

*Review Article***Glutathione as a Crucial Modulator of Phytohormone Signalling During Pathogen Defence in Plants**RIDDHI DATTA^{1,*} and SHARMILA CHATTOPADHYAY²¹Department of Botany, Dr. APJ Abdul Kalam Government College, New Town, Rajarhat, Kolkata 700 156, India²Plant Biology Laboratory, CSIR-Indian Institute of Chemical Biology, 4, Raja S. C. Mullick Road, Kolkata 700032, India

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Plant's resistance to different stress factors is regulated by a complex signalling network which connects the individual signalling pathways, enabling them to fine tune their defence response. For more than last two decades, glutathione (GSH) is gradually gaining importance as a crucial player in this network. The present review summarizes the central role of GSH in modulating plant's defence response to biotic stress, specially emphasizing the molecular mechanism of these regulations. Several transgenic approaches to constitutively enhance GSH levels have been followed and in most cases, these transgenic plants exhibited enhanced biotic stress tolerance. The post 2000 era envisaged a mechanistic approach in this field and GSH has been shown to modulate the defence signalling network by cross-communication with several stress-related phytohormones. GSH imparts stress tolerance against biotrophic infection via NPR1-dependent salicylic acid (SA) mediated pathway. GSH regulates SA accumulation at the level of *isochorismate synthetase 1 (ICS1)* expression and can also act in NPR1-independent pathway. A synergistic GSH-ethylene (ET) interplay during necrotrophic infection has also been reported. It has been demonstrated that GSH induces ET biosynthesis by modulating transcriptional and post-transcriptional regulations of its key enzymes. The cross-talk of GSH with jasmonic acid (JA) and abscisic acid (ABA) in alleviating stress has been reported as well. However, mechanistic details of the interaction between GSH and JA or ABA signaling pathways are not elucidated in details.

Keywords: Glutathione; Phytohormone Signalling; Pathogen Defence; Salicylic Acid; Ethylene; Jasmonic Acid

Introduction

Plants in their natural environment are continuously being threatened by a range of stress factors, including invasion by microbial pathogens, herbivorous insects as well as various abiotic stress conditions. Being immobile, plants have to respond to each of these attackers in a rapid and effective way in order to ensure survival. Plant's resistance to different stress factors is a multifaceted regulatory network which links the various signalling pathways thus enabling them to fine tune their defence responses. Previous studies also envisaged that plant's responses to various stress factors are regulated by multiple signalling pathways. A perfect synchronization of

these pathways switches on the transcription of appropriate defence related genes and their downstream machinery ultimately helping the system to tide over unfavourable conditions. It has been well-documented that an interconnecting signalling network, comprising the salicylic acid (SA), ethylene (ET) and jasmonic acid (JA) mediated signalling pathways, constitute the basic defence response strategy in plants (Glazebrook, 2005; Klessig *et al.*, 2000; Loake and Grant, 2007; Pieterse *et al.*, 2009; Thomma *et al.*, 1998; van Loon *et al.*, 2006). Glutathione (GSH; γ -glutamylcysteinyl glycine) is a low molecular weight non-protein tripeptide which is found in nearly all prokaryotic as well as eukaryotic cells. GSH represents the major pool of non-protein reduced

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sulphur and plays important roles in cell function and metabolism (Kunert and Foyer, 1993). It is gradually gaining importance as a vital player in this network and plays critical roles in combating biotic and abiotic stresses (Ghanta and Chattopadhyay, 2011).

This tripeptide thiol is a multifunctional metabolite and has drawn significant attention due to its wide distribution in most living organisms, abundance, broad redox potential and unique structural properties. The stability and ability of GSH to function as a cellular reductant has been derived from the single thiol group in the central cysteine. Along with ascorbate, GSH is considered as one of the most abundant redox couples in plant cells (May *et al.*, 1998). It has largely been reported for more than two decades that GSH plays a crucial role in cellular processes including development, growth and adverse environmental responses in plants. Abiotic stresses like extreme temperatures, heavy metal contaminated soils, drought, salinity or air pollutants lead to the generation of reactive oxygen species (ROS) and alter the intracellular redoxhomeostasis perturbing cellular physiology (Ogawa, 2005; Galant *et al.*, 2011). Plants generally respond to such conditions by producing GSH which acts as an antioxidant by quenching ROS. The ascorbate-GSH cycle that eliminates peroxides plays an important role in this respect (Noctor and Foyer, 1998). GSH also participates in the detoxification of a range of xenobiotics, herbicides, heavy metals and air pollutants like sulphur dioxide and ozone (Grill *et al.*, 1989; May *et al.*, 1998). GSH plays a critical role in biotic stress and its management as well (Dubreuil-Maurizi and Poinssot, 2012; Parisy *et al.*, 2007). In fact, a direct link between the biosynthesis of GSH and the expression of defence related genes has been reported in *Arabidopsis* (Ball *et al.*, 2004). Though the participation of GSH in plant responses to stress has long been reported (Dron *et al.*, 1988; Wingate *et al.*, 1988), yet the underlying molecular mechanism is still being explored.

GSH as a Central Regulator in Biotic Stress Tolerance

It has been demonstrated that significant changes in the GSH levels occur in the cells adjacent to the site of attempted pathogen ingress. This altered GSH levels then play an important role in regulating the induced defence response including the expression

of genes such as glutathione-S-transferases (GSTs) (Jabs *et al.*, 1996; Levine *et al.*, 1994; Mauch and Dudler, 1993) and glutathione peroxidases (GPX) (Levine *et al.*, 1994). Incompatible plant-pathogen interactions generate reactive oxygen species (ROS) and other products of lipid peroxidation which are detoxified by both GST and glutathione reductase (GR). It has been reported that during compatible barley-barley powdery mildew interactions activation of various antioxidative enzymes like GSTs and the ascorbate-GSH cycle occur presumably to lessen the detrimental effects of oxidative stress. On the other hand, these antioxidative reactions are either not activated or are only slightly activated in case of incompatible interactions (El-Zahaby, 1995). In general, pathogen invasion leads to enhanced accumulation of GSH in the cells which also increases the GSH/GSSG ratio and ultimately switches on the downstream defence related signalling cascade.

A transgenic approach to overexpress different GSH related genes in plants to constitutively enhance the GSH levels has widely been followed (Gomez *et al.*, 2004; Gullner *et al.*, 2001; Noctor *et al.*, 1998; Xiang *et al.*, 2001; Zhu *et al.*, 1999). In most cases, these transgenic plants exhibited enhanced stress tolerance. While most of these transgenic plants displayed no phenotypic abnormalities, some suggested a variation. In one such study, transgenic tobacco plants were found to develop severe necrosis due to a hypersensitive response (HR) by overexpressing the γ -ECS enzyme (Creissen *et al.*, 1999). This is perhaps because an excessive accumulation of GSH in the tissue led to oxidative stress. It has been reported that oxidative stress of intracellular origin can trigger HR and the excessive GSH redox potential (or GSSG accumulation) may lead to the activation of genetically programmed cell suicide pathways in the transgenic plants. This explanation is further supported by the fact that intracellular oxidative stress associated with GSSG accumulation can trigger the HR-like lesion formation (Chamnongpol *et al.*, 1998; Smith *et al.*, 1984; Willekens *et al.*, 1997).

The *A. thaliana cad2-1* and *rax1-1* mutants have mutations in the GSH biosynthesis enzyme. Ball *et al.*, (2004) reported that a changed GSH metabolism in these mutants leads to an alteration in the expression of 32 stress responsive genes. Another *A. thaliana* camalexin deficient mutant, *pad2-1*, was

isolated in the 1900s and was demonstrated to be susceptible to *Pseudomonas syringae* as well as *P. brassicae* infections (Glazebrook and Ausubel, 1994; Glazebrook *et al.*, 1997). About a decade later, it was demonstrated that the disease susceptibility of this mutant was not due to camalexin deficiency but due to a mutation in the GSH biosynthetic pathway gene and consequent GSH depletion (Parisy *et al.*, 2007). The *pad2-1* mutant again displayed decreased resistance to the feeding of insect larvae and this effect has been linked to decreased accumulation of glucosinolates (Schlaeppli *et al.*, 2008). This

susceptibility can be rescued by supplementation with exogenous GSH but not with other disulphide reductants like dithiothreitol (Schlaeppli *et al.*, 2008). It has subsequently been reported that formation of the glucosinolatethiogluco moiety encompasses a GSH-conjugate intermediate which is metabolized by a γ -glutamyl peptidase, GGP (Geu-Flores *et al.*, 2009). Also, this GSH depleted mutant is deficient in camalexin because camalexin synthesis requires GSH as a precursor (Böttcher *et al.*, 2009; Su *et al.*, 2011). In fact, synthesis of both camalexin and glucosinolates involve formation and metabolism of GSH-conjugate

Table 1: Different host-pathogen systems where a defensive role of GSH has been reported

Pathogen	Host plant	Reference
<i>Fusarium oxysporum</i>	<i>Cucumis melo</i> and <i>Lycopersicon esculentum</i>	Bolter <i>et al.</i> , 1993
<i>Drechslera avenae</i> and <i>Drechslera siccans</i>	<i>Avena sativa</i>	Gönner and Schlösser 1993
<i>Erysiphe graminis</i>	<i>Triticum aestivum</i>	Mauch and Dudler 1993
<i>Erysiphe graminis</i>	<i>Hordeum vulgare</i>	El-Zahaby 1995
<i>Cladosporium fulvum</i>	<i>Lycopersicon esculentum</i>	May <i>et al.</i> , 1996
Tobacco mosaic virus	<i>Nicotiana tabacum</i>	Fodor <i>et al.</i> , 1997
<i>Pseudomonas syringae</i> and <i>P. brassicae</i>	<i>Arabidopsis thaliana</i>	Glazebrook and Ausubel 1994; Glazebrook <i>et al.</i> , 1997; Ball <i>et al.</i> , 2004; Parisy <i>et al.</i> , 2007; Mhamdi <i>et al.</i> , 2010
<i>Alternaria brassicicola</i>	<i>Arabidopsis thaliana</i>	Van Wees <i>et al.</i> , 2003
<i>Spodoptera littoralis</i>	<i>Arabidopsis thaliana</i>	Schlaeppli <i>et al.</i> , 2008
<i>Pseudomonas syringae</i>	<i>Arabidopsis thaliana</i>	Chaouch <i>et al.</i> , 2010
<i>Phytophthora brassicae</i>	<i>Arabidopsis thaliana</i>	Roetschi <i>et al.</i> , 2001; Maughan <i>et al.</i> , 2010
RNA viruses	<i>Arabidopsis thaliana</i>	Wang <i>et al.</i> , 2011
<i>Pseudomonas syringae</i>	<i>Nicotiana tabacum</i>	Ghanta <i>et al.</i> , 2011
<i>Meloidogyne incognita</i>	<i>Medicago trunculata</i>	Baldacci-Crespel <i>et al.</i> , 2012
<i>Phytophthora cinnamomi</i>	<i>Eucalyptus</i>	Dempsey <i>et al.</i> , 2012
<i>Botrytis cinerea</i>	<i>Arabidopsis thaliana</i>	Simon <i>et al.</i> , 2013
<i>Pseudomonas syringae</i>	<i>Arabidopsis thaliana</i>	Mhamdi <i>et al.</i> , 2013
Caterpillar herbivory	<i>Arabidopsis thaliana</i>	Paudel <i>et al.</i> , 2013
<i>Botrytis cinerea</i>	<i>Mesembryanthemum crystallinum</i>	Kuźniak <i>et al.</i> , 2013
<i>Colletotrichum gloeosporioides</i> and <i>Ralstonia solanacearum</i>	<i>Arabidopsis thaliana</i>	Hiruma <i>et al.</i> , 2013
<i>Alternaria alternata</i>	<i>Mentha arvensis</i>	Sinha <i>et al.</i> , 2013
<i>Pseudomonas syringae</i> and <i>Botrytis cinerea</i>	<i>Nicotiana tabacum</i>	Ghanta <i>et al.</i> , 2014
<i>Pseudomonas syringae</i> pv <i>lachrymans</i>	<i>Cucumis sativus</i>	Kuźniak <i>et al.</i> , 2014
<i>Magnaporthe oryzae</i>	<i>Oryza sativa</i>	Zhang <i>et al.</i> , 2015
<i>Pseudomonas syringae</i>	<i>Arabidopsis thaliana</i>	Datta and Chattopadhyay 2015
<i>Botrytis cinerea</i>	<i>Arabidopsis thaliana</i>	Ferrari <i>et al.</i> , 2003; Datta <i>et al.</i> , 2015

which is hampered under low GSH conditions (Geu-Flores *et al.*, 2011). This explains why the *pad2-1* mutant displays constitutive camalexin deficiency and lower glucosinolates induction.

The proteins involved in imparting disease susceptibility of the GSH depleted *pad2-1* mutant to *P. syringae* infection has been reported recently. It has been identified that the mutant actually fails to efficiently regulate several proteins involved in the PTI-related first line of defence as well as ETI-related R-gene products, thus signifying the dynamic role of GSH in plant defence (Datta and Chattopadhyay, 2015). These studies cumulatively suggest that the accumulation of GSH is essential for disease resistance. Using high-resolution imaging techniques the temporal and spatial changes of subcellular GSH level during *Botrytis cinerea* infection in *A. thaliana* have been shown (Simon *et al.*, 2013). Another recent study demonstrated that increased GSH contributes to stress tolerance and global translational changes in *A. thaliana*. The translatoome analysis also identified several novel genes related to auxin, ABA, and JA biosynthetic pathways as well as signalling genes whose transcription is induced in response to exogenous GSH treatment, which was not reported in any previous transcriptomic data (Cheng *et al.*, 2015). Table 1 summarizes the different host-pathogen systems in which the role of GSH in imparting disease resistance has already been established.

GSH and its Cross-Talk with Phytohormones During Biotic Stress

Phytohormones are small molecules that are indispensable for the regulation of plant growth, development, reproduction, and survival. Diverse small-molecule phytohormones viz., SA, JA, ET, abscisic acid (ABA) and brassinosteroids play pivotal roles in regulating the plant defence signalling network (Dong, 1998; Dahl and Baldwin, 2007; Grant and Lamb, 2006; Howe and Jander, 2008; Loake and Grant, 2007; Pieterse *et al.*, 2009; van Wees *et al.*, 2003; van Loon *et al.*, 2006; Vlot *et al.*, 2008;). Extensive synergistic and/or antagonistic cross-communications among their signalling pathways enables the plant to finely regulate its immune response (Bostock, 2005; Kunkel and Brooks, 2002; Pieterse *et al.*, 2009; Reymond and Farmer, 1998). Although the detailed mechanisms of these cross-talks

are not fully described as yet, accumulating evidence points to imperative roles for GSH in phytohormone signalling during biotic stress (Ghanta *et al.*, 2014; Mhamdi *et al.*, 2013; Spoel and Loake, 2011). The different milestones attained in exploring the role of GSH-phytohormone cross-talk in plant defence signalling network has been summarized in Table 2.

GSH-SA Interplay

Plants synthesize SA in response to invasion by a diverse range of phytopathogens and it plays an essential role in establishing both local and systemic acquired resistance (SAR) (Loake and Grant, 2007). SA signalling is mediated by at least two mechanisms, the NPR1 dependent and the NPR1 independent pathways (Blanco *et al.*, 2009). Under normal condition, NPR1 exists as an oligomer. SA induces a change in the cellular redox potential, which leads to the reduction of NPR1 oligomer to its active monomeric form. It has been reported that the oligomerization of NPR1 is facilitated by its S-nitrosylation at cysteine-156 residue by S-nitrosoglutathione (GSNO). Conversely, the SA-induced monomerization of the NPR1 oligomer is catalyzed by thioredoxins (TRXs) through reduction or oxidation of its intermolecular disulphide bonds (Tada *et al.*, 2008). Monomeric NPR1 is then translocated from the cytosol into the nucleus where it acts as a transcriptional co-activator of several SA-responsive genes (Després *et al.*, 2003; Mou *et al.*, 2003). NPR1 is also a key molecule in modulating the SA-JA cross-talk during stress. In the cytosol, monomeric NPR1 negatively regulates JA-responsive gene expression, perhaps by inhibiting positive regulators of JA-responsive genes or by enabling the delivery of negative regulators of JA-responsive genes to the nucleus (Spoel *et al.*, 2003).

Fascinatingly, the interplay of SA with ROS and GSH under various stress conditions has been supported by different lines of evidence (Herrera-Vásquez *et al.*, 2015). One of the earliest reports suggesting GSH-SA interplay comes from a study on pea seedlings. In pea seedlings, a rise in the reduced GSH content and fall in the oxidized glutathione (GSSG) level, together with an increased GSH:GSSG ratio has been observed in response to exogenous SA treatment which signifies a modulation of GSH metabolism by SA (Srivastava and Dwivedi, 1998).

Table 2: Different milestones attained in exploring the role GSH-phytohormone cross-talk in plant defence signalling network

Milestones	Host system	References
GSH-SA interplay		
Exogenous SA treatment leads to an increase in GSH	Pea seedlings	(Srivastava and Dwivedi 1998)
SA induces GST transcription during plant defence via an ocs enhancer element in the GST promoter region	Arabidopsis	(Chen and Singh 1999)
Thermo-tolerance as a consequence of SA treatment coincides with an increase in GSH level but GSH:GSSG ratio remains unaltered	Tobacco	(Dat <i>et al.</i> , 2000)
INA (SA analogue) treatment increases the GSH level leading to a reduction of NPR1 and subsequent PR1 gene expression	Arabidopsis	(Mou <i>et al.</i> , 2003)
Exogenous treatments with SA, INA as well as pathogen infection increases GSH content and GSH: GSSG ratio	Arabidopsis; Tobacco-TMV infection	(Fodor <i>et al.</i> , 1997; Vanacker <i>et al.</i> , 2001; Mateo <i>et al.</i> , 2006)
Constitutive overexpression of SA induces GSH-mediated nickel tolerance	<i>Thlaspi</i> sp.	(Freeman <i>et al.</i> , 2005)
Protection of ozone-induced leaf injury by SA coincides with an increase in <i>de novo</i> GSH synthesis	Arabidopsis	(Yoshida <i>et al.</i> , 2009)
GRI-dependent GSH status plays a crucial role in leaf responses to intracellular H ₂ O ₂ including accumulation of SA, induction of PR genes and SA signalling pathway	Arabidopsis	(Mhamdi <i>et al.</i> , 2010)
Higher GSH level observed in SA-deficient plants during RNA virus infection	Arabidopsis-CMV	(Wang <i>et al.</i> , 2011)
GSH regulates the SA-mediated suppression of JA signalling	Arabidopsis- <i>Alternaria brassicicola</i> / <i>Botrytis cinerea</i>	(Koornneef <i>et al.</i> , 2008)
JA treatment decreases GSH level	Arabidopsis	(Spoel and Loake 2011)
Simultaneous SA and JA application increase GSH level suggesting a prioritization of the SA pathway	Arabidopsis	(Koornneef <i>et al.</i> , 2008)
GSH signaling acts through NPR1-dependent SA-mediated pathway to mitigate biotic stress	Tobacco	(Ghanta <i>et al.</i> , 2011b)
GSH regulates SA accumulation at the level of ICS1 expression and GSH also act independently of NPR1 to allow increased intracellular H ₂ O ₂ to activate SA signalling	Arabidopsis	(Han <i>et al.</i> , 2013a)
GSH-ET interplay		
An ET-responsive GST gene cluster was characterised in carnation	Carnation	(Itzhaki and Woodson 1993)
ET synthesis is hampered when the GSH pool shifts towards oxidized state by exogenous GSSG treatment	White spruce	(Belmonte <i>et al.</i> , 2005)
ACO transcripts increased in spruce somatic embryos grown in excess GSH condition	White spruce	(Stasolla <i>et al.</i> , 2004)
<i>S-adenosylmethionine synthase</i> transcript decreases in Brassica napus grown in excess GSSG condition	<i>Brassica</i>	(Stasolla <i>et al.</i> , 2008)
ET biosynthesis is assumed to be controlled by GSH via transcriptional regulation of ACO and <i>S-adenosylmethionine synthase</i>	<i>Brassica</i> ; Spruce	(Stasolla 2010)
ET controls GSH biosynthesis positively in ozone exposed <i>A. thaliana</i> leaves	Arabidopsis	(Yoshida <i>et al.</i> , 2009)
GSH-dependent lead resistance was impaired in ET signalling mutant, ein2-1	Arabidopsis	(Cao <i>et al.</i> , 2009)
Multistep involvement of GSH with SA and ET to combat stress	Tobacco- <i>Alternaria alternata</i>	(Ghanta <i>et al.</i> , 2014)
GSH induces ET biosynthesis by modulating the transcriptional and post-transcriptional regulations of its key enzymes, ACS and ACO	Arabidopsis- <i>Botrytis cinerea</i> /salt stress	(Datta <i>et al.</i> , 2015)

GSH-JA interplay		
JA treatment increases GSH synthesis but did not alter the GSH content in unstressed plants	Arabidopsis	(Xiang and Oliver 1998)
JA increases GSH metabolism under water stress	<i>Agropyron cristatum</i>	(Shan and Liang 2010)
Intracellular GSH is involved in methyl MeJA signalling		(Akter <i>et al.</i> , 2010)
GSNOR mediates JA and ET biosynthesis and JA-elicited responses in response to insect feeding	Arabidopsis	(Wünsche <i>et al.</i> , 2011)
MeJA treatment induces GPX expression		(Saisavoey <i>et al.</i> , 2014)
Increased GSH confers tolerance to drought and salt stress by enhancing global translation of JA-responsive genes	Arabidopsis	(Cheng <i>et al.</i> , 2015)
GSH modulates the antagonistic interaction between SA and JA pathways at the level of NPR1	Arabidopsis- <i>Pseudomonas syringae</i>	(Spoel <i>et al.</i> , 2003; Koornneef <i>et al.</i> , 2008)
GSH-ABA Interplay		
In two maize genotypes differing in stress tolerance, ABA differentially affected the GSH content, GSH:GSSG ratio, GR activity, and g-ECS transcript level	Maize	(Kellos <i>et al.</i> , 2008)
GSH content did not vary in potato tubers treated with ABA	Potato	(Stroinski <i>et al.</i> , 2010)
GSH-ABA interplay provides stress tolerance against abiotic stress factors	Arabidopsis; Wheat	(Chen <i>et al.</i> , 2012; Wei <i>et al.</i> , 2015)
GSH-SA interplay		
Exogenous SA treatment leads to an increase in GSH	Pea seedlings	(Srivastava and Dwivedi 1998)

Subsequently, SA and H₂O₂ were shown to induce GST transcription during plant defence via an *ocs* element which is an enhancer element present in the GST promoter region (Chen and Singh, 1999). In another study, thermo-tolerance as a consequence of SA treatment was shown to coincide with an increase in both GSH and GSSG levels in shoot while the GSH redox ratio remained unaltered (Dat *et al.*, 2000).

A treatment with 2, 6-dichloroisonicotinic acid (INA), the biologically active analogue of SA, augmented the GSH level in cells leading to the reduction of NPR1 and subsequent expression of the *PR1* gene (Mou *et al.*, 2003). Similarly, exogenous treatments with SA, INA as well as pathogen infection have been reported to increase GSH content and GSH:GSSG ratio in plants (Fodor *et al.*, 1997; Mateo *et al.*, 2006; Vanacker *et al.*, 2001). In several reports, changes in GSH levels were reported to occur during salinity as well as osmotic stresses (Borsani *et al.*, 2001). In another study, GSH-mediated nickel tolerance was shown to be induced due to constitutive overexpression of SA in *Thlaspi* hyper accumulators (Freeman *et al.*, 2005). Protection of ozone-induced leaf injury in *A. thaliana* by SA coincided with an increase in the *de novo* synthesis of GSH (Yoshida

et al., 2009). In fact, ozone exposure leads to ROS generation and subsequent cell death. SA and ET production is induced under such condition to decrease the magnitude of ozone-induced cell death via induction of GSH biosynthesis. It has been reported that unlike the wild-type, mutants deficient in ET signalling (*ein2*) or SA biosynthesis (*sid2*) generated high levels of superoxide, lower levels of GSH and exhibited visible leaf injury. The activities of the GSH biosynthetic enzymes were also affected in these mutants. Furthermore, ozone-induced leaf damage detected in *ein2* and *sid2* was alleviated by exogenous GSH treatment. GSH status has been demonstrated to regulate SA and other biotic stress response pathways in *A. thaliana*. It has been demonstrated that the GR1-dependent GSH status plays a crucial role in modulating multiple leaf responses to intracellular H₂O₂ including limitation of lesion formation, SA accumulation, induction of PR genes and signalling through SA and JA pathways (Mhamdi *et al.*, 2010). In another report, the role of GSH against RNA viruses in SA-deficient plants has been described. The levels of virus replication were found to be higher in the SA-deficient plants during the first 10 days, but lower than the wild-type seedlings 20

days after infection. It has been demonstrated that the higher level of GSH and ascorbic acid observed in SA-deficient plants perhaps contribute to their alleviated symptoms (Wang *et al.*, 2011).

GSH has also been shown to interfere with SA-mediated suppression of JA signalling in plants. The boost in GSH levels after SA treatment was shown to coincide accurately with the window of opportunity in which SA could suppress JA-induced *PDF1.2* expression. Inhibition of GSH biosynthesis by l-buthioninesulfoximine (BSO) strongly reduced this suppression of the JA-responsive *PDF1.2* gene by SA (Koornneef and Pieterse, 2008). Interestingly, JA can also influence the redox state of cells by decreasing the total amount of GSH and this shifts the GSH: GSSG ratio towards the oxidized state (Spoel and Loake, 2011). However, on simultaneous application of SA and JA, an increase in the GSH level was observed suggesting a prioritization of the SA pathway over the JA pathway (Koornneef *et al.*, 2008). Nonetheless, the mechanism of how does the SA-mediated cellular reduction modulates JA-inducible responses still remains obscure.

To obtain deeper insight into the mechanism how the GSH-SA interplay is involved in mitigating biotic stress, Ghanta *et al.* (2011b) used transgenic tobacco plants with enhanced GSH content and exhibiting resistance to pathogenesis as well. It was observed that the expression levels of *NPR1* and *NPR1*-dependent genes like *PR1*, *mitogen-activated protein kinase kinase*, *glutamine synthetase*, etc. were significantly enhanced in the transgenic plants as compared to the wild-type. Conversely, no significant alteration in the expression levels of *NPR1*-independent genes like *PR2*, *PR5*, and *short-chain dehydrogenase/reductase family protein* was observed. These observations suggested that GSH activates SA-mediated defence, presumably through the *NPR1*-dependent pathway (Ghanta *et al.*, 2011b; Ghanta and Chattopadhyay, 2011). In a subsequent study, the transgenic tobacco plants with enhanced GSH levels were reported to synthesize more SA than the wild-type plants (Ghanta *et al.*, 2011a). Activation of SA related genes and enhanced resistance to pathogenesis under augmented GSH condition was also observed in later studies (Ghanta *et al.*, 2014).

It has subsequently been reported that GSH

regulates SA accumulation at the level of *isochorismate synthetase 1 (ICS1)* expression and that an increase in the intracellular H_2O_2 level can function to activate the SA signalling (Han *et al.*, 2013a). The H_2O_2 -triggered changes in GSH status have been suggested not merely to be a passive response to oxidative stress. In fact, this modulation of GSH status links the elevated intracellular H_2O_2 production to activation of the *ICS1*-dependent SA pathway. The accumulated SA then leads to activation of *NPR1* function through reductive processes, to which GSH also contributes. This general model has been depicted in Fig. 1.

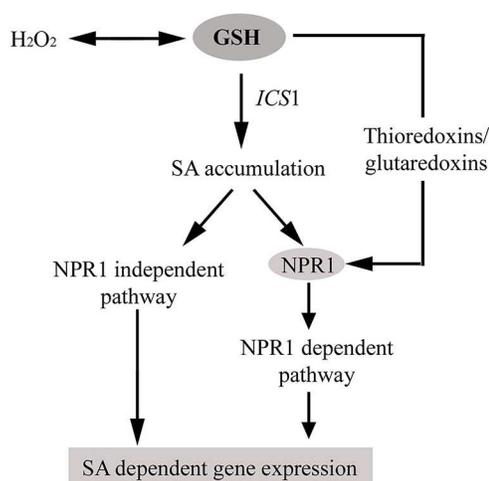


Fig. 1: GSH induces SA signalling via *NPR1* dependent and *NPR1* independent pathways in plants. GSH on one hand directly induces *NPR1* dependent pathway presumably through thioredoxins and glutaredoxins. On the other hand, oxidation by H_2O_2 modulates GSH status. This oxidative modulation is a part of the signal network required for optimal *ICS1* dependent SA accumulation that then leads to activation of *NPR1* dependent as well as independent pathways

GSH-ET Interplay

ET, a gaseous phytohormone, is known to play significant roles in plant defence and participate in cross-talk with other signalling molecules. ET and JA have been widely reported to act synergistically against necrotrophic pathogens (Penninckx *et al.*, 1998). In some cases however, a synergistic interaction between ET and SA has also been demonstrated to induce SAR and SA-mediated gene expression in plants (Lawton *et al.*, 1994; Verberne *et al.*, 2003; Vos *et al.*, 2006).

Reports demonstrating GSH-ET interplay dates back to the early 1990s when an ET-responsive GST gene cluster was characterized in carnation (Itzhaki and Woodson, 1993). In another report, ET synthesis was observed to be hampered in spruce somatic embryo when the GSH pool was shifted towards oxidized state by exogenous GSSG treatment (Belmonte *et al.*, 2005). Molecular studies revealed that ACC oxidase (ACO) transcripts increased in spruce somatic embryos grown in excess GSH (reduced) condition (Stasolla *et al.*, 2004). In a subsequent study, transcripts of S-adenosylmethionine synthase was found to be decreased in *Brassica napus* when grown in excess GSSG (oxidized) condition (Stasolla *et al.*, 2008). Hence, the biosynthesis of ET has been assumed to be controlled by GSH via transcriptional regulation of the two biosynthetic enzymes: S-adenosylmethionine synthase and ACO (Stasolla, 2010).

ET has also been reported to control GSH biosynthesis positively in ozone exposed *A. thaliana* leaves (Yoshida *et al.*, 2009). Again, the *ein2-1* mutant with impaired ET signalling has been shown to exhibit impaired GSH-dependent lead resistance, which was related to constitutive repression of γ -ECS gene and consequently reduced GSH content (Cao *et al.*, 2009). In transgenic tobacco with enhanced GSH content, up-regulation of ET related transcripts like *ACO*, *ERF4* and *WRKY1* and up-accumulation of proteins like ACC synthase (ACS) and ACO has been reported recently (Ghanta *et al.*, 2014). These transgenic plants have also been reported to exhibit tolerance against pathogenesis as well as osmotic stress thus demonstrating the involvement of GSH-ET interplay in imparting stress tolerance in plants (Ghanta *et al.*, 2014; Kumar *et al.*, 2014).

The molecular mechanism of the GSH-ET cross-talk during necrotrophic infection as well as abiotic stress has been solved only very recently. It has been demonstrated that GSH induces ET biosynthesis by modulating the transcriptional and post-transcriptional regulations of its key enzymes, ACS and ACO in *A. thaliana* (Datta *et al.*, 2015). Transgenic plants with enhanced GSH content were found exhibit up-regulation of *ACS2*, *ACS6*, and *ACO1* at transcript as well as protein levels while down-regulation was observed in the GSH depleted *pad2-1* mutant. Furthermore, GSH was shown to induce *ACS2* and

ACS6 transcription in a WRKY33 dependent manner. For *ACO1*, however, GSH increased the stability of *ACO1* mRNA without affecting its promoter activity. In addition, the ACO1 protein can be a subject for S-glutathionylation while S-glutathionylation of ACS2 and ACS6 proteins was not detected. Thus, a dual-level regulation of ET biosynthesis by GSH during stress has been proposed (Fig. 2; Datta *et al.*, 2015).

GSH- JA Interplay

The role of JA in plant defence has long been reported (Farmer and Ryan, 1992; Gundlach *et al.*, 1992; Turner *et al.*, 2002). JA-dependent signalling has been reported to play a crucial role in pathogen attack, especially necrotrophs, wounding and insect feeding (Glazebrook, 2005; Thomma *et al.*, 2001). JA has been known to function antagonistically with SA in defence signalling. JA treatment has been shown to increase the mRNA levels and the capacity for GSH synthesis but it did not alter the GSH content in unstressed plants (Xiang and Oliver, 1998). In a later study, it was observed that JA leads to an increase in GSH metabolism under water stress in *Agropyron cristatum* (Shan and Liang, 2010). Involvement of intracellular GSH has also been studied in methyl jasmonate (MeJA) signalling (Akteret *et al.*, 2010). Again, S-Nitrosoglutathione reductase (GSNOR) has been shown to mediate JA and ET biosynthesis in *Nicotiana attenuata* in response to insect feeding (Wünsche *et al.*, 2011). MeJA treatment has also been reported to induce expression of GPX in *Pueraria mirifica* (Saisavoey *et al.*, 2014). It has recently been demonstrated that increased GSH confers tolerance to drought and salt stress in *Arabidopsis* by enhancing global translation of JA-responsive genes (Cheng *et al.*, 2015). GSH has also been implicated in the antagonistic interaction between SA and JA pathways at the level of NPR1 as discussed earlier (Koorneef *et al.*, 2008; Spoel *et al.*, 2003).

Two possibilities could explain the dual effect of GSH on signalling through the SA and JA pathways in response to stress (Han *et al.*, 2013b). First, GSH status can act to modulate a master switch that regulates the oxidative activation of both pathways. A second scenario would involve regulation of both pathways in parallel. Whatever may be the case, the SA- JA interplay mediated by other redox-linked factors could act downstream to determine the relative

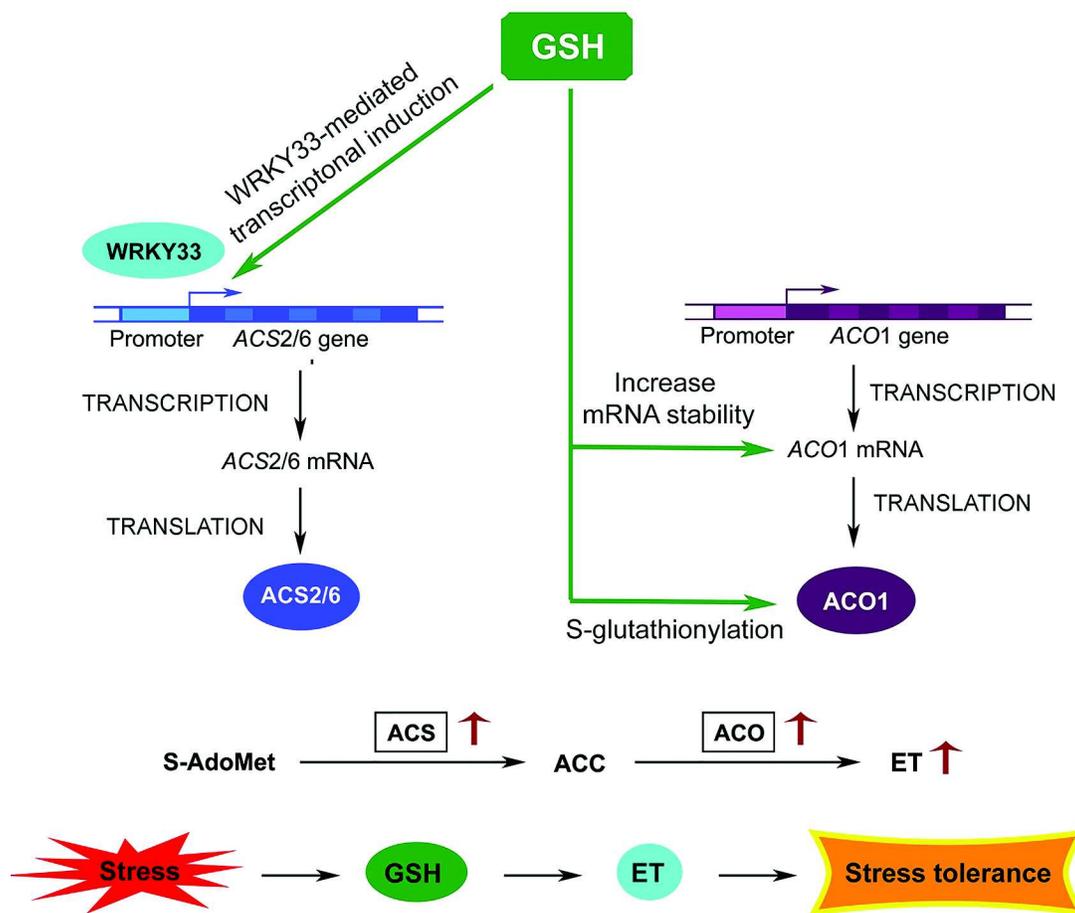


Fig. 2: Stress conditions lead to an increase in cellular GSH level in plants. Increased GSH then induces *ACS2* and *ACS6* transcription in a WRKY33 dependent manner during stress. This increases the transcript levels of *ACS2* and *ACS6*. Consequently, more ACS2 and ACS6 proteins are synthesized. On the other hand, GSH enhances the *ACO1* mRNA stability and consequently more ACO1 protein is synthesized. Also, ACO1 protein is S-glutathionylated. Together, this leads to increased synthesis of ET. Increased ET level then switches on the ET signalling pathway and increases stress tolerance in plants. Figure adapted and modified from Datta *et al.* 2015

dominance of these two key defence signalling pathways.

GSH-ABA Interplay

Apart from these three phytohormones, ABA also plays a significant role in environmental stress tolerance. ABA cross-communicates with the SA-JA-ET network by antagonizing the onset of SA-dependent defences and SAR (Mohr and Cahill, 2007; Yasuda *et al.*, 2008). Moreover, ABA attenuates the JA/ET-dependent gene expression (Anderson *et al.*, 2004) and affects JA biosynthesis and resistance against JA-inducing necrotrophic pathogens (Adie *et al.*, 2007; Flors *et al.*, 2008). Interplay between ABA

and GSH has also been reported. ABA has been demonstrated to differentially regulate the GSH content, GSH:GSSG ratio, γ -ECS transcript level and GR activity in two maize genotypes which varies in their stress tolerance potentials (Kellos *et al.*, 2008). However, it was subsequently reported that ABA treatment did not alter the GSH levels in potato tubers (Stroiński *et al.*, 2010). In several other studies, GSH-ABA interplay has been reported in providing stress tolerance against abiotic stress factors (Chen *et al.*, 2012; Wei *et al.*, 2015). But whether this interplay is also involved in imparting biotic stress tolerance remains to be studied in future.

Conclusion and Future Perspective

Dissecting the signalling network that operates during disease development in plants has revealed the association of various stress-related phytohormones along with several other signal molecules. GSH is mainly associated with the activation and modulation of different phytohormones and subsequent regulation of a various resistance genes. Most of the studies were focused on the cross-talk of GSH with SA, ET, and JA signalling pathways during stress. In SA and JA signalling pathways, GSH serves as an important intermediate to modulate their signalling cascades through NPR1 during specific stress responses. Again, in some cases, JA elicitation under stress condition

can also induce GSH biosynthesis in plants. On the other hand, GSH enhances ET biosynthesis by a two-step process in response to necrotrophic infection as well as abiotic stress. Identification of the GSH-mediated induction of the ABA signalling pathway can provide a distinct linkage between biotic and abiotic stress responses as well. It can also add a more elaborate view of the interrelationship among various stress hormones during disease resistance in plants. However, the molecular mechanisms of the GSH-JA and GSH-ABA cross-talks during various stress responses are still unsolved. Whether GSH can induce the signalling cascade of these phytohormones or their biosynthesis pathways during stress needs to be investigated in future.

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