but, to date, few such roles have been demonstrated experimentally.

Analysis of microarray data indicates that *Arabidopsis* CRFs are responsive to various abiotic stresses (Argueso et al., 2009). Similar expression patterns have been shown for CRFs from tomato (*Solanum lycopersicum*) and Chinese cabbage (*Brassica rapa*) (Shi et al., 2012a, 2014; Liu et al., 2013b; Gupta and Rashotte, 2014). Additional studies have provided more detailed information about the regulation of CRFs in response to specific abiotic stresses.

Lee et al. (2005) demonstrated that *CRF3* is induced at low temperatures and that this regulation is mediated by the cold responsive transcription factor ICE1. In *Arabidopsis*, *CRF4* has the greatest sequence similarity to *CRF3*. A separate study using reporter genes and quantitative PCR (qPCR) showed that this gene is highly induced by cold as well. A role in cold-acclimation was demonstrated in this instance as constitutive overexpression of *CRF4* enhanced freeze tolerance in non-acclimated plants (Compton, 2012).

The tobacco CRF referred to as Tobacco stress-induced gene 1 (*Tsi1*) was originally identified in a screen for salt-inducible transcripts. Overexpression of the Tsi1 protein was found to confer greater tolerance, not only to salt but also to pathogen attack which was taken to suggest that it was a positive regulator of two distinct responses (Park et al., 2001). Expression of the tomato orthologue of *Tsi1* (*SlCRF1*) is also induced by salt but a similar functional role in salt stress has not been demonstrated (Shi et al., 2012a).

*CRF6* is the most widely stress-regulated *Arabidopsis* CRF and is particularly responsive to oxidative stress (Zimmermann et al., 2004; Inze et al., 2012; Zwack et al., 2013; Ramireddy et al., 2014). In agreement with this trend, qPCR and promoter:GUS experiments have demonstrated *CRF6* induction by salt, heat shock, and H$_2$O$_2$ (Zwack et al., 2013). This expression pattern may be evolutionarily conserved as qPCR analyses showed that the tomato *CRF6* orthologue (*SlCRF5*) is also induced by heat and H$_2$O$_2$ as well as drought (Gupta and Rashotte, 2014). A recent study identified *Arabidopsis* *CRF6* as a member of the mitochondrial dysfunction (MD) stimulon, a set of 24 genes which are highly responsive to MD leading to the production of ROS (De Clercq et al., 2013). This retrograde signal is mediated largely by the transcription factors ANAC013 and ANAC017 which directly target *CRF6* and the closely related *CRF5* (Ng et al., 2013). This finding suggests that *CRF5* and *CRF6* along with their downstream targets may play a role in the response to stress-induced mitochondrial dysfunction, yet this remains to be experimentally tested.

**Conclusions**

Although the majority of cytokinin research has focused primarily on the regulation of developmental processes, the involvement of this hormone in stress responses has long been the subject of investigation. However, much about the relationship between cytokinin and stress tolerance and/or susceptibility remains unclear. Examinations of endogenous cytokinin levels under various conditions have suggested that cytokinin metabolism is highly regulated during the response to abiotic stress. Collectively, the findings of these hormone quantification studies seem to indicate that a transient spike of cytokinin occurs in the initial response to stress followed by a subsequent reduction in overall levels. This reduction, however, may not occur in the case of more severe stress conditions. Experiments involving the treatment of plants with exogenous cytokinin or biotechnological manipulation of endogenous levels have demonstrated both positive and negative effects on the tolerance of different stresses; therefore, generalizations about the effect of manipulating cytokinin levels with respect to overall stress tolerance are more difficult to make at this time.

Cytokinin signal transduction occurs via a multi-step His to Asp phosphorelay pathway and the signalling components have been identified in several species, but are most extensively characterized in *Arabidopsis*. The CHK receptor proteins from *Arabidopsis* (primarily AHK2 and 3) are antagonistic of drought, salt, and cold-stress tolerance; yet have a positive role in the adaptive response to high-light stress. Similarly, conflicting results have been found for type-A RRs as well. Overall, the current body of research suggests that the interactions between components of the cytokinin signalling pathway and stress responses are variable and context-specific. It is likely that many of these interactions occur as a result of cross-talk between cytokinin and ABA signalling and metabolism.

CRF proteins are emerging as potential integrators of cytokinin and stress responses. These transcription factors are (along with RRBs) co-regulators of cytokinin responses, yet little is known about the mechanisms of this co-regulation. It seems likely that CRFs are involved in the regulation of other transcriptional responses independent of RRBs. As such CRFs could serve to co-ordinate such responses along with the transcriptional output from cytokinin signalling.
References


