Jasmonate and salicylate as global signals for defense gene expression

Philippe Reymond and Edward E Farmer*

Remarkably, only a few low molecular mass signals, including jasmonic acid, ethylene and salicylic acid, upregulate the expression of scores of defense-related genes. Using these regulators, the plant fine-tunes its defense gene expression against aggressors which, in some cases, may be able to disrupt or amplify plant defense signal pathways to their own ends.

Addresses
Institut de Biologie et de Physiologie Végétales, Bâtiment de Biologie, Université de Lausanne, 1015 Lausanne, Switzerland
*e-mail: edwardelliston.farmer@ibpv.unil.ch

Current Opinion in Plant Biology 1998, **1**:404–411

http://biomednet.com/elecref/1369526600100404

Abbreviations

H_2O_2	hydrogen peroxide
JA	jasmonic acid
MeJA	methyl JA
MeSA	methyl SA
PR	pathogenesis related
ROI	reactive oxygen intermediate
SA	salicylic acid

Introduction

Plants contain many genes encoding defense-related proteins. These include resistance genes involved in gene-for-gene interactions leading to hypersensitive cell death, genes encoding signal transduction proteins, and downstream defense genes, for example, those encoding pathogenesis-related (PR) proteins, enzymes involved in the generation of phytoalexins, the enzymes of oxidative stress protection, tissue repair, and lignification, and others. Many of these genes are upregulated when the plant is attacked by herbivores or pathogens. Just how many inducible defense genes exist in plant genomes is difficult to estimate, because it is likely that some, if not many, of these genes have dual or multiple functions. A good example is the pathogen-inducible class I β-glucanase gene from tobacco [1]. This pathogen-inducible gene can be considered as a defense gene as its product, a β-1,3-glucanase, can disrupt the glucan mycelial wall of many fungi, helping the radicle to penetrate through the endosperm [2].

The picture which is emerging is that many inducible defense genes are regulated by a smaller number of signal pathways depending on the low molecular mass regulators jasmonic acid (JA, [3]), salicylic acid (SA, [4]), ethylene [5], and possibly hydrogen peroxide (H_2O_2, [6]). *Arabidopsis* mutants non-responsive to JA, SA, or ethylene have been crucial in dissecting the respective signal transduction pathways. Cross-talk between these pathways appears to be very common and important in the regulation of defense gene expression. Here, with the goal of trying to assess the relative importance of JA and SA in these processes, we use some of the available information from *Arabidopsis*. The data highlight the importance of both compounds as global regulators of inducible defense gene expression, but leave open the possibility that other small regulators might remain to be discovered.

Small regulators of inducible defense gene expression

Many of the inducible, defense-related genes defined to date are regulated by signal pathways involving one or more of the trio of regulators JA, ethylene and SA. The importance of these regulators in plant defense has been established in a number of experiments. JA is a 12-carbon fatty acid-derivative, which is synthesized via the octadecanoid pathway from the 18-carbon substrate linoleic acid. JA is essential for the defense of tomato against tobacco hornworm larvae [7] and for the defense of *Arabidopsis* against the fly *Bradysia* [8]. It has recently been shown that JA plays a crucial role in protecting *Arabidopsis* from weak fungal pathogens such as *Pythium mastophorum* [9••]. This discovery will likely be followed by other studies assessing the roles of JA in defense against different types of microbial pathogens. Additionally, although we use the term JA throughout this review, JA is unlikely to be a solitary signal *in vivo*; its volatile counterpart methyl jasmonate (MeJA), its octadecanoid precursor oxo-phytodienoic acid, and a newly discovered 16-carbon (hexadecanoid) regulator, dinor-oxo-phytodienoic acid, may all be powerful cellular regulators in plant tissues [10•,11].

Ethylene regulates many different processes in plants and has been implicated in defense responses [5]. Its roles in defense have been evaluated with mutants in the ethylene signal transduction pathway. Ethylene does not appear to play a major role in plants challenged with avirulent bacteria [12]. It was shown, however, that ethylene controls the amplitude and development of disease symptoms after inoculation with virulent bacteria or with fungal pathogens [12,13•,14••]. JA and ethylene co-operate to regulate the expression of many genes, and at least some JA-inducible genes are not inducible in plants unable to produce or sense ethylene [15,16].

SA has been shown to play a central role as a signalling molecule involved in both local defense reactions and in the induction of systemic resistance [4]. SA regulates many pathogenesis-related (PR) genes including those encoding PR1 and most acidic PR proteins [4,17], many of which are antifungal hydrolases targetted to the plant cell wall. Disruption of the SA signal pathway, for example in transgenic plants with reduced SA levels, leads to susceptibility

to viral (tobacco mosaic virus), fungal (*Phytophtora parasitica*, *Cercospora nicotianae*), and bacterial (*Pseudomonas syringae*) pathogens [18]. As mentioned above for JA, the volatile derivative of SA, methyl salicylate (MeSA), is also involved in plant defense. MeSA was shown to function as an airborne signal which activates the expression of defense-related genes in tobacco [19]. It is noteworthy that the gaseous regulator ethylene has volatile counterparts in MeJA and MeSA.

The role of H_2O_2 and related reactive oxygen intermediates (ROIs) in plant defense has recently been reviewed [6]. Although H_2O_2 does not seem to be a primary signal for the activation of defense genes involved in antimicrobial responses in wild-type plants, recent findings demonstrate the role of ROIs, including H_2O_2, in systemic immunity through a signal network of oxidative bursts [20••]. Not all defense-related genes are regulated by SA, JA or ethylene. Cases exist in which inducible defense gene expression appears to be independent of these known low molecular mass regulators. For example a novel, wound-inducible defense gene was recently discovered [21•] whose expression is independent of JA, ethylene, or SA. In addition, infection of tobacco with the pathogenic bacterium *Erwinia carotovora* induces a set of PR genes independently of SA [22•]. Besides JA, ethylene, and SA, therefore, there is the possibility for other endogenous low molecular mass signals in plant defense. We speculate that at least some defense-related genes will turn out to be regulated by low molecular mass signals which have not yet been characterized. JA, ethylene and SA, however, account for the expression of many defense genes and it is of interest to try to estimate their relative contributions to defense gene expression.

In order to assess the relative contributions of JA and SA to inducible defense gene expression in one plant, *Arabidopsis*, we have compiled a list of genes that are upregulated by wounding, pathogens or elicitors, JA or SA [Table 1]. For simplicity, data on ethylene were not included. The genes represented in Table 1 are grouped into six categories starting with those encoding PR proteins. All genes from this category are induced by pathogens or by elicitors of plant defense, whereas only one them, encoding a thionin (small antimicrobial proteins whose mechanism of action is as yet unclear), has been shown to be wound-inducible. The next group comprises genes involved in response to oxidative stress. For instance, the glutathione *S* transferase *GST1* is known to be upregulated by H_2O_2 [6]. At present, none of these genes is reported to be induced by JA or SA. The next two categories contain genes that are implicated in secondary metabolism. Of these, the first are genes of the aromatic metabolism including several components of the phenylpropanoid pathway. None of them is yet reported to be SA-inducible but many are pathogen-inducible. The second class of genes involved in secondary metabolism belongs to a specialised branch of aromatic metabolism, the tryptophan pathway, and includes genes potentially involved in the biosynthesis of the phytoalexin camalexin and of the defense molecules glucosinolates. SA does not induce the expression of most of these genes, whereas pathogens do. The next category is a group of genes involved in fatty acid signalling and metabolism, most of them JA-inducible. It has been proposed that JA can act as a metabolic regulator positively controlling its own synthesis and that of its precursors [10,23]. The last category contains genes involved in signal transduction, regulatory roles, or other functions. Some of these genes (*NIM1*/*NPR1*, *NDR1*) have been shown to be essential for plant defense and are upregulated by pathogens. Two genes involved in ethylene synthesis (*SAM*, *ACC2*) are JA-inducible, indicating that one defense signal can control the production of an other one (see next section).

More data could potentially be included in Table 1; we have not included inducible genes of as yet unassigned functions, the role of JA and SA in defense gene induction has not always been reported, and some published data may have been inadvertantly overlooked. Moreover, many defense-related genes from other species [17] may later be found to be upregulated in *Arabidopsis*. We note that different research groups use different methods to induce gene expression and our table does not take into account the quantity or concentration of JA or SA used. In some cases treatment of tissues with massive doses of regulators could have caused artifacts. Interesting patterns can be seen in Table 1. Of the 55 genes listed, 23 are reported to be wound-inducible and 41 are pathogen-inducible (or in a few cases, elicitor-inducible). Nine are reported to be induced by both wounding and pathogens/elicitors. There are 18 genes reported to be JA-inducible and eight reported to be SA inducible, illustrating the global importance of both JA and SA as defense gene regulators. Interestingly, no low molecular mass regulators are yet reported for 31 of the genes indicated, and it is unclear whether these genes will turn out to be JA- or SA-inducible.

In the near future, quantitative methods for the global analysis of gene expression will have a dramatic impact. cDNA microarray technology [24] will extend our knowledge of inducible defense gene expression and will also help in the discovery of new defense-related transcripts. The genes presented in Table 1 could form the basis of a cDNA microarray. Such a chip would give an insight into the relative impact of pathogens, wounding, JA, SA, ethylene, and combinations of these molecules on the dynamics of global defense gene expression.

Pathway cross-talk

There is clearly much cross-talk between signal pathways leading to inducible defense gene expression. The regulators JA, SA, and ethylene control and potentiate each other's activities. Cross-talk may help the plant to prioritize the activation of a particular signal pathway over another. For example, during pathogenesis, the plant might need to

Table 1

Inducible *Arabidopsis* defense-related genes.

Gene	Induction by:				Gene product	Accession*	Reference
	W	JA	P/E	SA			
Pathogenesis-related proteins							
THI2.1	yes	yes	yes	no	Thionin	L41244	[39,40]
PDF1.2	no	yes	yes	no	Defensin	T04323	[41]
PR1	no	no	yes	yes	PR-1	M90508	[40–42]
BGL2	n.r.	n.r.	yes	yes	β-1,3-glucanase (PR-2)	M90509	[28,42]
CHIA1	no	yes	yes	n.r.	Class I basic chitinase (PR-3)	M38240	[43]*
CHIA4	n.r.	n.r.	yes	n.r.	Class IV chitinase (PR-3)	Y14590	[44]
HEL	n.r.	yes	yes	yes	Hevein-like protein (similar to PR-4)	U01880	[45]†
PR5	n.r.	no	yes	yes	Acidic thaumatin-like protein (PR-5)	M90510	[40,42]
TLP1	n.r.	n.r.	yes	yes	Basic thaumatin-like protein (similar to PR-5)	L34693	[46]
CHIB1	no	yes	yes	no	Class III chitinase (PR-8)	M34107	[47]†
CXc750	n.r.	n.r.	yes	n.r.	Unknown, small basic protein	X72022	[48]
ELI9	n.r.	n.r.	yes	n.r.	Hydroxyproline-rich glycoprotein	n.r.	[49]
Oxidative stress							
GST1	yes	no	yes	n.r.	Glutathione S-transferase (oxidative damage protection)	Z26426	[8,50]
GST5	yes	n.r.	n.r.	n.r.	Glutathione S-transferase (oxidative damage protection)	D44465	[51]
AP3	n.r.	n.r.	yes	n.r.	Anionic peroxidase (cell wall strengthening)	n.r.	[49]
AP1	n.r.	n.r.	yes	n.r.	Ascorbate peroxidase (H_2O_2 metabolism)	D14442	[52]
OZI1	n.r.	n.r.	yes	n.r.	Unknown (ozone-induced)	U20347	[53]
Aromatic metabolism							
DHS1	yes	yes	yes	n.r.	DAHP synthase (shikimate pathway)	M74819	[8,54]
CM1	n.r.	n.r.	yes	n.r.	Chorismate mutase (shikimate pathway)	Z26519	[55]
PAL1	yes	yes	yes	n.r.	Phenylalanine ammonia lyase (phenylpropanoid pathway)	L33677	[8,28]
PAL2	no	n.r.	yes	n.r.	Phenylalanine ammonia lyase (phenylpropanoid pathway)	L33678	[55,56]
C4H	yes	n.r.	n.r.	n.r.	Cinnamate 4-hydroxylase (phenylpropanoid pathway)	D78579	[57]
AR2	yes	n.r.	n.r.	n.r.	NADPH:Cytochrome P450 reductase (C4H activation)	X66017	[57]
4CL	yes	n.r.	yes	n.r.	4-coumarate:CoA ligase (phenylpropanoid pathway)	U18675	[49,56]
CHS	no	yes	no/yes	n.r.	Chalcone synthase (flavonoid pathway)	M20308	[9••,28,56,58]
TAT	yes	yes	n.r.	n.r.	Tyrosine aminotransferase (tyrosine biosynthesis?)	n.r.	[59•]
ELI5	n.r.	n.r.	yes	n.r.	Tyrosine decarboxylase (phenolic synthesis)	n.r.	[49]
ELI3	n.r.	n.r.	yes	n.r.	Aromatic alcohol:$NADP^+$ oxidoreductase (benzyl alcohols)	X67816	[49]

Table 1 ***continued***

Inducible *Arabidopsis* defense-related genes.

Gene	Induction by:				Gene product	Accession*	Reference
	W	JA	P/E	SA			
Tryptophan pathway							
ASA1	yes	n.r.	yes	no	Anthranilate synthase α (camalexin synthesis?)	M92353	[50,60]
ASB	n.r.	n.r.	yes	no	Anthranilate synthase β (camalexin synthesis?)	L22585	[50,61]
PAT1	n.r.	n.r.	yes	no	Phosphorybosylanthranilate transferase (camalexin synthesis?)	U58942	[50]
PAI	n.r.	n.r.	yes	no	Phosphorybosylanthranilate isomerase (camalexin synthesis?)	U18970	[50]
TSA	n.r.	n.r.	yes	no	Tryptophan synthase α (glucosinolate synthesis?)	U18993	[50]
TSB	n.r.	n.r.	yes	no	Tryptophan synthase β (glucosinolate synthesis?)	M23872	[50]
RAR047	n.r.	yes	yes	yes	Sulfotransferase (glucosinolate synthesis?)	Z46823	[62]
Fatty acid signalling and metabolism							
FAD7	yes	yes	n.r.	no	Plastid ω-3 fatty acid desaturase (JA synthesis)	D14007	[63]
LOX1	no	yes	yes	n.r.	Lipoxygenase (JA synthesis?)	L04637	[23]
LOX2	yes	yes	yes	yes	Lipoxygenase (JA synthesis)	L23968	[64]†
AOS	yes	n.r.	n.r.	n.r.	Allene oxide synthase (JA synthesis)	X92510	[65]
HPL	yes	yes	n.r.	n.r.	Hydroperoxide lyase (aldehyde and oxoacid production)	n.r.	[58]
ACO	yes	yes?	n.r.	n.r.	β-oxidation (JA synthesis?)	n.r.	[59•]
CK	yes	no	n.r.	n.r.	Choline kinase (membrane repair?)	n.r.	[59•]
Signal, regulatory functions, others							
NIM1/NPR1	n.r.	n.r.	yes	no	Transcription factor inhibitor IκB homologue	U87794	[66]
NDR1	n.r.	n.r.	yes	n.r.	Signal protein in defense responses	AF021346	[67]
WAK1	no	n.r	yes	yes	Cell wall-associated kinase	L04999	[68]
MEK1	yes	n.r.	n.r.	n.r.	MAP kinase kinase	AF000977	[69]
CAM	n.r.	n.r.	yes	n.r.	Calmodulin-like protein	L12115	[70]
ROF1	yes	n.r.	n.r.	n.r.	Rotamase FκBP homologue, calmodulin binding domain	U49453	[71]
SAM	yes	n.r.	yes	n.r.	S-adenosylmethionine synthetase (ethylene synthesis)	M33217	[49,72]
ELI14	n.r.	n.r.	yes	n.r.	S-adenosyl-L-homocysteine hydrolase (ethylene synthesis)	M62756	[49]
ACC2	yes	n.r.	n.r.	n.r.	ACC synthase (ethylene synthesis)	M95595	[73]
NIT2	n.r.	n.r.	yes	n.r.	Nitrilase (auxin biosynthesis)	U09958	[74]
JR3	yes	yes	n.r.	n.r.	Aminohydrolase (hydrolysis of auxin conjugates?)	Y13577	[59•]
VSP	yes	yes	yes	no	Vegetative storage protein	Z18377	[75]†
COR1	yes	yes	n.r.	n.r.	Similar to hydrolases, P-loop, ATP/GTP binding site	AF021244	[76]

*GeneBank accession number is listed when available. W, wounding; JA, jasmonic acid; P/E, pathogen or elicitor; SA, salicylic acid; n.r., not reported; PR, pathogenesis-related protein; *BP Thomma and WF Broekaert, personal communication, †S Vidal, C Norman, and ET Palva, personal communication.

channel a large amount of energy into the synthesis of pathogen-inducible gene products (PR proteins, etc.), simultaneously suppressing the expression of wound-inducible genes directed against other pests. Consistent with this, the inhibitory effect of SA on JA-regulated gene expression has been previously reported for the induction of proteinase inhibitors in wounded tomatoes [25]. Similarly, genes activated by JA are hyperinducible in transgenic plants expressing a bacterial salicylate hydroxylase gene (*NahG*) and which fail to accumulate wild-type levels of SA during pathogenesis (S Vidal, C Norman, and ET Palva, personal communication). Inhibition of JA-dependent gene expression by SA is not always the case. Application of 2,6-dichloroisonicotinic acid, an SA analogue, increases JA levels and induces JA-reponsive genes in rice [26•]. The evidence that SA can often inhibit JA-inducible gene expression in plants raises the possibility that the converse might occur. In other words, wounding of a plant might turn on a JA-dependent pathway and inhibit a subsequent SA-dependent induction of defense genes by pathogens. Until more studies with monocots become available, it might be premature to generalize what we know about signal pathway cross-talk for all plants.

Many other examples of cross-talk exist. Ethylene can potentiate the level of expression of many defense genes in different plants. The sensitivity of *Arabidopsis* plants to SA-inducible *PR1* accumulation is enhanced by ethylene [27]. In tobacco, the genes encoding pathogenesis related proteins PR1b and PR5 are synergistically induced by MeJA and ethylene, or by the combination of MeJA and SA [15]. In tomato, ethylene co-operatively stimulates the expression of wound- and JA-inducible proteinase inhibitor genes [16]. These potentiating effects of signals on gene expression, combined with inhibitory cross-talk, may help to fine-tune defense gene expression against specific pathogens. The result is that not all aggressors induce the same defense genes. For example, the *Arabidopsis* chalcone synthase gene *CHS* is not activated by virulent or avirulent *Pseudomonas syringae* strains [28] but its expression is activated by the fungal pathogen *Pythium mastophorum* ([9••], see Table 1 where pathogen induced expression of CHS is indicated 'no/yes'). The plant is thus able to distinguish between potential pathogens and direct the expression of inducible defense genes accordingly.

Genetic studies in *Arabidopsis* are extending our knowledge of the genes involved in cross-talk and, in parallel, suggesting the presence of novel defense genes. Genes involved in cross-talk between JA and SA pathways include *NPR1* and *CPR6* [29••]. CPR6 may function with NPR1 in regulating JA-inducible genes, including *PDF1.2* and *THI2.1*, as well as SA-inducible genes, such as *PR1* and *BGL2*, all of which appear to be involved in defense against oomycetes such as *Peronospora parasitica*. Crosses between *cpr6* and *npr1* resulted in plants which expressed *PR1*, *BGL2* and *PR5* but were susceptible to an avirulent strain of *Pseudomonas syringae* pv *maculicola*, providing genetic evidence that a set of unidentified antibacterial genes must be regulated via NPR1 [29••].

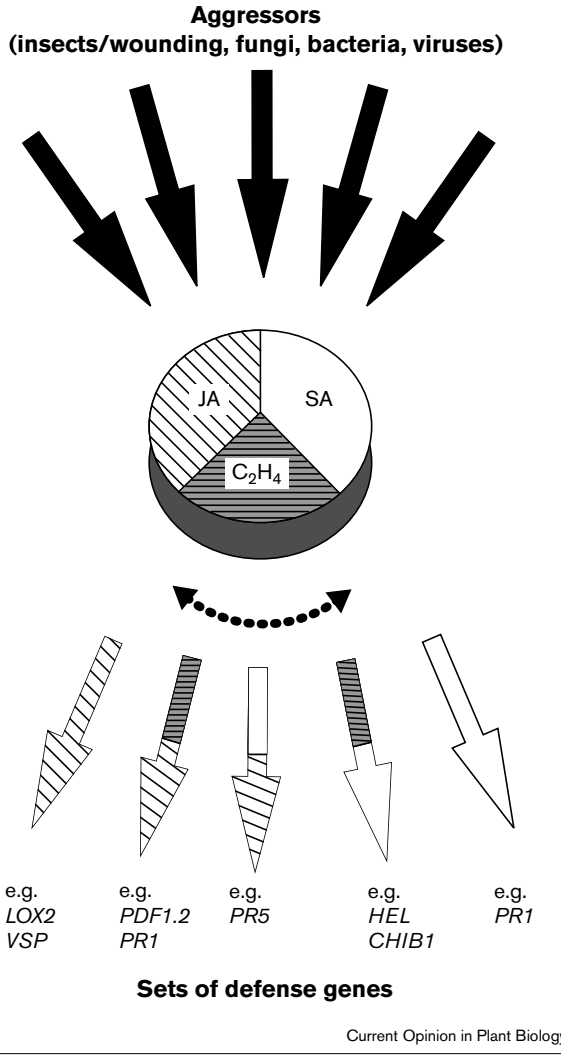
At present the causes and effects of cross-talk between defense gene activation pathways appear to be complex. In conclusion, studies on cross-talk between JA- , SA- and ethylene-dependent signal pathways have highlighted the possibility that the plant fine-tunes its defense by upregulating different sets of overlapping genes against different aggressors, as illustrated in Figure 1.

Signal wars in plant defense?

Why do plants regulate so many of their inducible defense-related genes with such a limited number of signal pathways, depending strongly on JA, SA and ethylene? Why and when during evolution these pathways have appeared is unknown. Heavy dependence on a trio of regulators may leave plants vulnerable to signal interference by pathogens. Pathogens might take advantage from being able to synthesize, mimic, degrade or jam the plants' signals. Such signalling wars are common in biology; a recent example concerns the proteolytic destruction of mitogen-activated protein kinases by a toxin from anthrax [30]. Do signal wars occur in plant defense? It is interesting that some plant-associated microorganisms are capable of producing SA, ethylene, and JA analogues. Some *Pseudomonas syringae* pathovars synthesize the pathogenicity factor coronatine [31], an analogue of the 18-carbon jasmonate family signal 12-oxo-phytodienoic acid [32]. Coronatine, at least to some extent, mimics JA, powerfully inducing a number of JA-inducible proteins [33]. An advantage for the bacteria might be that the induction of a jasmonate pathway could, as a consequence, lead to the inhibition of the SA-dependent pathway and permit the bateria to resist the plant's defensive gene products. Anyway, the production of coronatine by some bacterial pathogens is a good indication that signal mimicry can occur in plant pathosystems. Similarly, ethylene is produced by a variety of microorganisms [34] including the plant pathogen *Pseudomonas syringae* [35]. The implications of ethylene production by plant pathogens are not yet apparent. Since ethylene can potentiate defense gene expression, further work on the biological effects of 'bacterial' ethylene might be fruitful.

Ethylene and JA analogues are not the only defense signals produced by microorganisms. SA is synthesized by some bacteria including several pseudomonads. SA, an iron chelator, can promote iron uptake in some bacteria. Thus, there is a possibility that, early in evolution, plant cells might have used SA as a siderophore. The *P. aeruginosa* SA biosynthetic genes [36] were expressed in root-colonizing *P. fluorescens*, and this modified soil bacterium promoted systemic resistance of tobacco against tobacco necrosis virus [37]. Whether bacteria producing SA gain any (dis)advantage in their ability to stimulate resistance in plants has yet to be established. On the other hand, certain bacterial strains can induce systemic resistance in plants in an SA-independent pathway [38].

Figure 1



Tunable dial model for the regulation of defense gene expression by the three signals jasmonic acid (JA, hatched lines), ethylene (C_2H_4, grey) and salicylic acid (SA, white). Depending on the nature of a particular aggressor the plant is able to fine-tune (dotted arrow) the induction of defense genes either by employing a single signal molecule (single-pattern arrow) or by a combination of these regulators (multi-pattern arrow). Examples found in the literature are shown to illustrate several such cases. The induction of many JA-inducible genes during pathogenesis requires ethylene (e.g. *PDF1.2* [41]) but this is not always the case (e.g. *LOX2, VSP*, S Vidal, C Norman, ET Palva, personal communication). The gene encoding the pathogenesis-related protein PR1 is upreglated by SA alone [41] in *Arabidopsis* but is reported to be induced by a combination of ethylene and MeJA in tobacco [15]. In an other case *PR5* can be synergistically induced by MeJA and SA in tobacco [15]. SA and ethylene are required for full induction of *HEL* and *CHIB1* (S Vidal, C Norman, ET Palva, personal communication) in *Arabidopsis*. An emerging hypothesis is that, by producing, mimicking or destroying any one of the trio of signals, pathogens and pests could reset the dial and alter the spectrum of genes induced.

In summary, the fact that all three signals (SA, ethylene, JA or their analogues) can be produced in different plant-associated bacteria is evidence that interkingdom signal interference can exist and may play important roles in plant disease.

Conclusions

It is now clear that, along with SA, JA is a global regulator of many defense genes and is an essential part of the plants' defense against a variety of pathogens and insects. The relative contribution of both signal molecules to inducible defense gene expression depends on the pathogen and the spectrum of genes activated in response to a particular aggressor may reflect this fact. Having placed the control of many inducible defense genes under a few global regulators, plants may be vulnerable to signal disruption by pathogens and insects.

Acknowledgements

We thank WF Broekaert, S Vidal, and ET Palva for communicating unpublished information. We also thank D Haas, P Bariola, and H Weber for valuable comments on the manuscript. This work was supported in part by the Swiss National Science Foundation, the Leenaards Foundation and the Etat de Vaud.

References and recommended reading

Papers of particular interest, published within the annual period of review, have been highlighted as:

- • of special interest
- •• of outstanding interest

1. Vögeli-Lange R, Fründt C, Hart CM, Nagy F, Meins F: **Developmental, hormonal and pathogenesis-related regulation of the tobacco class I β-1,3-glucanase B promoter**. *Plant Mol Biol* 1994, **25**:299-311.

2. Vögeli-Lange R, Fründt C, Hart CM, Beffa R, Nagy F, Meins F: **Evidence for a role of β-1,3-glucanase in dicot seed germination**. *Plant J* 1994, **5**:273-278.

3. Creelman RA, Mullet JE: **Biosynthesis and action of jasmonates in plants**. *Annu Rev Plant Physiol Plant Mol Biol* 1997, **48**:355-81.

4. Durner J, Shah J, Klessig DF: **Salicylic acid and disease resistance in plants**. *Trends Plant Sci* 1997, **2**:266-274.

5. Ecker JR: **The ethylene signal transduction pathway in plants**. *Science* 1995, **268**:667-675.

6. Lamb C, Dixon RA: **The oxidative burst in plant disease resistance**. *Annu Rev Plant Physiol Plant Mol Biol* 1997, **48**:251-275.

7. Howe GA, Lightner J, Browse J, Ryan CA: **An octadecanoid pathway mutant (JL5) of tomato is compromised in signaling for defense against insect attack.** *Plant Cell* 1996, **8**:2067-2077.

8. McConn M, Creelman RA, Bell E, Mullet JE, Browse J: **Jasmonate is essential for insect defense in *Arabidopsis*.** *Proc Natl Acad Sci USA* 1997, **94**:5473-5477.

9. •• Vijayan P, Shockey, J, Lévesque A, Cook RJ , Browse J: **A role for jasmonate in pathogen defense of *Arabidopsis*.** *Proc Natl Acad Sci USA* 1998, **95**:7209-7214.
Both the JA insensitive *coi1* mutant and the *fad3-2 fad7-2 fad8* triple mutant (which cannot synthesize JA) are susceptible to the fungus *Pythium mastophorum*. These new data provide evidence that JA plays an essential role in defense against at least some fungi.

10. • Weber H, Vick BA, Farmer EE: **Dinor-oxo-phytodienoic acid: a new hexadecanoid signal in the jasmonate family.** *Proc Natl Acad Sci USA* 1997, **94**:10473-10478.
Identification of a new member of the jasmonate family whose levels increase rapidly during wounding of *Arabidopsis* and potato plants. It is suggested that members of octadecanoid and hexadecanoid pathways may control defense processes in parallel.

11. Farmer EE, Weber H, Vollenweider S: **Fatty acid signalling in *Arabidopsis*.** *Planta* 1998, **206**:167-174.

12. Bent AF, Innes RW, Ecker JR, Staskawicz B: **Disease development in ethylene-insensitve *Arabidopsis thaliana* infected with virulent**

and avirulent *Pseudomonas* and *Xanthomonas* pathogens. *Mol Plant–Microbe Interact* 1992, **5**:372-378.

13. Lund ST, Stall RE, Klee HJ: **Ethylene regulates the susceptible**
• **response to pathogen infection in tomato.** *Plant Cell* 1998, **10**:371-382.

The authors show that symptom development in tomato plants inoculated with bacterial or fungal pathogens is ethylene-dependent. Lesion size is reduced in plants insensitive to ethylene. It would be interesting to see the results of similar experiments in JA-insensitive plants.

14. Knoester M, van Loon LC, van den Heuvel J, Hennig J, Bol JF,
•• Linthorst HJM: **Ethylene-insensitive tobacco lacks nonhost resistance against soil-borne fungi.** *Proc Natl Acad Sci USA* 1998, **95**:1933-1937.

A very interesting paper on the role of ethylene in non-host resistance. Ethylene-insensitive tobacco plants are susceptible to the non or weak pathogen *Pythium sylvaticum*. This paper complements the recent publication of Vijayan *et al*. [**9••**] on the role of jasmonate in defense.

15. Xu Y, Chang P-FL, Liu D, Narasimhan ML, Raghothama KG, Hasegawa PM, Bressan RA: **Plant defense genes are synergistically induced by ethylene and methyl jasmonate.** *Plant Cell* 1994, **6**:1077-1085.

16. O'Donnell PJ, Calvert C, Atzorn R, Wasternack C, Leyser HMO, Bowles DJ: **Ethylene as a signal mediating the wound response of tomato plants.** *Science* 1996, **274**:1914-1917.

17. Kombrik E, Somssich IE: **Pathogenesis-related proteins and plant defense.** In *The Mycota V Part A: Plant Relationships*. Edited by Carroll G, Tudzynski P. Berlin, Heidelberg: Springer-Verlag; 1997:107-128.

18. Delaney TP, Uknes S, Vernoij B, Friedrich L, Weyman K, Negrotto D, Gaffney T, Gut-Rella M, Kessmann H, Ward E, Ryals J: **A central role of salicylic acid in plant disease resistance.** *Science* 1994, **266**:1247-1250.

19. Shulaev V, Silverman P, Raskin I: **Airborne signalling by methyl salicylate in plant pathogen resistance.** *Nature* 1997, **385**:718-721.

20. Alvarez ME, Pennell RI, Meijer PJ, Ishikawa A, Dixon RA, Lamb C:
•• **Reactive oxygen intermediates mediate a systemic signal network in the establishment of plant immunity.** *Cell* 1998, **92**:773-784.

This study reveals the presence and the importance of systemic oxidative micro-bursts which occur in *Arabidopsis* after infiltration of avirulent *Pseudomonas*. The paper emphasizes the role of reactive oxygen intermediates as key components in systemic acquired resistance.

21. O'Donnell PJ, Truesdale MR, Calvert CM, Dorans A, Roberts MR,
• Bowles DJ: **A novel tomato gene that rapidly responds to wound- and pathogen-related signals.** *Plant J* 1998, **14**:137-142.

This paper reports that a tomato glucosyl transferase (GTase) potentially involved in signal transduction is rapidly induced on wounding and by the AVR9 avirulence peptide. The signal pathway leading to inducible expression of GTase appears to be JA-, ethylene-, and SA-independent, making a good model for the search for novel low molecular mass regulators of inducible gene expression.

22. Vidal S, Ponce de Leon I, Denecke J, Palva ET: **Salicylic acid and the**
• **plant pathogen *Erwinia carotovora* induce defense genes via antagonistic pathways.** *Plant J* 1997, **11**:115-123.

Treatment of tobacco plants with cell wall-degrading enzymes from the plant pathogen *Erwinia carotovora* trigger local and systemic induction of a defense-related β-1,3-glucanase. The same induction is found in *NahG* plants that cannot accumulate wild type levels of SA, suggesting the presence of an SA-independent pathway in this plant–pathogen interaction. This pathway is likely to be JA-dependent (S. Vidal, C Norman, ET Palva, personal communication).

23. Melan MA, Dong X, Endara ME, Davis KR, Ausubel FM, Peterman TK: **An *Arabidopsis thaliana* lipoxygenase gene can be induced by pathogens, abscisic acid, and methyl jasmonate.** *Plant Physiol* 1993, **101**:441-450.

24. Schena M, Shalon D, Davis R, Brown P: **Quantitative monitoring of gene expression patterns with a complementary DNA microarray.** *Science* 1995, **270**:467-470.

25. Doares SH, Narvaes-Vasquez J, Conconi A, Ryan CA: **Salicylic acid inhibits synthesis of proteinase inhibitors in tomato leaves induced by systemin and jasmonic acid.** *Plant Physiol* 1995, **108**:1741-1746.

26. Schweizer P, Buchala A, Metraux J-P: **Gene-expression patterns and**
• **levels of jasmonic acid in rice treated with the resistance inducer 2,6-dichloroisonicotinic acid.** *Plant Physiol* 1997, **115**:61-70.

This study shows that treatment of rice plants with the SA-analogue 2,6-dichloroisonicotinic acid leads to increased JA levels and expression of JA-inducible genes. It is one of the few such studies using a monocot.

27. Lawton KA, Potter SL, Uknes S, Ryals J: **Acquired resistance signal transduction in *Arabidopsis* is ethylene independent.** *Plant Cell* 1994, **6**:581-588.

28. Dong X, Mindrinos M, Davis KR, Ausubel FM: **Induction of *Arabidopsis* defense genes by virulent and avirulent *Pseudomonas syringae* strains and by a cloned avirulence gene.** *Plant Cell* 1991, **3**:61-72.

29. Clarke JD, Liu Y, Klessig DF, Dong X: **Uncoupling PR gene**
•• **expression from NPR1 and bacterial resistance: characterisation of the dominant *Arabidopsis* cpr6-1 mutant.** *Plant Cell* 1998 **10**:557-569.

This paper reports the characteristics of the *cpr6-1* mutant in *Arabidopsis*, which contains elevated salicylic acid (SA) levels and shows constitutive expression of SA-dependent PR genes. Data show that *CPR6* is an important regulator of multiple signal transduction pathways involved in plant defense and provides evidence that resistance to virulent *Pseudomonas s.* pv. *maculicola* must be accomplished with the help of as yet unidentified antibacterial gene products.

30. Duesbery NS, Webb CP, Leppla SH, Gordon VM, Klimpel KR, Copeland TD, Ahn NG, Oskarsson MK, Fukasawa K, Paull KD, Vande Woude GF: **Proteolytic inactivation of MAP-kinase-kinase by anthrax lethal factor.** *Science* 1998, **280**:734-737.

31. Bender CL, Stone HE, Sims JJ, Cooksey DA: **Reduced pathogen fitness of *Pseudomonas syringae* pv. *tomato* Tn5 mutants defective in coronatine production.** *Physiol Mol Plant Pathol* 1987, **30**:273-283.

32. Weiler EW, Kutchan TM, Gorba T, Brodschelm W, Niesel U, Bublitz F: **The *Pseudomonas* phytotoxin coronatine mimics octadecanoid signalling molecules in higher plants.** *FEBS Lett* 1994, **345**:9-13.

33. Feys BJF, Benedetti CE, Penfold CN, Turner JG: ***Arabidopsis* mutants selected for resistance to the phytotoxin coronatine are male sterile, insensitive to methyl jasmonate, and resistant to a bacterial pathogen.** *Plant Cell* 1994, **6**:751-759.

34. Fukuda H, Ogawa T, Tanase S: **Ethylene production by micro-organisms.** *Adv Microbial Physiol* 1993, **35**:275-306.

35. Nagahama K, Yoshino K, Matsuoka M, Sato M, Tanase S, Ogawa T, Fukuda H: **Ethylene production by strains of the plant-pathogenic bacterium *Pseudomonas syringae* depends upon the presence of indigenous plasmids carrying homologous genes for the ethylene-forming enzyme.** *Microbiology* 1994, **140**:2309-2313.

36. Serino L, Reimann C, Baur H, Beyeler M, Visca P, Haas D: **Structural genes for salicylate biosynthesis from chorismate in *Pseudomonas aeruginosa*.** *Mol Gen Genet* 1995, **249**:217-228.

37. Maurhofer M, Reimmann C, Schmidli-Sacherer P, Heeb S, Haas D, Défago G: **Salicylic acid biosynthetic genes expressed in *Pseudomonas fluorescens* strain P3 improve the induction of systemic resistance in tobacco against tobacco necrosis virus.** *Phytopathol* 1998, **88**:678-684.

38. Pieterse CMJ, van Wees SCM, Hoffland E, van Pelt JA, van Loon LC: **Systemic resistance in *Arabidopsis* induced by biocontrol bacteria is independent of salicylic acid accumulation and pathogenesis-related gene expression.** *Plant Cell* 1996, **8**:1225-1237.

39. Vignutelli A, Wasternack C, Apel K, Bohlmann H: **Systemic and local induction of an *Arabidopsis* thionin gene by wounding and pathogens.** *Plant J* 1998, **14**:285-295.

40. Epple P, Apel K, Bohlmann H: **An *Arabidopsis thaliana* thionin gene is inducible via a signal transduction pathway different from that for pathogenesis-related proteins.** *Plant Physiol* 1995, **109**:813-820.

41. Penninckx IAMA, Eggermont K, Terras FRG, Thomma BPHJ, De Samblanx GW, Buchala A, Métraux JP, Manners JM, Broekaert WF: **Pathogen-induced systemic activation of a plant defensin gene in *Arabidopsis* follows a salicylic acid-independent pathway.** *Plant Cell* 1996, **8**:2309-2323.

42. Uknes S, Mauch-Mani B, Moyer M, Potter S, Williams S, Dincher S, Chandler D, Slusarenko A, Ward E, Ryals J: **Acquired resistance in *Arabidopsis*.** *Plant Cell* 1992, **4**:645-656.

43. Samac DA, Shah DM: **Effect of chitinase antisense RNA expression on disease susceptibility of *Arabidopsis* plants.** *Plant Mol Biol* 1994, **25**:587-596.

44. Gerhardt LBA, Sachetto-Marting G, Contarini MG, Sandroni M, Ferreira RP, Lima VM, Cordeiro MC, Oliveira DE, Margis-Pinheiro MM: ***Arabidopsis thaliana* class IV chitinase is early induced during the interaction with *Xanthomonas campestris*.** *FEBS Lett* 1997, **419**:69-75.

45. Potter S, Uknes S, Lawton K, Winter AM, Chandler D, DiMaio J, Novitzky R, Ward E, Ryals J: **Regulation of a hevein-like gene in *Arabidopsis*.** *Mol Plant-Microbe Interact* 1993, **6**:680-685.

46. Hu X, Reddy ASN: **Cloning and expression of a PR5-like protein from *Arabidopsis*: inhibition of fungal growth by bacterially expressed protein.** *Plant Mol Biol* 1997, **34**:949-959.

47. Samac DA, Shah DM: **Developmental and pathogen-induced activation of the *Arabidopsis* acidic chitinase promoter.** *Plant Cell* 1991, **3**:1063-1072.

48. Aufsatz W, Grimm C: **A new, pathogen-inducible gene of *Arabidopsis* is expressed in an ecotype-specific manner.** *Plant Mol Biol* 1994, **25**:229-239.

49. Trezzini GF, Horrichs A, Somssich IE: **Isolation of putative defense-related genes from *Arabidopsis thaliana* and expression in fungal elicitor-treated cells.** *Plant Mol Biol* 1993, **21**:385-389.

50. Zhao J, Last RL: **Coordinate regulation of the tryptophan biosynthetic pathway and indolic phytoalexin accumulation in *Arabidopsis*.** *Plant Cell* 1996, **8**:2235-2244.

51. Watahiki MK, Mori H, Yamamoto KT: **Inhibitory effects of auxins and related substances on the activity of an *Arabidopsis* glutathione S-transferase isozyme expressed in *Escherichia coli.*** *Physiol Plant* 1995, **94**:566-574.

52. Lummerzheim M, de Oliveira D, Castresana C, Miguens FC, Louzada E, Roby D, Van Montagu M, Timmerman B: **Identification of compatible and incompatible interactions between *Arabidopsis thaliana* and *Xanthomonas campestris* pv. *campestris* and characterization of the hypersensitive response.** *Mol Plant-Microbe Interact* 1993, **6**:532-544.

53. Sharma YK, Davis KR: **Isolation of a novel *Arabidopsis* ozone-induced cDNA by differential display.** *Plant Mol Biol* 1995, **29**:91-98.

54. Keith B, Dong X, Ausubel FM, Fink GR: **Differential induction of 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase genes in *Arabidopsis thaliana* by wounding and pathogenic attack.** *Proc Natl Acad Sci USA* 1991, **88**:8821-8825.

55. Eberhard J, Ehrler TT, Epple P, Felix G, Raesecke HR, Amrhein N, Schmid J: **Cytosolic and plastidic chorismate mutase isozymes from *Arabidopsis thaliana*: molecular characterization and enzymatic properties.** *Plant J* 1996, **10**:815-821.

56. Mizutani M, Ohta D, Sato R: **Isolation of a cDNA and a genomic clone encoding cinnamate 4-hydroxylase from *Arabidopsis* and its expression manner *in planta*.** *Plant Physiol* 1997, **113**:755-763.

57. Mizutani M, Ohta D: **Two isoforms of NADPH:cytochrome P450 reductase in *Arabidopsis thaliana*.** *Plant Physiol* 1998, **116**:357-367.

58. Rojo E, Titarenko E, Leon J, Berger S, Vancanneyt G, Sanchez-Serrano JJ: **Reversible protein phosphorylation regulates jasmonic acid dependent and independent wound signal transduction pathways in *Arabidopsis thaliana.*** *Plant J* 1998, **12**:153-165.

59. • Titarenko E, Rojo E, Leon J, Sanchez-Serrano JJ: **Jasmonic acid dependent and -independent signaling pathways control wound-induced gene activation in *Arabidopsis thaliana*.** *Plant Physiol* 1997, **115**:817-826.

Differential display was used to identify several new wound- and JA-inducible transcripts. Amongst these genes are several which are wound- but not JA-inducible. They will be useful to help define signal pathways for JA-independent gene expression.

60. Niyogi KK, Fink GR: **Two anthranilate synthase genes in *Arabidopsis*: defense-related regulation of the tryptophan pathway.** *Plant Cell* 1992, **4**:721-733.

61. Niyogi KK, Last RL, Fink GR, Keith B: **Suppressors of *trp1* fluorescence identify a new *Arabidopsis* gene, *TRP4*, encoding the anthranilate synthase ß subunit.** *Plant Cell* 1993, **5**:1011-1027.

62. Lacomme C, Roby D: **Molecular cloning of a sulfotransferase in *Arabidopsis thaliana* and regulation during development and in response to infection with pathogenic bacteria.** *Plant Mol Biol* 1996, **30**:995-1008.

63. Nishiuchi T, Hamada T, Kodama H, Iba K: **Wounding changes the spatial expression pattern of the *Arabidopsis* plastid ω-3 fatty acid desaturase gene (FAD7) through different signal transduction pathways.** *Plant Cell* 1997, **9**:1701-1712.

64. Bell E, Mullet JE: **Characterization of an *Arabidopsis* lipoxygenase gene responsive to methyl jasmonate and wounding.** *Plant Physiol* 1993, **103**:1133-1137.

65. Laudert D, Pfannschmidt U, Lottspeich F, Holländer-Czytko H, Weiler EW: **Cloning, molecular and functional characterization of *Arabidopsis thaliana* allene oxide synthase (CYP 74), the first enzyme of the octadecanoid pathway to jasmonates.** *Plant Mol Biol* 1996, **31**:323-335.

66. Ryals J, Weymann K, Lawton K, Friedrich L, Ellis D, Steiner HY, Johnson J, Delaney TP, Jesse T, Vos P, Uknes S: **The *Arabidopsis NIM1* protein shows homology to the mammalian transcription factor inhibitor IκB.** *Plant Cell* 1997, **9**:425-439.

67. Century KS, Shapiro AD, Repetti PP, Dahlbeck D, Holub E, Staskawicz BJ: ***NDR1*, a pathogen-induced component required for *Arabidopsis* disease resistance.** *Science* 1997, **278**:1963-1965.

68. He Z-H, He D, Kohorn BD: **Requirement for the induced expression of a cell wall associated receptor kinase for survival during the pathogen response.** *Plant J* 1998, **14**:55-63.

69. Morris PC, Guerrier D, Jeung J, Giraudat JL: **Cloning and characterisation of MEK1, an *Arabidopsis* gene encoding a homologue of MAP kinase kinase.** *Plant Mol Biol* 1997, **35**:1057-1064.

70. Mindrinos MN, Yu GL, Ausubel FM: ***Arabidopsis thaliana* as a model system to study host-pathogenic bacterial interaction.** In *Arabidopsis thaliana as a model for plant-pathogen interactions.* Edited by Davis KR, Hammerschmidt R. St Paul:The American Phytopathological Society; Symposium Series; 1993:37-48.

71. Vucich VA, Gasser CS: **Novel structure of a high molecular weight FK506 binding protein from *Arabidopsis thaliana*.** *Mol Gen Genet* 1996, **252**:510-517.

72. Kim CS, Kwak JM, Nam HG, Kim KC, Cho BH: **Isolation and characterization of two cDNA clones that are rapidly induced during the wound response of *Arabidopsis thaliana.*** *Plant Cell Rep* 1994, **13**:340-343.

73. Liang X, Abel S, Keller JA, Shen NF, Theologis A: **The 1-aminocyclopropane-1-carboxylate synthase gene family of *Arabidopsis thaliana*.** *Proc Natl Acad Sci USA* 1992, **89**:11046-11050.

74. Bartel B, Fink GR: **Differential regulation of an auxin-producing nitrilase gene family in *Arabidopsis thaliana*.** *Proc Natl Acad Sci USA* 1994, **91**:6649-6653.

75. Berger S, Bell E, Sadka A, Mullet JE: ***Arabidopsis thaliana Atvsp* is homologous to soybean *VspA* and *VspB*, genes encoding vegetative storage protein acid phosphatases, and is regulated similarly by methyl jasmonate, wounding, sugars, light and phosphate.** *Plant Mol Biol* 1996, **111**:525-531.

76. Benedetti CE, Costa CL, Turcinelli SR, Arruda P: **Differential expression of a novel gene in response to coronatine, methyl jasmonate, and wounding in the *coi1* mutant of *Arabidopsis*.** *Plant Physiol* 1998, **116**:1037-1042.