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2 to Aphid Infestation 3 Christine H. Foyer^{1*}, Brwa Rasool¹, Jack Davey² and Robert D. Hancock^{2*} 4 5 ¹ Centre for Plant Sciences, School of Biology, Faculty of Biological Sciences, 6 University of Leeds, LS2 9JT. United Kingdom. 7 ² Cell and Molecular Sciences, The James Hutton Institute, Invergowrie, Dundee, 8 DD2 5DA. United Kingdom. 9 10 Email addresses: c.foyer@leeds.ac.uk, ml10bmar@leeds.ac.uk, 11 rob.hancock@hutton.ac.uk 12 13 *Corresponding Authors: CH Foyer Tel: +44 (0)113 343 1421, Fax: +44 (0)113 343 14 15 2882; RD Hancock Tel: +44 (0)1382 568 779, Fax: +44 (0)1382 568 704 16 Running title: Aphid-abiotic stress interactions 17 Number of tables: 0 18 19 Number of figures: 3 Word count: 7083 20 21 Highlight Summary: Within natural environments plants respond to multiple biotic 22 and abiotic stresses simultaneously, using an integrated signalling and response 23 24 network that involves multiple points of reciprocal control. Here we explore how these multiple stress response pathways are managed and co-ordinated at a molecular 25

Cross Tolerance to Biotic and Abiotic Stresses in Plants: A Focus on Resistance

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- 26 level to create short/medium term defences and long term memories of
- 27 environmental hazards with a specific focus on how other biotic and abiotic stresses
- 28 impact on plant-aphid interactions.

Abstract

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Plants co-evolved with an enormous variety of microbial pathogens and insect herbivores under daily and seasonal variations in abiotic environmental conditions. Hence, plant cells display a high capacity to respond to diverse stresses through a flexible and finely balanced response network that involves components such as reduction-oxidation (redox) signalling pathways, stress hormones and growth regulators, as well as calcium and protein kinase cascades. Biotic and abiotic stress responses use common signals, pathways and triggers leading to cross tolerance phenomena, whereby exposure to one type of stress can activate plant responses that facilitate tolerance to several different types of stress. While the acclimation mechanisms and adaptive responses that facilitate responses to single biotic and abiotic stresses have been extensively characterised, relatively little information is available on the dynamic aspects of combined biotic/abiotic stress response. In this review, we consider how the abiotic environment influences plant responses to attack by phloem-feeding aphids. Unravelling the signalling cascades that underpin cross tolerance to biotic and abiotic stresses will allow the identification of new targets for increasing environmental resilience in crops.

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49 **Key words**: aphids, secondary metabolites, nitrogen deficiency, drought, high light

stress, UV irradiation, oxidative stress, reactive oxygen species

Introduction

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Stress may be defined as any external factor that has a negative influence on plant growth and/or reproduction (Madlung and Comai, 2004). Environmental stresses have a significant negative impact on current agriculture. Under field conditions, commercially grown crops achieve an average of only about 50% of their potential yield due to the negative effects of abiotic environmental stresses such as drought, poor soil quality, temperature extremes and flooding (Hatfield and Walthall, 2015). Biotic stress also contributes significantly to the yield gap with field losses to insect pests estimated at more than 10% (Kerchev et al., 2012a) a figure that rises to 50-80% in the absence of control measures (Bruce, 2010). In order to mitigate these diverse agricultural limitations, extensive effort has been expended examining the signalling and response pathways of plants to biotic and abiotic stresses. The majority of this work has necessarily focussed on single stresses in highly controlled environments in order to build our understanding of key processes and signalling elements. To date much less focus has been placed on the integrated response of plants to multiple stresses typically encountered under field conditions, however fundamental knowledge is now sufficiently advanced to tackle these questions. It is clear from studies on single stresses that there is significant overlap in signalling and response pathways to different biotic and abiotic stresses that include cellular redox status, reactive oxygen species, hormones, protein kinase cascades and calcium gradients as common elements (Atkinson and Urwin, 2012). This overlap in signalling pathways is associated with cross tolerance phenomena in which exposure to one type of stress enhances plant resistance to other biotic or abiotic stresses (Pastori and Foyer, 2002). These observations imply the possibility of engineering or breeding for multiple stress resistance in crop plants. However, to achieve these goals a thorough understanding of how plants integrate information from multiple signals and optimise response to simultaneous stresses is required. In the present review we discuss knowledge concerning plant signalling and response to multiple stresses with particular reference to the impact of abiotic stresses on plant resistance to aphids.

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Factors that underpin multiple stress resistance

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Plants are able to withstand multiple mild and even severe environmental stresses simultaneously (Atkinson and Urwin, 2012). In a competitive growing environment a key factor underlying such resistance is the capacity of sessile plants to recognise, integrate and respond to biotic and abiotic environmental variables by constantly adjusting physiology and metabolism to optimise growth and reproduction in an ever changing environment. This capacity is facilitated by cross-tolerance phenomena, in which enhanced tolerance to a range of different environmental stresses is triggered by exposure to a single stress (Pastori and Foyer, 2002; Mittler, 2006). Cross-tolerance is achieved by the synergistic co-activation of the plant innate immune system involving a network of non-specific stress-responsive pathways that cross biotic-abiotic stress boundaries (Bostock, 2005). The innate immune system of plants additionally facilitates the induction of the systemic acquired immune response (SAR) that primes the immune response of tissues distal to the site of pathogen attack in a process analogous to that of cross-tolerance. Both crosstolerance and SAR comprise an arsenal of inducible defences activated by stress perception and associated cell signalling pathways (Figure 1). Cross-tolerance and SAR are linked in many cases to an enhanced production of reactive oxygen species (ROS) such as superoxide (O_2^-) and hydrogen peroxide (H_2O_2) that are perceived via thiol-modulated redox- and nitric oxide-mediated (NO) signalling pathways (Foyer and Noctor, 2009). For example, exposure to the atmospheric pollutant ozone generates ROS in the apoplast of plant cells, activating a plethora of biotic and abiotic stress responses through interactions with plant hormones such as ethylene (ET), salicylic acid (SA), abscisic acid (ABA), auxin and JA (Baier et al., 2005; Fujita et al., 2006; Bartoli et al., 2013a). This redox-hormone signalling hub, which receives and integrates information from a wide range of environmental stimuli is linked to downstream changes in gene expression that are presumably optimised to meet the prevailing environmental conditions as well as the developmental stage of the plant. The concept that the transcriptional response of a plant results from integration of all of the prevailing external factors is often overlooked in experiments where researchers focus on responses to a single variable. This is illustrated by a recent meta-analysis of the transcriptional response of Arabidopsis to aphid infestation (Foyer et al., 2015). Highly limited overlap in gene expression changes were observed between experiments even when comparing identical interactions between M. persicae and the Col-0 genotype and these were reflective of variability in other environmental variables such as growth temperature, day length, light intensity and relative humidity between laboratories (Foyer et al., 2015).

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Changes in gene expression result in downstream consequences in plant developmental and defence programmes mediated via changes in protein and metabolite content. Plant metabolite composition is strongly impacted by the prevailing abiotic environment affecting the quality of plants as hosts for insect herbivores through both direct effects on the quality of the insect diet as well as

indirectly via their signalling function in plants. Conversely infestation by pathogens or pests can induce specific compounds that may play a role in abiotic stress signalling or adaptation.

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The metabolite composition of leaves and other organs is considered to be an important determinant of the success of aphid infestation. Aphid feeding can exert a strong influence on leaf metabolite profiles (Foyer et al., 2012), greatly increasing the contents of some stress-associated primary and secondary metabolites such as trehalose (Hodges et al., 2013). Trehalose metabolism is important in sugar signalling and underpins the regulation of carbon partitioning during plant responses to abiotic stress (Nuccio et al., 2015). It also influences the resistance of A. thaliana plants to M. persicae where loss of TREHALOSE PHOSPHATE SYNTHASE11 (TPS11) gene function, which is required for sugar signalling activities, prevented trehalose accumulation in aphid-infested leaves and decreased resistance to aphid infestation through modulation of the PAD4-dependent biotic stress response pathways (Singh et al., 2011). Interestingly trehalose plays a role in starch metabolism, where the external application of trehalose results in the accumulation of starch in plant tissues and in addition to promoting trehalose accumulation, M. persicae infestation of Arabidopsis results in local starch accumulation. In tps11 mutant lines that exhibited lower resistance to M. persicae than wild-type lines, starch accumulation was impaired in response to aphid infestation. Similarly pgm1 mutant plants that were unable to accumulate starch due to impaired glucose metabolism exhibited reduced M. persicae resistance (Singh et al., 2011). Taken together these data suggest that changes at the primary metabolic level can have broad pleiotropic effects on aphid susceptibility. Polyphenols are well known to respond to abiotic stresses such as nutrient availability, drought, salinity, light and temperature (Nakabayashi and Saito, 2015). Polyphenols and their oxidation products are also considered important in aphid resistance (Miles and Oertli, 1993; Lattanzio *et al.*, 2000; Kerchev *et al.*, 2012b) through the nonspecific formation of radicals or by crosslinking of cell walls suggesting that certain abiotic environments might induce a relatively broad and non-specific basal aphid resistance. Conversely, many secondary metabolites are specific in their anti-aphid action. For example, the aphid-induced indole alkaloid gramine accumulated only in response to infestation by the aphid *Schizaphis graminum* on different barley genotypes with varying resistance characteristics. Feeding by the russian wheat aphid (*Diuraphis noxia*), the rose-grain aphid (*Metopolophium dirhodum*) or the bird cherry-oat aphid (*Rhopalosiphum padi*) failed to elicit gramine accumulation. Gramine accumulation was additionally triggered by exposure to abiotic drought stress or the addition of ABA (Larsson et al., 2011) and drought stressed barley plants were a poorer host for *Schizaphis graminum* than control plants (Cabrera et al., 1995).

Non-protein amino acids, such as 5-hydroxynorvaline that is induced in maize (*Zea mays*) leaves in response to herbivory by aphids (*Rhopalosiphum maidis*, the corn leaf aphid) and caterpillars (*Spodoptera exigua*, beet armyworm), and by abotic stresses such as drought stress, can impede aphid reproduction (Yan et al., 2015). Moreover, glucosinolates and the products of their hydrolysis by myrosinases play important roles in constitutive and inducible defences in crucifers. In the absence of stress, myrosinases and their substrates are not localised in the same cell types, the enzymes are transported to the cells that contain glucosinolates in response to mechanical damage and other triggers such as jasmonic acid (Thangstad et al., 2004; Redovniković et al., 2008). Furthermore, it has been demonstrated that feeding by *Myzus persicae* on Arabidopsis induces the accumulation of indole

glucosinolates and that the addition of indole glucosinolates to artificial diets reduces the fecundity of *M. persicae* (Kim and Jander, 2007). However the association between indole glucosinolates in plant tissues and aphid performance is less clear. For example, atr1D mutants of Arabidopsis that contain elevated levels of indole glucosinolates supported slower reproduction of M. persicae than wild-type plants (Kim et al., 2008). Similarly, drought caused a significant increase in the indole glucosinolate content of Arabidopsis plants as well as reduced aphid fecundity (Pineda et al., 2016). However a similar negative impact of drought treatment was observed in knockout mutant lines that were blocked in the production of indole glucosinolates (Pineda et al., 2016). In our own experiments, treatment of kale with 1 mM methyl-jasmonate (Me-JA) resulted in increases of glucobrassicin (indol-3ylmethylglucosinolate) neoglucobrassicin (1-methoxy-indol-3and ylmethylglucosinolate) of more than 35- and 550-fold, respectively. However, aphid fecundity on Me-JA treated plants was significantly higher (Student's t-test, p<0.05) than that on untreated plants (Figure 2).

Camalexin, a characteristic indole alkaloid of Arabidopsis, is considered to be important in plant defences against bacteria, fungi and insects (Rogers et al., 1996; Kettles et al., 2013). For example, aphid reproductive performance was decreased on the *dcl1* Arabidopsis mutants, which accumulate high levels of camalexin (Kettles et al., 2013). However, aphid fecundity was increased in the *A. thaliana* phytoalexindeficient *pad3* relative to the wild type plants (Glazebrook and Ausubel, 1994; Kettles et al., 2013). Camalexin accumulation has been observed under conditions that cause amino acid starvation or those inducing oxidative stress (Zhao et al., 1998).

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Plant responses to aphid infestation

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Aphids, which are the largest group of phloem feeding insects, are major agricultural pests causing extensive damage to crop, garden and wild plants (Foyer et al., 2015). During feeding, aphids secrete metabolites, proteins, pathogenic bacteria and viruses into the host plant (Furch et al., 2015; Sugio et al., 2015; Whitfield et al., 2015). While the feeding process is thought to cause relatively little damage to the host plant tissues, the impact of feeding on vigour and productivity depend largely on the intensity of infestation. In agricultural environments, aphid-induced damage generally results in crop losses of about 15% (Leather et al., 1989). The majority of damage is associated with their role as vectors for more than 100 disease-causing viruses such as potato leaf roll virus and cucumber or cauliflower mosaic virus (van Emden et al., 1969). Furthermore, because aphids feed exclusively on the phloem, their diet is rich in sugar but relatively poor in nitrogen requiring the ingestion of large volumes so that the insects can acquire sufficient nitrogen (Douglas 2006). These large volumes of phloem sap are secreted as honeydew, which attracts saprophytic fungi which colonise the leaf surface inhibiting photosynthetic performance (Dedryver et al., 2010).

In order to feed, aphids penetrate the leaf epidermis and probe between the mesophyll cells with their piercing-sucking mouthparts that are called stylets to reach the phloem sieve elements from which they feed (Figure 3). Along the stylet track mesophyll cells are regularly probed and small amounts of cell content are ingested, a behaviour that is believed to orientate the aphid stylet towards the phloem (Hewer et al., 2011). Aphids produce a rapidly-gelling "sheath saliva" around the stylets during probing activity which is rich in conjugated carbohydrates, phospholipids, pectinases, phenoloxidases and β-glucosidases, all of which have the potential to

induce plant defence responses (Miles, 1999) however it remains unclear whether aphid sheath components are recognised by plant hosts (Bak et al., 2013). In addition to the rapidly-gelling sheath saliva, aphids also secrete "watery saliva" at the puncture points and feeding locations (Tjallingii, 2006). The enzymes present in the watery saliva prevent the induction of the plant wound responses in the penetrated tissues and so impede the repair of feeding-associated damage (Will et al., 2009). However, aphid saliva also contains components that act as elicitors that induce plant defence responses (Miles, 1999; de Vos and Jander, 2009). For example, Mp10, an elicitor present in green peach aphid saliva induces chlorosis and local cell death in Nicotiana benthamiana (Bos et al., 2010). Moreover, oligogalacturonides are released from the plant cell walls as a result of the action of enzymes secreted by the stylet sheath. Oligogalacturonides and other products of the cell wall breakdown have the potential to induce defence responses that limit aphid infestation (Heil, 2009). Proteins derived from endosymbiotic bacteria that have been found in aphid saliva may also participate in the elicitation of plant defence responses, for example GroEL a chaperonin associated with the obligate aphid endosymbiont Buchnera aphidicola triggers plant immunity resulting in reduced aphid fecundity on hosts (Chaudhary et al., 2014). Plants perceive the presence of fungal pathogens mainly through the presence

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Plants perceive the presence of fungal pathogens mainly through the presence of chitin in the fungal cell wall, which acts as an elicitor. Chitin is also a major constituent of the insect exoskeleton and chitin oligosaccharides act as microbe-associated molecular patterns (MAMP), inducing a suite of responses which play important roles in defence against fungal pathogens (Boller and Felix, 2009; Wan et al., 2008). In Arabidopsis, plant perception of chitin is dependent on LysM RECEPTOR-LIKE KINASE 1 (LysM RLK1) that specifically binds

chitooligosaccharides released from fungal cell walls and insect exoskeletons by the action of chitinases. These important pathogenesis-related (PR) proteins are induced not only by biotic but also by abiotic stress (Ahmed et al., 2012). It has been suggested that in addition to catalysing chitin oligosaccharide release from pests and pathogens, plant chitinases may also release similar polysaccharides from endogenous glycoproteins. In support of this hypothesis Arabidopsis plants engineered to express Trichoderma endochitinase and hexoaminidase exhibit enhanced tolerance to several abiotic stresses however tolerance was lost in a LysM RLK1 mutant background (Brotman et al., 2012). The significance of endogenous chitinases was highlighted in a study in Malus hupehensis where infection by the fungal pathogen Botryosphaeria berengeriana, infestation by the apple aphid Aphis citricota, as well as treatment with SA, methyl jasmonate, and 1-aminocyclopropane-1-carboxylic acid increased the expression of MHCHIT1, a class I chitinase gene (Zhang et al., 2012). Transgenic tobacco plants that constitutively over-expressed MHCHIT1 had enhanced resistance to Botrytis cinerea and to treatment with the drought-inducing compound, polyethylene glycol, suggesting that the pathways induced by the MHCHIT1 gene product were involved in cross tolerance responses to abiotic and biotic stresses (Zhang et al., 2012).

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The induction of MAMP-type responses is not specific to the detection of micro-organisms. Similar molecular patterns and related responses such as the hypersensitive response (HR) can be triggered by a range of abiotic and biotic stresses, including aphid feeding (Klinger et al., 2009; Villada et al., 2009). The oxidative burst that is characteristic of HR involves the production and accumulation of reactive oxygen species (ROS) as well as changes in calcium fluxes, leading to the production of pathogenesis-related (PR) proteins linked to genetically-programmed

cell suicide responses (Smith and Boyko, 2007). Relatively little is known about the resistance responses that are mediated by the plant disease resistance (R) genes involved in aphid resistance. Incompatible plant-pathogen interactions involve the recognition of the products of avirulence genes produced by the attacking or invading organism by R genes, most of which encode nucleotide-binding site leucine-rich repeat (NBS-LRR) proteins (Martin et al., 2003; McHale et al., 2006). For example, an NBS-LRR gene is thought to be involved in the incompatible interaction between potato aphid (Macrosiphum euphorbiae) and tomato that leads to poor aphid growth and reproductive performance (Rossi et al., 1998). Furthermore, the AIN gene that mediates the hypersensitive response of Medicao trunculata to Acyrthosiphon kondoi and A. pisum as well as the AKR and TTR genes which specifically provide resistance to A. kondoi and Therioaohis maculate respectively all map to a genomic region containing a cluster of NBS-LRR coding sequences (Klinger et al., 2009). Similarly, the VAT gene encodes a NBS-LRR protein, which is implicated in the resistance response of melon to the aphid Aphis gossypii (Villada et al., 2009). Resistance responses dependent on the presence of the VAT gene included apoplastic callose production, lignin decomposition and localised programmed cell death (Villada et al., 2009; Dogimont et al., 2014).

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In other plant species although R genes against insects have been defined through genetic studies individual genes have not been identified and cloned. For example, while several genes that confer resistance to fungi and rusts have been cloned from wheat and mostly identified as NBS-LRRs, none of the 65 R genes providing resistance to insects have been identified (Harris et al., 2015). In contrast, a number of genes that act downstream of R genes in wheat have been identified and functionally characterised. For example, the wheat genes *Hfr-1* and *Wci-1* encoding

lectins thought to interfere with feeding are expressed in response to Hessian fly (Mayetiola destructor) or bird cherry-oat aphid (Rhopalosiphum padi) in a biotype specific manner. Both of these genes additionally respond to treatment with SA or its analogue benzothiadiazole while Wci-1 was also responsive to MeJA and ABA (Subramanyam et al., 2006). Within the context of abiotic-biotic stress crosstalk an interesting additional observation was that expression of Wci-1 was upregulated by mechanical wounding while Hfr-1 upregulation was observed following water-deficit. Similarly, the presence of the Rag1 aphid resistance gene in soybean led to the constitutive expression of many defence-related transcripts, including those associated with ABA signalling. In resistant cultivars containing the Rag1 gene, aphid feeding triggered the significant expression of only one additional gene, whereas aphid feeding in the susceptible cultivar caused increased abundance of many transcripts (Studham and MacIntosh, 2013).

The SA, ABA and JA signalling network is considered to be particularly important in triggering appropriate responses against herbivory (de Vos et al., 2005; Kerchev et al., 2013; Studham and MacIntosh, 2013; Hillwig *et al.*, 2016). While each hormone has a defined role to play in activating defences, the dynamic adjustment of the relative contribution of each pathway is required to ensure that elicited defence responses are appropriate to prevailing biotic and abiotic environments. SA is required for the induction of effective defences against biotrophic and hemi-biotrophic pathogens. Plants exposed to pathogens, herbivores and to abiotic stresses accumulate SA and PR proteins such as β-1,3-glucanase (Loake and Grant, 2007). However, SA does not provide an effective defence against necrotrophic pathogens (Coquoz et al., 1995; Yu, et al., 1997), which require activation of JA-dependent responses. The NON-EXPRESSOR OF PR1

(NPR1) protein is important in the elaboration of SA-mediated defence responses (Kinkema et al., 2000; Mou et al., 2003). *NPR1* and *NPR1*-related transcripts such as *MhNPR1* in apple were increased in response to a range of different abiotic and biotic stresses including aphid infestation (Zhang et al., 2014). Although overexpression of AtNPR1 decreased dehydration and salt tolerance in rice (Quilis et al., 2008), the constitutive expression of *MhNPR1* in tobacco enhanced tolerance to salinity and drought stresses, together with increasing resistance to *Botrytis cinerea* (Zhang et al., 2014).

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In addition to its functions in protection against invasion by necrotrophic pathogens, the JA-dependent pathways of defence are associated with wounding and responses to herbivory (Creelman and Mullet, 1995; Devoto and Turner, 2005). Although many studies show that JA and SA act in an antagonistic manner in the regulation of plant defences (Spoel et al., 2003), abiotic stress-associated oxidative signalling can induce both pathways together (Han et al., 2013a). ABA has roles in oxidative signalling and protection against aphids (Kerchev et al., 2013, Studham and MacIntosh, 2013). ABA, which can act antagonistically to SA (Ton et al., 2009; Zabala et al., 2009), is important in drought and key physiological responses such as stomatal closure, via the activation of NADPH oxidases (Kwak et al., 2003; Petrov and Van Breusegem, 2012). Mutants defective in ABA biosynthesis such as aba2 fail to accumulate JA or associated oxylipins following pathogen challenge (Adie et al., 2007). Furthermore aba2 mutants support smaller aphid colonies than the wild type controls (Kerchev et al., 2013). The aba1 mutant also supported reduced aphid colonisation associated with increased accumulation of the indole glucosinolates glucobrassicin and 4-methoxy glucobrassicin (Hillwig et al., 2016). Both of these compounds and particularly 4-methoxy glucobrassicin are toxic when provided in

artificial diets (Kim and Jander, 2007). However, as discussed above *M. persicae* can tolerate high concentrations of indole glucosinolates *in planta* (Figure 2).

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Many hormones such as auxin and ABA promote ROS production as part of their mechanism of action through the activation of superoxide-producing enzymes such as NADPH oxidases, also called respiratory burst oxidase homologues (RBOH) (Bartoli et al., 2013b; Xia et al., 2015). For example, the RbohD and RbohF proteins were found to be important in generating a ROS burst and long-distance systemic signal following aphid infestation (Miller et al., 2009; Jaouannet et al., 2015). Together with cell wall peroxidases that also produce ROS, germin-like oxalate oxidases, and polyamine oxidases these enzymes generate an oxidative burst in the apoplast (Bolwell et al., 2002; Torres et al., 2002; Apel and Hirt, 2004; Sierla et al., 2013). The steady state concentrations of ROS within the cytoplasm are generally very low because of the activity of an elaborate network of low molecular weight antioxidants and antioxidant enzymes (Noctor and Foyer, 1998; Foyer and Noctor, 2009). Plant cells contain many low molecular weight antioxidants such as ascorbic acid and glutathione. The capacity of the cellular antioxidant defences including the activities of enzymes such as superoxide dismutases (SOD), ascorbate peroxidases (APX), glutathione peroxidases (GPX), catalases (CAT) and peroxiredoxins (PRX) (Noctor and Foyer, 1998; Foyer and Noctor, 2005) are important in regulating the innate immune response to aphids and other pathogens. Mutants that are defective in antioxidant enzymes, or that have a low abundance of ascorbate, show enhanced resistance to biotrophic pathogens (Pavet et al., 2005). For example, mutants lacking the major leaf form of catalase (CAT2) exhibit enhanced resistance to bacterial pathogens (Chaouch et al., 2010), together with constitutive activation of pathogenesis-related (PR) genes and lesion development linked to SA accumulation

(Chen et al., 1993; Chamnongpol et al., 1998). Similarly, leaves with low ascorbate show enhanced resistance to aphid infestation (Kerchev et al., 2013).

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ROS signals are in part mediated through GSH-dependent post-translational modifications of signalling proteins (Mhamdi et al., 2013; Han et al., 2013 a, b) as well as through protein kinase signalling cascades (Apel and Hirt, 2004; Foyer et al., 2015). Different components of mitogen-activated protein kinase (MAPK) cascades that comprise of MAPK, MAPK kinase (MAPKK/MKK) and MAPKK kinase (MAPKKK/MEKK) are activated by H₂O₂. For example, the MEKK1-MKK4/MKK5-MPK3/MPK6 signalling cascades that regulate pathogen defences via regulation of transcription factors such as WRKY22 and WRKY29 (Asai et al., 2002) are responsive to oxidative signalling (Rentel et al., 2004; Nakagami et al., 2005; Xing et al., 2008; Pitzschke et al., 2009;). There are more than 80 MAPKKK genes in the A. thaliana genome and most have been implicated in plant defence responses (Taj et al., 2010). Furthermore, systematic transcriptional analyses of aphid infestation in Arabidopsis revealed a significant role for MAPK cascades in plant responses to this stress (Foyer et al., 2015). The roles of cell wall associated kinases (WAKS) and Domain of Unknown Function (DUF)26 receptor-like kinases in the responses of Arabidopsis leaves to aphid infestation was highlighted in a recent metadata analysis of available transcriptome responses to aphid infestation (Foyer et al., 2015).

Protein phosphatases, which regulate the degree of protein phosphorylation, participate in cell signalling, particularly in oxidative and stress-regulated pathways (He et al. 2004; Nakagami et al., 2005; Segonzac et al. 2014), as well as in wounding responses (Rojo et al. 1998). Protein phosphatase (PP)2A, which has been shown to regulate oxidative signalling leading to the elaboration of pathogen responses (Li et

al., 2014), also plays a role in plant resistance to aphids (Rasool et al., 2014). PP2A-B'γ was found to function downstream of metabolic ROS signals and act as a negative control of SA-linked responses in *A. thaliana* (Trotta et al., 2011; Li et al., 2014). Moreover, metabolite profiling analysis indicated that PP2A-B'γ modulates amino acid and secondary metabolism, particularly camalexin synthesis under oxidative stress (Li et al., 2014).

Biotic and abiotic factors alter the expression of a large number of transcription factors. For example, the *A. thaliana* homeodomain-leucine zipper (HD-Zip) transcription factor, ATHB13 influences resistance to both biotic and abiotic stresses (Gao et al., 2014; Cabello et al., 2012; Cabello and Chan, 2012). While Arabidopsis plants in which this transcription factor was overexpressed by activation tagging had a similar susceptibility to *Pseudomonas syringae*, they were found to exhibit a higher resistance to *M. persicae* and downy mildew (Gao et al., 2014). Similarly, the WRKY53 transcription factor, which is expressed in response to biotic and abiotic stress triggers in cereals, contains upstream *cis*-acting regulatory elements responsive to environmental cues such as drought and ultraviolet radiation (Van Eck, et al., 2014). Downstream targets of WRKY53 include components involved in HR such as the ORK10/LRK10 Ser/Thr receptor kinase and the apoplastic peroxidase POC1, which are expressed in response to pathogens and aphids (Van Eck, et al., 2014).

The expression of Redox Responsive Transcription Factor1 (RRTF1) is increased by ROS-generating necrotrophic pathogens but not by biotrophic and mutualistic infections (Matsuo et al., 2014). Moreover, transgenic lines overexpressing RRTF1 showed increased susceptibility to *Alternaria brassicae* infection (Matsuo et al., 2014). In contrast, aphid fecundity was reduced on null

mutants deficient in the RRTF1 protein compared to that on the wild type controls, even though RRTF1 transcripts were greatly increased within the first hours of aphid feeding (Kerchev et al., 2014).

Effects of the abiotic environment on plant responses aphids

While it has been postulated that abiotic stress increases herbivory, a metaanalysis of insect performance on woody plants subjected to drought, pollution, and/or shading, showed that overall these stresses had few significant effects on insect growth rates or other parameters such as colonization density (Koricheva et al., 1998). However, this analysis also revealed that abiotic stresses adversely affected chewing insects and that the reproductive potential of phloem feeding insects was reduced by drought (Koricheva et al., 1998). Moreover, much uncertainty remains concerning how climate change will alter the performance of insect herbivores and influence plant resistance to aphids and other insects. The development of the *Brassica* specialist feeder, *Brevicoryne brassicae* was not greatly altered by elevated plant growth temperatures, such as those that might be predicted to occur as a result of climate change. However, the weights of *M. persicae* adult and progeny were lower at the higher temperatures and the development time was decreased (Himanen et al., 2008).

Like global temperatures, atmospheric carbon dioxide (CO₂) levels are increasing annually. Growth under high atmospheric CO₂ typically decreases plant tissue N contents while increasing C/N ratios but these effects had little impact on aphid performance on oilseed rape (Himanen et al., 2008). However, in a free air enrichment (FACE) study of pea aphid (*Acyrthosiphon pisum*) performance on *Vicia*

faba, the atmospheric composition had a significant impact on aphid performance in a genotype-dependent manner. One genotype was unaffected by enrichment of either CO₂, O₃ or both gasses together however, a second genotype was significantly more abundant when CO₂ and O₃ were enriched simultaneously although enrichment of either gas in isolation had either no (CO₂) or a negative (O₃) impact on aphid abundance (Mondor et al., 2005). However, it was unclear whether differences in aphid fecundity were due to the direct impact of altered atmospheres or via indirect influences on the host plant. In a recent report, M. trunculata plants grown at ambient temperature (26°C) with CO₂ fertilisation (640 µmol mol⁻¹) were observed to have a significant increase in both total and essential amino acids relative to plants grown at ambient CO₂ (400 µmol mol⁻¹) concentrations. Plants grown under elevated CO2 were more suitable hosts for A. pisum than those grown at ambient CO₂; however, when plants were grown at elevated temperature (30°C) the effect of CO₂ fertilisation on amino acid content was lost as was the enhanced susceptibility of plants to aphid infestation (Ryalls et al., 2015) suggesting that at least under some conditions effects may be plant mediated. These data further illustrate the complexity of biotic-abiotic crosstalk under variable environmental conditions and demonstrate potential difficulties in predicting herbivore pest status under changing environments. Considerable cross talk exists between plant responses to ozone and to aphids leading to speculation that future selection of ozone-resistsnt cultivars may also influence the ability of plant defences to prevent infestation (Menendez et al., 2009).

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While the relative importance of abiotic and biotic soil components can differ between plants and their herbivores, a study of the interactions between the aphid *Schizaphis rufula* and its host dune grass *Ammophila arenaria* revealed that aphid

population characteristics were dependent on the abiotic properties of the soils in different growing regions, irrespective of whether soil biota were present (Vandegehuchte et al., 2010). Moreover, herbivore-induced resistance is likely to be constrained in plants growing on degraded soils because of JA-linked responses to prevailing abiotic and biotic stresses (Held and Baldwin, 2005). Of the abiotic properties of the soils, the availability of water and essential nutrients such as nitrogen and phosphate are the most important in determining plant growth and productivity (Comadira et al., 2015).

Nitrogen availability

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Soil nitrogen contents can have a strong influence on aphid fecundity (Gash, 2012), as well as influencing the competition between phytophagous species. For example, the presence of leaf-chewing insects had a negative impact on aphid infestation on plants growing on all fertilizer treatments, except for ammonium nitrate fertilizer treatment (Staley, et al., 2011). The availability of essential nutrients in the soil is likely to have a significant impact on the success of herbivores because of direct effects of host nutrient availability on the diet, as well as on plant composition of secondary metabolites and on the nature of preformed and inducible defences. Herbivore feeding itself can cause carbon and nitrogen allocation changes in plants that are exacerbated under conditions of nitrogen deficiency. Moreover, the emission of volatiles is decreased in plants grown with low fertilization (Gouinguene and Turlings, 2002). In situations where essential resources such as nitrogen and phosphate are scarce, one might predict that the plant response to aphids is adjusted by shortages in essential metabolites. The specialist aphid Rhopalosiphum padi performed more poorly on N-limited barley seedlings, with aphids taking longer to locate the phloem (Ponder et al., 2000). Similarly, the generalist feeder M. persicae

was unable to establish a successful infestation of nitrogen-deficient barley plants even though the leaves were found to be rich in amino acids, sugars and tricarboxylic acid cycle intermediates (Comadira et al., 2015). Nitrogen deficiency has a large impact on leaf transcriptome profiles, such that transcripts encoding cell wall, sugar and nutrient signalling, protein degradation and secondary metabolism are overrepresented in nitrogen-deficient leaves. The extensive reorganisation of leaf metabolism and gene expression that occurs under nitrogen deficiency induces defences that protect the metabolite-rich nitrogen-deficient leaves from M. persicae attack (Comadira et al., 2015). Some significant similarities were observed between the gene expression profiles of N-deficient barley leaves and those of A. thaliana leaves infested by M. persicae (Foyer et al., 2015). For example, transcripts encoding WRKY 18, 33, 40, 51 and 53 were significantly induced following either Nlimitation in barley or by aphid infestation in Arabidopsis leaves. Conversely, while the transcript data show that N-limitation resulted in higher levels of flavonoid metabolism transcripts in barley, flavonoid metabolism was effectively suppressed by M. persicae feeding in A. thaliana leaves (Foyer et al. 2015). Transcripts encoding WAKs and DUF26 kinases were significantly abundant in both stress situations, adding support to the hypothesis that WAKs, DUF26 kinases and WRKY transcription factors play important roles for basal resistance to aphids (Foyer et al., 2015).

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The presence of the root nematode, *H. schachtii* decreased aphid performance on *A. thaliana* when nitrate levels were low but not under conditions of higher nitrate fertilization (Kutyniok et al., 2014). While host choice by the aphids was not influenced by the presence of nematodes under the higher nitrate fertilization regime, the aphids preferred nematode-free plants to nematode-infested plants under the

lower nitrogen conditions (Kutyniok et al., 2014). The presence of aphids on the shoots enhanced nematode infestation compared to controls under the low but not high nitrate availability, (Kutyniok and Müller, 2013), suggesting that the carbon-nitrogen interactions in the roots and shoots exert a strong influence on herbivore preferences and the susceptibilities of roots and shoots to herbivory.

Water availability, drought and salinity

Drought can have a strong negative influence on the success of phloem feeding insects (Koricheva et al., 1998) although it has additionally been proposed that under conditions of pulsed water stress such insects can perform better than on unstressed plants (Huberty and Denno, 2004). Interestingly, aphid performance was found to be highest in *Brassica* plants subjected to moderate drought stress (Tariq et al., 2013). Moreover, plant water status in *B. oleracea* did not have a great influence on the ability of the specialist *Brevicoryne brassicae* to induce leaf glucosinolate accumulation although it was significant with respect to glucosinolate accumulation following feeding by the generalist *M. persicae*. While the responses of plants infested with *B. brassicae* were not changed by water availability (flooding or drought), the ability of plants to induce this response following *M. persicae* infestation was negatively affected by both treatments (Khan et al., 2011). High salinity led to a significant decrease in aphid fecundity on cotton plants, an effect that was linked to increased levels of secondary metabolites such as flavonoids (Wang et al., 2015).

Any negative impact of drought on aphid performance is likely to be related to increases in ABA and ABA-signalling pathways that are known to decrease aphid fecundity (Kerchev et al., 2013). Protein elicitors such as harpin are able to induce plant SAR and HR responses, including resistance to the green peach aphid and can

also trigger drought tolerance through ABA-dependent pathways. For example, constitutive over-expression of the harpin-encoding gene, *HRF1* in rice enhanced drought tolerance through abscisic acid (ABA) signalling (Zhang et al., 2011).

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Light intensity and quality, including UV irradiation

Although light is an essential driving force for photosynthesis, excess light has a damaging impact on photosynthetic efficiency by inducing photoinhibition and producing transcriptome changes indicative of a wide-ranging stress response (Foyer et al., 1994; Niyogi, 1999; Suzuki et al., 2012). Signals concerning light availability arise in the chloroplast and are transmitted to the nucleus in order to regulate gene expression (Karpinski et al., 2013). High light stress triggers oxidative signalling, MPK3/MPK6, lipoxygenase and hormone signalling, particularly through SA, ABA and auxin-dependent pathways (Mühlenbock et al. 2008; Suzuki et al. 2012). For example, singlet oxygen (¹O₂) generated by the photosynthetic electron transport chain triggers signalling pathways leading to defence responses including programmed cell death (Lee et al., 2007). The plant response to high light is qualitatively similar to HR (Chang et al. 2009; Frenkel et al. 2009) leading to SAR (Nomura et al., 2012) and systemic acquired acclimation (SAA) responses (Mateo et al. 2004; Rossel et al. 2007). Moreover, plants pre-treated with high light retain a "memory" of the high light stress that persists when plants are returned to low light conditions (Szechyńska-Hebda et al., 2010; Zhao et al., 2014). The creation of such "light memory" signalling pathways is poorly understood but ROS, hormonal and electrophysiological signalling are thought to have important roles (Szechyńska-Hebda et al., 2010). Growth under high light also increases the levels of secondary metabolites, raffinose, polyamines and glutamate in leaves (Edreva et al., 2008;

Zavala and Ravetta, 2001; Wulff-Zottele et al., 2010; Jänkänpää et al., 2012) and light quality also has a marked effect on leaf metabolite profiles (Kopsell and Sams, 2013). *M. persicae* fecundity was similar on tobacco plants when infestation occurred in plants grown under high or low light levels, presumably because the high-light grown leaves had more amino acids and sugars compared to those grown under low light (unpublished data). In contrast, aphid fecundity was decreased when infection took place on Arabidopsis plants that had previously been grown under high light (1000 μmol m⁻² s⁻¹) and returned to low light (250 μmol m⁻² s⁻¹) conditions (Rasool et al., 2014).

The content of UV-B radiation within the light spectrum can also have an impact on herbivory. Growth under UV-irradiation altered the attractiveness *B. oleracea* plants to herbivorous insects such as thrips, whiteflies, and aphids (Kuhlmann and Müller, 2009). However, the fecundity of the green peach aphid was significantly decreased on the *B. oleracea* plants grown under high (80%) and low (4%) UV-B levels compared to ambient UV-B (Kuhmann and Müller, 2010). In contrast, the reproduction of specialist cabbage aphid (*Brevicoryne brassicae*) was decreased only under high UV-B (80%) levels (Kuhmann and Müller, 2010).

Discussion and perspectives

It has long been supposed that plants experiencing adverse environmental conditions are likely to be more susceptible to attack by herbivores and pathogens. Certainly herbivore performance and behaviour are affected by the quality of their host plants, which in turn is determined by the prevailing environmental conditions. However, in many cases even mild exposures to abiotic stresses trigger innate immune responses and so enhance plant defences. Each stress influences the

morphological, metabolic, transcript and protein landscapes of the leaves and other organs in ways that show a high degree of overlap with the responses to other stresses allowing for cross tolerance phenomena. In reality, relatively few stress-specific signalling pathways have been found in plant responses to biotic and abiotic triggers. The use of common signalling pathways that enhance general defences to a wide range of stresses dictates that exposure to a single environmental stress is sufficient to trigger rapid defence responses to a range of stresses as well as generating epigenetic memories of stress that can persist from generation to generation. Plant responses to aphids therefore involve overlap and interaction points between hormone, redox, nitric oxide, kinase and calcium signalling pathways that have common features with abiotic stress responses. The analysis of current literature discussed above suggests that few stresses pre-dispose plants to aphid infestation.

Most of the common plant defence responses to the imposition of abiotic stress such as decreased growth and enhanced production of secondary metabolites are likely to have a negative impact on the ability of aphids to colonise and thrive on their plant hosts. In particular, abiotic stresses that lead to strengthening of the cell wall and/or altered accumulation of assimilate in the phloem are likely to impede aphid feeding. It is therefore important to understand the impact of abiotic stress on factors that are crucial to aphid success. Climate change factors such as elevated atmospheric CO₂ concentrations might diminish aphid success, particularly if the higher capacity for carbon gain achieved by the inhibition of photorespiration is accompanied by nitrogen limitation and limitations on primary nitrogen assimilation (Foyer et al., 2009).

Redox regulation and signalling through different pathways, particularly thiol-mediated post-translational modification processes, is important in the regulation of growth and defence responses because it is intrinsically linked to the action of hormones such as ABA, SA and JA that facilitate resistance to different pathogens and herbivores. Redox regulation is also likely to participate in a raft of different epigenetic control mechanisms that influence the plant response to aphids. For example, processes such as S-glutathionylation of histones and GSTs, together with GSH - and glutaredoxin-dependent mechanisms for the reductive activation of methionine sulfoxide reductases that facilitate the reduction of methionine sulfoxide to methionine, provide an additional layer of stress-mediated control of gene regulation. We have previously highlighted the importance of ascorbate as a major redox buffer in priming leaf local and systemic transcript profile responses to aphids (Kerchev et al. 2013). Ascorbate is also an important co-factor for the 2-oxoglutarate dehydrogenase family of enzymes that includes the ten-eleven translocation (TET) methylcytosine dioxygenases. These enzymes catalyze the conversion of 5-methyl cytosine (5-mC) to 5-hydroxmethyl cytosine (5-hmC), which is considered to be the initial step of active DNA methylation. Moreover, ascorbate has been shown to be a reprogramming enhancer in animals because of its ability to induce a blastocyst-like state in embryonic stem cells, promoting widespread DNA demethylation in gene promoters by modulating epigenetic modifiers (Gao et al., 2015). In this way, the impacts of biotic and abiotic stresses on the cellular ascorbate pool and the redox state of the cell can therefore generate molecular memories of stress with lasting consequences.

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Recent advances in molecular genetic techniques mean that we are close to the identification of receptors and the associated cell signalling pathways that underpin many stress-induced responses that influence aphid performance. For example, a better understanding of the stress-dependent regulation and functions of wall-associated kinases is likely to provide new insights into the biotic/abiotic stress interactions that influence aphid fecundity.

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Figure Legends

Figure 1 Schematic model of the perception and common signalling pathways that trigger enhanced biotic and abiotic stress cross tolerance. Biotic threats are frequently perceived by the recognition of pathogen associated molecular patterns (PAMP) by receptor-like kinases (RLK) which in turn activate respiratory burst oxidase homologues (RBOH) via Ca²⁺ and kinase signalling cascades (not shown) leading to the accumulation of apoplastic ROS that diffuse across the plasma membrane to enter the cytoplasm. Unfavourable abiotic environments similarly result in the accumulation of ROS primarily produced in organelles such as the chloroplasts (Chl), mitochondria (Mit) and peroxisomes (not shown). ROS accumulation promotes NO production and NO can react with O₂- to produce other reactive nitrogen species (RNS). ROS and RNS react with protein thiol groups providing one of the perception mechanisms for redox signals that promote hormonal signalling leading to the combined activation of stress associated genes and subsequent tolerance to biotic and abiotic stress.

Figure 2 The impact of methyl-jasmonate treatment on indole glucosinolate content and aphid fecundity on curly kale. Plants were grown under glass for three weeks prior to treatment with 1 mM methyl-jasmonate or water (control) as a foliar spray. Five days after treatment 5 plants were harvested and the relative quantity of indole glucosinolate estimated by LC/MS as previously described (Panel A, Viger *et al.*, 2015). Ten further plants were transferred to controlled environment chambers and a single one-day *M. persicae* nymph (genotype G) was applied to each plant which were caged as previously described (Kerchev *et al.*, 2012b). Following 15 days, the total number of aphids present were recorded (panel B). Bars represent mean values \pm SE.

Figure 3 Schematic of potential elicitor release during aphid feeding. Hydrolytic enzymes in gelling sheath saliva have the capacity to release cell wall oligosaccharides allowing 'damaged self' recognition and furthermore, sheath proteins and peptides can be recognised by the plant immune system and will be present both in the apoplast and through the function of sheath saliva in sealing cell puncture wounds small amounts will also be present intracellularly. proteins and

peptides from watery saliva will be primarily present in cells punctured epidermal, mesophyll and companion cells punctured during location of the sieve element as well as within the sieve elements themselves. Similarly, proteins of bacterial symbiont origin will be localised within these cells.





